SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 7.300e 10 245-259 PRO0019B 11.36 5.320e-09 113- 127 PRO0019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PRO0011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	W KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e- 09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246B 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-10 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254 .	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e- 09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e- 10 421-435
250	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e- 13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
267	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 241-257

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE PAMI.	PD02952C 15.76 9.731e- 16 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366c-
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
		Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e-
			09 517-534 BL00028 16.07 7.429e-09 489- 506
296	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 8.333e- 16 111-136 BL00215A 15.82 2.723e-11 10-35
			BL00215B 10.44 9.526e- 11 152-165 BL00215B 10.44 7.375e-10 59-72
			BL00215A 15.82 9.824e- 10 205-230
302	PF00953	Glycosyl transferase.	PF00953C 19.70 8.773e- 34 236-269 PF00953A 19.68 5.000e-25 102-
		·	129 PF00953B 6.17 1.000e-13 182-194
304	PF00152	tRNA synthetases class	PF00152D 21.30 8.364e- 28 422-461 PF00152C 28.03 9.250e-21 220-
			257 PF00152B 15.67 2.658e-13 159-184
			PF00152A 19.68 5.714e- 11 44-67
305	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.250e- 35 37-76
305	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 5.840e- 09 92-135
307	PR00454	ETS DOMAIN SIGNATURE	PRO0454C 11.24 7.808e- 09 1167-1186
30B	PR00237	RHODOPSIN-LIKE GPCR SUPERFAMILY SIGNATURE	PR00237E 13.03 5.091e- 13 188-212 PR00237G 19.63 7.207e-13 268- 295 PR00237A 11.48 4.375e-11 24-49 PR00237C 15.69 3.057e- 10 101-124 PR00237D 8.94 4.750e-10 137-159
			PR00237F 13.57 5.364e- 10 230-255 PR00237B 13.50 9.438e-10 57-79
309	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 7.577e- 24 315-339 BL00522F 14.90 1.310e-15 470- 494 BL00522A 25.52 1.265e-14 179-226
			BL00522E ⁻ 19.63 8.615e- 14 430-460 BL00522B 27.30 9.625e-12 267- 313
310	BL00326	Tropomyosins proteins.	BL00326D 8.76 5.235e- 10 856-897
312	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 4.706e- 14 151-174 BL00290B 13.17 9.000e-12 211- 229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 34-85 BL00345A 13.96 9.217e-16 1-20
315	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 5.091e- 15 63-76
317	BL01020	SAR1 family proteins.	BL01020C 15.35 3.198e- 17 79-130
318	BL00216	Sugar transport	BL00216B 27.64 4.696e- 11 164-214
320	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 4.814e- 10 216-235

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
		SIGNATURE	
321	BL00027	'Homeobox' domain	BL00027 26.43 5.688e-
		proteins.	10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
	1	CATALYTIC DOMAIN	12 558-577
		SIGNATURE	7.01010
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-
			30 183-236 BL01241 35.81 3.222c-13 282-
		1	335
326	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000e-
320	DEGGALZ	proteins.	12 515-566 BL00412D
		Figure	16.54 5.705e-11 516-
		İ	567 BL00412D 16.54
			7.848e-10 518-569
		Ì	BL00412D 16.54 1.827e-
			09 514-565 BL00412D
			16.54 1.918e-09 513-
	1		564 BL00412D 16.54
330	Pransas	Cadherins extracellular	2.102e-09 520-571 BL00232B 32.79 9.557e-
328	BL00232	repeat proteins domain	20 151-199 BL00232B
		proteins.	32.79 2.246e-18 41-89
		· Processes.	BL00232B 32.79 5.985e-
	1 .		18 370-418 BL00232B
	İ		32.79 5.500e-16 258-
			306 BL00232B 32.79
			9.384e-15 475-523
		1	BL00232C 10.65 2.537e-
			12 256-274 BL00232C 10.65 4.326e-11 368-
			386 BL00232C 10.65
	•		7.261e-11 473-491
	Į.	Ì	BL00232C 10.65 7.457e-
		ł	11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
			09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e-
333	Drozad C		18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e- 32 70-115 BL01016E
	1	proceins.	14.88 5.286e-19 149-
•			177 BL01016H 13.71
	Ì		7.577e-13 291-301
	1	}	BL01016D 8.86 3.298e-
	1		11 127-140 BL01016G
	ì	i	7.14 5.622e-10 261-271
	1	.	BL01016A 5.65 7.167e-
	1	I	10 4-19 BL01016F 13.34 1.563e-09 200-
	1	İ	212 BL01016B 8.93
	1	1	8.855e-09 38-50
339	BL01115	GTP-binding nuclear	BL01115A 10.22 5.500e-
		protein ran proteins.	11 17-61
340	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 1.231e-
	1	ZINC-FINGER METAL-	33 10-49
		BINDING NU.	
341	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
		repeat proteins.	09 55-109
342	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2.400e-
	1	ZINC-FINGER METAL-	30 16-55
343	I DWGGGGG	BINDING NU.	DW000012 26 60 = 605
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-
346	DDOOLOO	BUDGING VIVE	40 20-68
340	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e- 11 135-154
		CATALYTIC DOMAIN	11 133-124
347	PR00109	SIGNATURE TYROSINE KINASE	PR00109B 12.27 4.764e-
	1 - 100103	- TWO TIN BUTTOR	1

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	7.000e-09 255-267 PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 342-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in 20-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	br0001a	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e- 15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
380	BL00107	Protein kinases ATP- binding region proteins.	10 88-118 BL00107A 18.39 1.000e- 23 276-307 BL00107B 13.31 1.692e-12 342-
381	BC00455	Putative AMP-binding	358 BL00455 13.31 5.714e-
382	PR00624	domain proteins. HISTONE H5 SIGNATURE	12 50-66 PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e- 09 67-80
386	PD02870	RECEPTOR INTERBEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e- 10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e- 13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.657e- 09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e- 11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e- 09 272-285 BL00215B 10.44 8.500e-09 165- 178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e- 11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e- 09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e- 10 118-142
401	PF00676	Dehydrogenase E1 component.	PF00676B 24.71 8.071e- 18 331-369 PF00676D 14.40 3.854e-15 486- 506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G 15.98 6.092e-14 4555- 4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e- 10 4519-4534 BL00514H 14.95 4.955e-10 4584- 4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e- 10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e- 09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e- 18 358-406 BL00232B 32.79 5.500e-16 246-

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SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESOLIS-
			294 BL00232B 32.79
	1		9.384e-15 463-511
			BL00232C 10.65 2.537e- 12 244-262 BL00232C
			10.65 4.326e-11 356-
			374 BL00232C 10.65
da.			7.261e-11 461-479
63*		İ	BL00232C 10.65 7.457e-
			11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
409	BL01160	(Hemagglutinin). Kinesin light chain	BL01160B 19.54 9.695e-
403	PROTICO	repeat proteins.	09 126-180
410	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
		dissociation stimulators	09 252-275
		CDC24 family sign.	
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e- 09 86-100
412	BL00603	Thymidine kinase	BL00603B 11.39 8.500e-
444	200000	cellular-type proteins.	09 542-557
415	BL00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
		synthase subdomain	31 245-291 BL00866C
		proteins.	23.26 9.000e-25 331-
41.0	PR00239	MOLLUSCAN RHODOPSIN C-	366 PR00239E 1.58 6.114e-
41.8	FRUUZJY	TERMINAL TAIL SIGNATURE	09 590-602
421	PF00791	Domain present in 20-1	PF00791B 28.49 7.955e-
		and Unc5-like netrin	14 23-78 PF00791B
		receptors.	28.49 3.653e-12 273- 328 PF00791B 28.49
			4.273e-11 156-211
	·		PF00791B 28.49 7.818e-
			11 89-144 PF00791B
			28.49 1.524e-10 56-111
			PF00791C 20.98 3.559e- 09 37-76 PF00791C
*	i i		20.98 5.235e-09 170-
	1		209 PF00791C 20.98
			5.235e-09 381-420
		•	PF00791B 28.49 6.202e- 09 189-244 PF00791B
	1		28.49 7.028e-09 435-
	1	l	490 PF00791B 28.49
	1		8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTBINASE.	DM00892C 23.55 7.207e-
435	DD007.00	TYROSINE KINASE	28 1645-1679 PR00109D 17.04 5.881e-
425	PR00109	CATALYTIC DOMAIN	10 228-251
1		SIGNATURE	
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
	<u> </u>	(RING finger), proteins.	11 31-40
431	BF00033	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e- 34 490-536 BL00039A
		dependent helicases proteins.	18.44 5.615e-19 205-
	1		244 BL00039B 19.19
			8.920e-16 251-277
	1	Į.	BL00039C 15.63 5.781e-
	10000153	6112 Power For Carolina Paris	15 333-357 PR00452B 11.65 7.652e-
432	PR00452	SH3 DOMAIN SIGNATURE	12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
			10 382-405
436	BL00415	Synapsins proteins.	BL00415N 4.29 B.643e-
	1	1	11 195-239 BL00415N
443	PD00924	UPDA (DECO DEOPERCE	4.29 3.036e-09 809-853 PR00834F 10.91 6.040e-
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	11 221-234
446	PF01140	Matrix protein (MA),	PF01140D 15.54 9.663e-
			<u></u>

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
		p15.	10 183-218 PF01140D 15.54 3.093e-09 246-
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PRC0568G 13.95 5.551e- 09 39-53
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL007901 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.72le- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.57le- 09 393-40B
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PRG0049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT CLQ DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e- 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e- 12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e- 09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		polyprotein).	15 21-71
498	ВЬ00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.353e- 11 299-318
501	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e- 12 131-146
505	B1.00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e- 19 705-722
509	DM01417_	6 kw INDUCING XPMC2 MUSHROOM SPAC22G7.04.	DM01417B 20.62 2.938e- 16 362-395 DM01417D 11.08 3.800e-13 322- 338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 346-370
511	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 293-317
512	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e- 09 366-390
513	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 110-160 PD01841B 14.35 1.000e-40 181- 222 PD01841D 17.87 1.000e-40 243-295 PD01841F 13.36 1.000e- 40 333-382 PD01841G
			24.26 1.000e-40 386- 440 PD01841L 18.42 1.000e-40 968-1010 PD01841I 23.00 4.545e- 37 762-804 PD01841E 18.60 3.750e-36 295- 333 PD01841J 14.94 6.023e-35 851-888 PD01841H 21.30 2.909e- 33 490-527 PD01841K 14.81 7.080e-33 924- 954 PD01841C 13.78 9.386e-23 222-243 PD01841M 10.82 8.594e- 21 1054-1073 PD01841I 23.00 2.667e-13 549- 591
514	PR00153	CYCLOPHILIN PEPTIDYL- PROLYL CIS-TRANS ISOMERASE SIGNATURE	PR00153C 11.01 7.188e- 13 95-111 PR00153E 9:10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e- 12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e- 12 1018-1052
517	BL00242	Integrins alpha chain proteins.	BL00242C 16.86 8.320e- 09 12-42
523	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B 15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic glycoprotein extracellular domain proteins.	BL00319C 17.12 8.375e- 10 61-95
526	PF00789	Domain present in ubiquitin-regulatory proteins.	PF00789B 19.70 3.308e- 12 322-343 PF00789C 20.98 5.269e-09 367- 392
528	BL01162	Quinome oxidoreductase / zeta-crystallin proteins.	BL01162C 22.80 1.500e- 16 120-164

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
529	PR00910	LUTEOVIRUS ORFG PROTEIN SIGNATURE	PR00910A 2.51 3.893e-
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A 15.82 8.660e-11 123- 148
533	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A 15.82 8.660e-11 97-122
534	BL00098	Thiolases acyl-enzyme intermediate proteins.	BL00098C 21.65 2.800e- 38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e- 35 245-288 BL00098E 22.12 1.000e-34 314- 352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e- 11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e- 22 321-340 PR00370D 16.33 6.143e-21 185- 204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e- 21 27-46 PR00370C 12.72 3.500e-20 140- 157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028 16.07 6.294e-14 341- 358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e- 11 397-414 BL00028 16.07 4.462e-11 453- 470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e- 10 313-330
537	BL00762	WHRP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e- 10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.000e- 40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146
543	BP000N8	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95
545	BL00250	TGF-beta family , proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	8L01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN PAMILY SIGNATURE	PR00326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	1 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Bukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PP00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURB	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752 BL00030	XPA protein. Eukaryotic RNA-binding	DL00752B 19.17 9.703e- 10 885-929 BL00030A 14.39 7.000e-
		region RNP-1 proteins.	09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw ski2w ski2 nucleolar helicase.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PFC0013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASK.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-382 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

CRO YD NO	1.0000000000000000000000000000000000000	DESCRIPTION	RESULTS*
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	CIAUCAN
			5.000e-11 61-73
			BL00242D 13.57 4.986e-
			10 291-316
601	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 5.610e-
		REPEAT SIGNATURE	09 198-213
602	PR00278	PANCREATIC HORMONE	PR00278A 12.43 4.569e-
	1	SIGNATURE	10 331-348
603	BL00479	Phorbol esters /	BL00479C 12.01 3.250e-
		diacylglycerol binding	12 170-183
		domain proteins.	
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e-
			09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e-
			10 295-339
606	PR00926	MITOCHONDRIAL CARRIER	PR00926F 17.75 1.000e-
		PROTEIN SIGNATURE	13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
			15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.411e-
ULL	DAMITZOD	PROTEIN.	10 877-897 DM01206B
		PROTEIN.	10.69 8.027e-10 861-
		1	881 DM01206B 10.69
	1		9.137e-10 873-893
			DM01206B 10:69 1.456e-
	1	•	09 859-879 DM01206B
			10.69 1.797e-09 879-
	1		899 DM01206B 10.69
			4.076e-09 865-885
			DM01206B 10.69 7.038e- 09 898-91B DM01206B
	İ		10.69 7.949e-09 871-
			891 DM01206B 10.69
			8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING	PD02699A B.91 2.023e-
		BINDING DNA	28 129-158 PD02699C
			24.84 1.000e-27 317-
			364 PD02699B 18.28
		<u> </u>	1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN	PRO0380A 14.18 4.086e-
		SIGNATURE	22 288-310 PR00380D
			1 0 D2 7 7716_17 APE_ENR
	1		9.93 3.721e-17 486-508 PR00380R 12.64 2.241e-
			PR00380B 12.64 2.241e-
			1
			PR00380B 12.64 2.241e- 16 410-428 PR00380C
617	PR00380	KINESIN HEAVY CHAIN	PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 PR00380A 14.18 4.086e-
617	PR00380	Kinesin heavy chain Signature	PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D
617	PR00380		PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508
617	PR00380		PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e-
617	PR00380		PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C
617	PR00380		PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436-
		SIGNATURE	PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	PR00380	SIGNATURE CORONAVIRUS NUCLEOCAPSID	PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e-
		SIGNATURE	PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
		SIGNATURE CORONAVIRUS NUCLEOCAPSID	PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B
		SIGNATURE CORONAVIRUS NUCLEOCAPSID	PRO0380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535-
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM012C6B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN . PROTEIN TYROSINE	PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PR00700B 16.80 3.160e-
618	DM01206 PR00700	CORONAVIRUS NUCLEOCAPSID PROTEIN . PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455' PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455 DM012C6B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PR00700B 16.80 3.160e- 21 561-582
618	DM01206 PR00700	CORONAVIRUS NUCLEOCAPSID PROTEIN. PROTEIN TYROSINE PHOSPHATASE SIGNATURE Receptor tyrosine kinase	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PRO0700B 16.80 3.160e- 21 561-582 BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543-
618 621 622	DM01206 PR00700 BL00239	CORONAVIRUS NUCLEOCAPSID PROTEIN. PROTEIN TYROSINE PHOSPHATASE SIGNATURE Receptor tyrosine kinase class II proteins.	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PR00700B 16.80 3.160e- 21 561-582 BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
618	DM01206 PR00700	CORONAVIRUS NUCLEOCAPSID PROTEIN. PROTEIN TYROSINE PHOSPHATASE SIGNATURE Receptor tyrosine kinase class II proteins.	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PRO0700B 16.80 3.160e- 21 561-582 BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566 PRO0407K 9.94 8.448e-
618 621 622	DM01206 PR00700 BL00239 PR00407	CORONAVIRUS NUCLEOCAPSID PROTEIN. PROTEIN TYROSINE PHOSPHATASE SIGNATURE Receptor tyrosine kinase class II proteins. EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PRO0700B 16.80 3.160e- 21 561-582 BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566 PRO0407K 9.94 8.448e- 09 326-339
618 621 622	DM01206 PR00700 BL00239	CORONAVIRUS NUCLEOCAPSID PROTEIN. PROTEIN TYROSINE PHOSPHATASE SIGNATURE Receptor tyrosine kinase class II proteins.	PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455' PRO0380A 14.18 4.086e- 22 288-310 PRO0380D 9.93 3.721e-17 486-508 PRO0380B 12.64 2.241e- 16 410-428 PRO0380C 13.18 2.976e-13 436- 455 DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555 PRO0700B 16.80 3.160e- 21 561-582 BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566 PRO0407K 9.94 8.448e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23
627	PR00103	CAMP-DEPENDENT PROTEIN KINASE SIGNATURE	9.308e-29 216-240 PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PROOCEIA 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 8.500e- 14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	3L00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BF00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	B1,01129	Hypothetical yabO/yceC/afhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBÜTYRÎC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			20 422-443
654	PD01719	PRECURSOR GLYCOPROTEIN SIGNAL RE.	PD01719A 12.89 4.452e- 11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	Bb00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-1C 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PRO0819B 10.83 8.988e-
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT BPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-40 RBPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			629 PR00320C 13.01 8.435e-11 696-711 PR00320C 13.01 2.800e- 10 614-629 PR00320C 13.01 6.400e-10 572- 587 PR00320B 12.19 3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e- 09 249-263
679	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642 11.59 7.900e-12 187- 198
680	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 8.754e- 10 286-296
681	BL00019	Actinin-type actin- binding domain proteins.	BL00019D 15.33 4.200e- 19 227-257
682	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURB	PR00700D 12.47 4.000e- 09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 8.500e- 10 538-553
689	BL01024	Protein phosphatase 2A regulatory subunit PR55 proteins.	BL01024A 10.26 1.000e- 40 22-69 BL01024B 8.91 1.000e-40 86-127 BL01024C 7.80 1.000e- 40 146-185 BL01024D 13.22 1.000e-40 185- 222 BL01024E 11.96 1.000e-40 222-266 BL01024F 9.42 1.000e- 40 266-317 BL01024G 11.09 1.000e-40 317- 349 BL01024H 13.88 1.000e-40 389-442
691	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.071e- 31 152-195
692	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
693	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 45-57
694	BL00211	ABC transporters family proteins.	BL00211A 12.23 5.050e- 09 58-70
696	BL00680	Methionine aminopeptidase subfamily 1 proteins.	BL00680 14.37 5.304e- 17 173-195
697	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14,27 3.418e- 11 242-265
698	DM01930	2 kw FINGER SMCX SMCY YDR096W.	DM01930B 15.41 1.367e- 37 170-215 DM01930F 14.16 B.232e-28 267- 303 DM01930B 19.86 9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X SIGNATURE	PR00869A 12.80 1.281e- 16 245-263
701	PR00048	C2H2-TYPE ZINC PINGER SIGNATURE	PR00048A 10.52 2.174e- 10 77-91 PR00048A 10.52 6.870e-10 133- 147 PR00048A 10.52 8.826e-10 105-119 PR00048A 10.52 5.320e- 09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e- 25 326-356 BL00523A 13.36 5.050e-16 38-55 BL00523B 8.64 5.909e- 15 86-98 BL00523C 12.64 5.500e-13 137-

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	NO.		
			148 BL00523D 9.89 1.844e-11 290-302
		,	BL00523G 9.46 5.500e-
			10 513-523 BL00523F
į			10.85 6.351e-09 413-
703	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.412e-
-		SIGNATURE	12 376-390 PR00048B
			6.02 1.000e-10 334-344
		•	PR00048B 6.02 1.474e-
707	PD00787	SYNTHASE BIOSYNTHESIS	PD00787A 14.84 8.941e-
		TRANSFERASE.	14 66-82
708	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761E 14.32 8.500e- 10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE	DM01354Y 10.69 4.977e-
		II ORF2.	38 425-465 DM01354X
			13.86 7.300e-34 376-
	1		415 DM01354V 12.97 4.923e-17 311-358
	İ	•	DM01354W 12.64 5.596e-
713	Propers	DEND have sub-firm 1.	10 356-376
113	BL00039	DEAD-box subfamily ATP- dependent helicases	BL00039D 21.67 7.545e- 27 450-496 BL00039A
		proteins.	18.44 2.537e-18 147-
		1	186 BL00039C 15.63
	1	· }	2.216e-14 280~304 BL00039B 19.19 1.947e-
			13 194-220
715	BL00383	Tyrosine specific protein phosphatases	BL00383E 10.35 4.981e-
	1	proteins.	10 130-101
717	PF00777	Sialyltransferase	PF00777C 18.60 4.035e-
718	DM00031	family. IMMUNOGLOBULIN V REGION.	21 106-161 DM00031A 16.80 3.750e-
		Interest State Control	39 20-68 DM00031B
			15.41 2.688e-28 84-118
			DM00031C 12.79 1.300e- 12 131-142
719	BL00243	Integrins beta chain	BL00243B 17.54 1.000e-
		cysteine-rich domain proteins.	40 131-172 BL00243C 16.42 1.000e-40 172-
		proceins.	208 BL00243D 24.07
	į	•	1.000e-40 222-274
		1.	BL00243F 22.63 1.000e- 40 314-358 BL00243I
		1	31.77 6.571e-39 607-
		1	650 BL00243E 16.70
		İ	3.077e-35 274-304 . BL00243G 21.38 3.625e-
	1.	1	34 358-400 BL00243H
	1		17.53 5.235e-29 567-
			593 BL00243A 17.61
			3.250e-21 63-84 BL00243H 17.53 7.167e-
			16 477-503 BL00243H
		İ	17.53 2.304e-11 524-
			550 BL00243H 17.53 5.304e-11 606-632
			BL00243I 31.77 1.380e-
720	DD0003.7	13 In Dogman	09 610-653
	PR00217	43 KD POSTSYNAPTIC PROTEIN SIGNATURE	PR00217C 10.91 8.022e- 09 20-36
722	PR00704	CALPAIN CYSTEINE	PR00704D 11.05 5.909e-
		PROTEASE (C2) FAMILY	34 135-161 PR00704P
•		SIGNATURE	13.61 7.000e-26 190- 218 PR00704E 12.55
			8.071e-26 165-189
			· · · · · · · · · · · · · · · · · · ·

SEQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00704B 17.94 2.241e- 23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e-
725	PR00194	TROPOMYOSIN SIGNATURE	18 99-116 PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A 16.74 1.310e-11 277- 292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e- 11 323-338 PR00320B
			12.19 4.343e-10 323- 338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e- 16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 9.082e- 10 787-798
738	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039A 18.44 2.565e- 28 26-65 BL00039D 21.67 2.105e-20 338- 384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e- 11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B 10.45 9.571e-17 353- 383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e- 12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e- 40 256-305 BL00965B 17.77 1.600e-25 126- 153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL0002ID 24.56 4.563e- 25 231-273 BL00021B 13.33 5.345e-21 60-78
748	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e- 10 135~157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C 17.06 9.444e-11 370- 415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e- 16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SARI family proteins.	BL01020C 15.35 9.020e- 12 99-150
762	3L00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e- 29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e- 10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			180 BL01208B 15.83 4.162e-09 85-100
770	BL00031	Nuclear hormones	BL00031A 19.55 9.571e-
,,,	B00003T	receptors DNA-binding	32 ·208-241 BL00031B
	1	region proteins.	22.25 5.500e-27 242~
			274
772	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.450e-
		RAS SIGNATURE	18 4-26 PR00449E
]		13.50 3.520e-14 142-
	1		165 PR00449C 17.27
)		3.032e-13 44-67
	1		PR00449D 10.79 8.579e-
	1		13 107-121 PR00449B
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-
113	PF00282	Siliacases proceins.	23 299-329 BL00523A
	1		13.36 2.200e-13 47-64
	1		BL00523B 8.64 2.607e-
	1		13 91-103 BL00523D
	1	1	9.89 7.923e-12 224-236
	1		BL00523C 12.64 4.512e-
	,	1	10 141-152 BL00523F
		1	10.85 5.821e-10 373-
375	DY 00000	Ting finger call tree	384 BL00028 16.07 7.686e-
775	BL00028	Zinc finger, C2H2 type, domain proteins.	09 568-585
776	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
	} =====================================	domain proteins.	09 621-638
777	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
	} .	domain proteins.	09 595-612
778	BF00030	Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
	1	region RNP-1 proteins.	11 322-341 BL00030A
	1		14.39 7.000e-10 220-
779	PR00079	GLUCOSE-6-PHCSPHATE	PR00079B 12.98 2.929e-
713	PROUDTS	DENTYDROGENASE SIGNATURE	26 193-222 PR00079E
	1		16.65 4.150e-23 348-
			375 PR00079C 8.68
			6.351e-16 246-264
			PR00079D 13.51 7.070e-
-			16 264-281 PR00079A
			16.12 6.769e-13 169-
781	BL00215	Mitochondrial energy	183 BL00215A 15.82 9.250e-
,01	2000213	transfer proteins.	17 10-35 BL00215A
			15.82 6.000e-16 221-
•			246 BL00215A 15.82
			7.857e-12 108-133
-			BL00215B 10.44 9.526e-
			11 168-181
783	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
795	87.006.00	REPEAT PRESYNA. DRAH-box subfamily ATP-	159-173 BL00690B 13.38 1.000e-
785	BT00630	dependent helicases	12 147-165 BL00690A
		proteins.	6.87 5.320e-10 114-124
	1		BL00690C 7.51 3.189e-
	1		09 218-228
786	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17,27 8.500e-
	i	RAS SIGNATURE	16 50-73 PR00449A
	1		13.20 5.235e-14 8-30
			PR00449E 13.50 2.853e-
	1		11 150-173 PR00449D
	1		10.79 1.545e-09 111-
788	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 8.767e-
, 00	N-101200	PROTEIN.	10 1-21
790	BL00915	Phosphatidylinositol 3-	BL00915C 22.43 9.182e-
		and 4-kinases proteins.	39 725-764 BL00915B
	J <u></u>	Taraboo processor	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			22.78 5.050e-33 633- 671 BL00915D 27.02
			1.529e-21 795-831
			BL00915A 10.09 1.000e-
			13 395-407
791	PR00208	GLIADIN AND LMW GLUTENIN	PR00208A 12.59 6.294e-
		SUPERFAMILY SIGNATURE	10 120-138 PR0020BA
			12.59 6.294e-10 121- 139 PR00Z08A 12.59
			6.294e-10 122-140
			PR00208A 12.59 6.294e-
		, i	10 123-141 PR00208A
			12.59 6.294e-10 124-
			142 PR00208A 12.59
			6.294e-10 125-143 PR00208A 12.59 6.294e-
			10 126-144 PR00208A
ļ			12.59 6.294e-10 127-
			145 PR00208A 12.59
1	[6.294e-10 128-146
			PR00208A 12.59 6.294e-
			10 129-147 PR00208A 12.59 7.41le-09 130-
			148 PR00208A 12.59
•			7.658e-09 131-149
			PR00208A 12.59 7.904e-
			09 132-150 PR00208A
			12.59 8.274e-09 118- 136 PR00208A 12.59
	į		B.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e-
			16 302-320 PR00205A
]		14.73 1.257e-11 284-
ļ			300 PR00205C 13.65
796	BL00412	Neuromodulin (GAP-43)	1.333e-11 337-352 BL00412D 16.54 4.000c-
130	DD0414	proteins.	12 196-247 BL00412D
1		•	16.54 5.705e-11 197-
	•	·	248 BL00412D 16.54
			7.848e-10 199-250
	1		BL00412D 16.54 1.827e-
	ļ		16.54 1.918e-09 194-
ŀ	1		245 BL00412D 16.54
L	<u>_</u>	[. .	2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e-
708	DY 03 053	Colmonin for la social	13 40-58 BL01052C 18.51 1.000e-
799	BL01052	Calponin family repeat proteins.	40 87-127 BL01052A
]		16.12 1.529e-32 3-35
} .	1	,	BL01052B 15.31 1.257e-
İ	j		25 52-78 BL01052D
			10.26 5.737e-25 174-
800	BL00348	nE3 tumor anti-man	194 BL00348F 23.19 3.714e-
500	200348	p53 tumor antigen proteins.	09 197-240
801	BL00309	Vertebrate galactoside-	BL00309C 18.65 1.621e-
1	\	binding lectin proteins.	09 62-87
802	PR00245	OLFACTORY RECEPTOR	PR00245D 10.47 5.224e-
		SIGNATURE	09 187-199
804	PF00774	Dihydropyridine	PF00774A 16.47 8.457e-
}	1	sensitive L-type calcium	10 110-156
808	PR00667	channel (Beta subuni. RETINAL PIGMENT	PR00667C 11.71 9.875e-
808	* KUU00/	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR	09 12-28
ļ		SIGNATURE	
B10	PD02346	PHOTOSYSTEM II PROTEIN	PD02346F 12.89 4.340e-
{		PRECURSOR	09 317-354
	·	·	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.	PHOTOSYNTHESIS.	
Bli	BL00685	CBF-A/NF-YB subunit	BL00685B 14.41 6.779e-
		proteins.	14 54-95 BL00685A
			11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE	PR00080A 9.32 9.419e-
		SUPERFAMILY SIGNATURE	10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17
815	PD00056	PROTEIN ZINC-FINGER	22-65
023	1200000	METAL-BINDI	PD00066 13.92 7.923e~ 15 158-171 PD00066
		1	13.92 5.200e-14 46-59
		•	PD00066 13.92 7.000e-
			·14 18-31 PD00066
			13.92 7.000e-13 130-
			143 PD00066 13.92
	ļ		7.500e-13 214-227 PD00066 13.92 9.000e-
			13 102-115 PD00066
			13.92 4.429e-12 186-
			199 PD00066 13.92
016			1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase	BL01195C 20.12 3.348e-
820	BLC0520	proteins. Interleukin-10 family	20 100-139 BL00520A 6.21 6.471e-
	2200320	proteins.	09 1-14
822	BL00972	Ubiquitin carboxyl-	BL00972A 11.93 8.113e-
	į	terminal hydrolases	09 224-242
		family 2 proteins.	
825	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 2.268e-
829	PD02855	SIGNATURE FLAVOPROTEIN PROTEIN	10 101-115
ULS	FDUZ833	DNA/PANTOTHEN.	PD02855A 18.37 4.732c- 28 88-124 PD02855B
		,	8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING	PR00405B 11.83 7.000e-
		PROTEIN SIGNATURE	21 44-62 PR00405C
	•]	19.41 1.000e-13 65-87
			PR00405A 17.71 7.283e-
831	2R00019	LEUCINE-RICH REPEAT	PR00019A 11.19 1.000e-
		SIGNATURE	09 47-61 PR00019B
			11.36 1.720e-09 136-
			150 PR00019B 11.36
832	PR00011	TYPE III EGP-LIKE	3.880e-09 44-58
032	PROUULL	SIGNATURE	PR00011B 13.08 3.438e- 16 164-183 PR00011D
			14.03 6.850e-16 164-
			183 PRO0011A 14.06
į			8.364e-14 164-183
l			PR00011C 24.25 5.415e~
			12 231-260 PR00011D
ŀ			14.03 9.852e-11 212-
834	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
		PRECURSOR RE.	12 232-246
835	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 4.000e-
026	DD00206	PRECURSOR RE.	10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN	PD00306A 10.26 7.000e-
837	DM00215	PRECURSOR RE. PROLINE-RICH PROTEIN 3.	12 216-230
		ANDDING-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR	PD02784B 26.46 8.302e-
		RIBONUCLEOPROTRIN.	09 73-116
840	PR00700	PROTEIN TYROSINE	PR00700B 16.80 5.091e-
}		PHOSPHATASE SIGNATURE	22 369-390 PR00700D
		i	12.47 5.765e-21 491-
. [510 PR00700C 13.17
Į.		l	4.750e-14 449-467 PR00700F 11.18 8.500e-
			-100700% 11.10 0.3008-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		<u> </u>
_			11 538-549 PR00700E
			17.57 3.100e-10 522-
	2220100	TOWNOGING WINNESS	538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	PR00109B 12.27 5.404e- 13 134-153
		SIGNATURE	13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S	PD02785B 14.43 1.000e-
022	1202103	122 RNA-BINDING HEP.	40 58-112 PD02785A
			15.23 1.915e-28 8-57
845	BLC0826	MARCKS family proteins.	BL00826C 7.63 6.738e-
		1	09 203-230
846	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.429e-
L	<u> </u>	(RING finger), proteins.	10 15-24
849	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.000e-
		(RING finger), proteins.	08 340-349
850	PR00308	TYPE I ANTIFREEZE	PR00308A 5.90 6.506e-
	-	PROTEIN SIGNATURE	09 12-27 PD02411 21.89 7.000e-
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	16 246-280
852	BL00420	Speract receptor repeat	BL00420B 22.67 1.000e-
032		proteins domain	40 723-778 BL00420B
		proteins.	22.67 1.321e-38 933-
		[988 BL00420B 22.67
		1	8.457e-28 482-537
			BL00420B 22.67 4.500e-
			27 587-642 BL00420B
		Ì	22.67 9.625e-27 270-
			325 BL00420B 22.67 4.205e-26 163-218
	••		BL00420B 22.67 5.731e-
			23 55-110 BL00420B
		1	22.67 6.464e-20 377-
			432 BL00420B 22.67
			2.800e-15 830-885
		1	BL00420C 11.90 1.900e-
	1	\	13 355-366 BL00420C
			11.90 1.900e-12 808- 819 BL00420C 11.90
	1	\ ·	3.550e-12 248-259
			BL00420C 11.90 2.831e-
	,	1.	11 141-152 BL00420C
		1	11.90 5.119e-11 1018-
	ł		1029 BL00420C 11.90
			7.955e-10 567-578
853	BL00420	Speract receptor repeat	BL00420B 22.67 1.000e- 40 756-B11 BL00420B
		proteins domain proteins.	22.67 1.321e-38 966-
		hroceine.	1021 BL00420B 22.67
			8.457e-28 482-537
	•	i '	BL00420B 22.67 4.500e-
1	į.		BD004208 22.67 4.5008-
			27 620-675 BL00420B
			27 620-675 BL00420B 22.67 9.625e-27 270-
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e-
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377-
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e-
			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259
,			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-
· · · · · · · · · · · · · · · · · · ·			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C
· · · · · · · · · · · · · · · · · · ·			27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	110.	 	7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE	PR00388A 10.45 2,778e-
		CLASS II	09 64-83
· ·		PHOSPHODIESTERASE	
859	BL00030	SIGNATURE	
039	BD00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B
		region kill-1 proteins.	7.03 1.900e-11 167-177
]	BL00030A 14.39 2.000e-
		1	10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e-
			17 23-41 PR00988C
			13.64 8.714e-16 107- 123 PR00988F 12.23
			7.828e-15 198-212
		ĺ	PR00988E 8.27 9.769e-
		·	12 176-188 PR00988D
			5.95 8.250e-11 163-174
	İ		PR00988B 11.60 4.512e-
863	BL00215	Mitochondrial energy	BL00215B 10.44 8.07le-
	1	transfer proteins.	12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN	PR00775E 8.06 1.000e-
		SIGNATURE	24 198-221 PR00775B
			3.52 1.837e-23 107-130 PR00775D 8.91 4.484e-
			17 171-189 PR00775A
			9.90 8.342e-17 86-107
			PR00775C 10.68 9.379e-
			17 153-171 PR00775G
		·	10.64 6.850e-15 267- 286 PR00775F 12.76
			6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e- 09 89-121
867	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.596e-
		ZINC-FINGER METAL-	29 14-53
		BINDING NU.	
868	BL01287	RNA 3'-terminal phosphate cyclase	BL01287A 17.95 2.688e-
		proteins.	26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e-
<u>-</u>			10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes	BL00188 30.29 9.036e-
	.	attachment site	32 665-711
876	BL00028	proteins. Zinc finger, C2H2 type,	Dr. o.o.o.o.o.o.o.o.o.o.o.o.o.o.o.o.o.o.o
		domain proteins.	BL00028 16.07 7.686e- 09 298-315
877	PD02102	SUBUNIT E V-ATPASE	PD02102A 16.74 4.176e-
		VACUOLAR ATP SYNTHASE	10 97-141
070		HYDROL.	· · · · · · · · · · · · · · · · · · ·
879	BL01189	Ribosomal protein S12e	BL01189A 14.27 1.000e-
	. *	proteins.	40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e-
		* . E	25 62-104 BL00284B
	I		17.99 6.182e-12 35-56
889	BL00216	Sugar transport	BL00216B 27.64 4.375e-
896	PR00391	proteins.	21 35-85
0.70	= 100331	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN	PR00391E 12.50 7.785e-
		SIGNATURE	15 211-231 PR00391B 8.39 1.000e-13 83-104
			PR00391D 12.21 9.328e-
			13 191-207 PR00391A
000		- <u>-</u>	7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-
		•	

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 7.800e- 26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-
901	PD00066	PROTEIN ZINC-PINGER METAL-BINDI.	11 236-260 PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92
		÷	8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 9.321e- 11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e- 09 97-111
904	PR00381	KINESIN LIGHT CHAIN SIGNATURE	PRO0381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398 PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329
906	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e~ 09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	3L00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09 500-511
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181	PROTOCHLOROPHYLLIDS REDUCTASE PHOTOSYNT.	PD0218iD 12.85 8.609e- 09 36-54
926	BL00019	Actinin-type actin- binding domain proteins.	BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510c-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A 12.56 2.373e-10 34-45
928	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

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		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325 BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.857e- 10 137-146
930	BL01085	Ribulose-phosphate 3- epimerase family proteins.	BL01085D 16.55 4.600e- 24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3- epimerase family proteins.	BLC1085D 16.55 4.600e- 24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085B 18.87 8.676e- 20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTRIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e- 12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e- 10 5-49
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e- 09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e- 09 407-420
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e- 18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e- 10 66-111
955	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.250e-
956	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.250e-
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e- 15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e- 10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e- 14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e- 13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e- 11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e- 09 55-70
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69 5.671e-09 38-58
969	PF01008	Initiation factor 2 subunit.	PF01008B 25.59 4.724e- 31 417-460 PF01008C 12.25 5.333e-18 506- 526 PF01008A 20.14 5.875e-15 369-390

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e- 12 130-145 BL01159 13.85 4.122e-10 171- 186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e- 09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e- 19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e- 13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312R 8.32 3.423e- 36 169-199 PR003121 15.78 5.286e-35 332- 361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e- 35 263-291 PR00312J 13.73 5.688e-34 363-
			392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e- 33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e- 32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e- 09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e- 09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e- 40 156-202 BL01150A 14.10 8.200e-39 100- 138
986	BL0079S	Involucrin proteins.	BL00795C 17.06 7.211e- 14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e- 10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e- 10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e- 09 3-48
987	BL00939	Ribosomal protein Lle proteins.	BL00939F 17.27 5.393e- 09 B10-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e- 11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e- 09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e- 24 73-94 PR00926D 10.53 3.250e-23 126- 145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

SEQ ID N	O: ACCESSION	DESCRIPTION	RBSULTS*
	NO.		
			20 174-193 PR00926B
}		1	16.07 2.125e-18 24-39 PR00926A 10.41 1.000e-
			15 11-25 PR00926F
			17.75 5.565e-09 120-
			143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e-
			40 88-143 BL00406C
			6.75 1.000e-40 147-202 BL00406D 12.58 3.700e-
		1	40 270-325 BL00406E
			8.44 7.375e-38 327-377
		<u> </u>	BL00406A 9.95 3.348e-
1006	BL00406	Nation probable	29 11-46
1000	BE00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C
		1	6.75 1.000e-40 147-202
		•	BL00406E 8.44 1.000e-
			35 248-298 BL00406A
1007	PR00304	TAILLESS COMPLEX	9.95 3.348e-29 11-46
2000	1100304	POLYPEPTIDE 1	PR00304D 11.04 8.714e- 22 384-407 PR00304C
		(CHAPERONE) SIGNATURE	8.69 4.667e-20 98-118
		j	PR00304B 11.60 7.577e-
			19 68-87 PR00304A
	į	· ·	9.20 3.382e-16 46-63
·	l		PR00304E 7.79 6.870e-
1009	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 2,929e-
		ZINC-FINGER METAL	32 9-48
1011	PD01066	BINDING NU.	
1011	POTOR	PROTBIN ZINC FINGER ZINC-FINGER METAL	PD01066 19.43 2.929e- 32 68-107
		BINDING NU.	32 00 10,
1012	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 6.143e-
1016	PD01168	(RING finger), proteins.	10 64-73
	1501100	PROTEIN ALANYL.	PD01168H 12.08 1.000e- 11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 1.391e-
		ACTIVATION.	32 261-302 PD00930A
	1		25.62 9.550e-22 157-
1022	BL00175	Phosphoglycerate mutase	183 BL00175A 15.42 5.179e-
		family phosphohistidine	12 6-26 BL00175C
1005		proteins.	23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA	PR00305D 16.34 1.439e-
1026	BL00353	SIGNATURE HMG1/2 proteins.	10 158-185 BL00353B 11.47 2.436e-
		oz/z procerns.	18 238-288 BL00353C
		1	14.83 8.844e-11 288-
1020			335
1028	BL00183	Ubiquitin-conjugating	BL001B3 28.97 1.310e-
1033	PF00580	enzymes proteins. UvrD/REP helicase.	33 43-91 PF00580A 13.37 4.720e-
-			09 111-133
1034	PR00413	HALOACID	PR00413E 15.78 3.429e-
		DEHALOGENASR/EPOXIDE	09 154-171
		HYDROLASE FAMILY	
1037	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.657e-
		ZINC-FINGER METAL-	09 5-44
		BINDING NU.	1 - 2 - 2
1038	PD01796	PROTEIN TRANSMEMBRANE	PD01796 15.01 4.259e-
1039	BL00299	COBALT ZINC CADMIU.	11 55-82
-UJ	B700533	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP-	PR00970A 17.73 6.143e-
		RIBOSYLTRANSFERASE	20 56-78 PR00970D
			

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	NO.	SIGNATURE	9.96 2.154e-18 154-171
			PR00970F 12.30 1.000e- 16 224-241 PR00970G
			9.97 9.229e-15 242-258
			PR00970B 16.37 1.290e-
			13 86-105 PR00970C 11.05 1.643e-11 115-
			130 PR00970E 11.23
ļ			9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10
1043	PR00048	C2H2-TYPE ZINC FINGER	243-254 PR00048A 10.52 6.786e-
		SIGNATURE	13 114-128 PR00048A
			10.52 1.000e-09 172-
1045	BL00615	C-type lectin domain	186 BL00615A 16.68 1.720e-
		proteins.	11 218-236 BL00615B
	•		12.25 1.857e-10 317-
1046	BL01092	Adenylate cyclases	331 BL01092N 13.54 8.924e-
		class-I proteins.	10 3-40
1047	BL01216	ATP-citrate lyase /	BL01216D 21.75 4.316e-
	•	succinyl-CoA ligases family proteins.	28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	- DM00031B 15.41 7.618e-
1050			12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e-
- 444			31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B
		region knews processis.	7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins	BL00223C 24.79 8.754e-
		domain proteins.	23 262-317 BL00223A 15.59 9.478e-14 46-80
			BL00223A 15.59 5.557e-
			11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding	BL00455 13.31 6.211e-
10.05		domain proteins.	13 280-296
1065	PR00019 .	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B
		SIGNATURE	11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 4.600e-
		PROTEIN FAMILY SIGNATURE	16 151-172 PR00326C 9.79 1.290e-14 200-216
		[PR00326B 16.74 8.548e-
			14 172-191 PR00326D
•			19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1	PD02870B 18.83 8.518e-
2072	7770000	PRECURSOR.	11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins	BL01009D 14.19 4.300e-
		SCP/Tpx-1/Ag5/PR-1/Sc7	20 127-148 BL01009A
		proteins.	13.75 6.586e-13 57-75
			BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C	PR00724A 10.91 1.000e-
		SERINE PROTEASE (S10)	08 366-379
1078	BL00215	FAMILY SIGNATURE Mitochondrial energy	BL00215A 15.82 1.000e-
		transfer proteins.	12 170-195 BL00215A
1079	BL00678		15.82 7.529e-10 79-104
1017	8/ 90044	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e- 10 23-57
1094	BI:00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133- 156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e-
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	BPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e- 12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-12B PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

SEQ ID NO	D: ACCESSION	DESCRIPTION	RESULTS*
	NO.		KEDODIO
			32 159-188 PR00314A
1139	- DV 03334		14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e- 13 13-57
1141	BL00107	Protein kinases ATP-	BL00107A 18.39 4.00Ge-
	22020,	binding region proteins.	19 451-482 BL00107B
			13.31 3.377e-12 519-
		1	535
1148	PR00685	TRANSCRIPTION INITIATION	PR00685A 13.62 4.676e-
4455		PACTOR IIB SIGNATURE	09 21-42
1155	PD01652	RECEPTOR CELL NK	PD01652B 8.50 9.396e-
		GLYCOPROTEIN IMMUNOGLOB.	10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR	PD02894A 21.96 7.873e-
		PROTEIN SIGNAL BE.	28 81-127 PD02894B
			13.93 1.188e-27 178-
			211
1159	BL00623	GMC oxidoreductases	BL00623E 15.00 3.531e-
		proteins.	20 391-414 BL00623C
		•	10.86 4.240e-20 155-
1161	PD01937	DNA PROTEIN POLYMERASE	176
1101	FDULYST	ENDONUCLEASE DNA	PD01937A 6.68 3.475e- 09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE	PD01937A 6.68 3.475e-
]	RNDONUCLEASE DNA	09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e-
	- 1		10 214-239 PR00624D
			11.94 1.961e-09 312-
1167	BL00226		337
1107	BLUUZZ6	Intermediate filaments proteins.	BL00226B 23.86 7.384e-
1177	BL01032	Protein phosphatase 2C	09 302-350 BL01032G 8.33 1.422e-
		proteins.	10 34-48
1178	PR00320	G-PROTEIN BETA WD-40	PR00320A 16.74 1.794e-
		REPEAT SIGNATURE	10 205-220 PR00320C
	1	1 .	13.01 7.840e-10 205-
			220 PR00320B 12.19 .
		· ·	8.457e-10 35-50 PR00320A 16.74 7.146e-
			09 35-50 PR00320B
			12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e-
		<u> </u>	19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e-
1184	BL00720		11 152-187
1104	BL00720	Guanine-nucleotide dissociation stimulators	BL00720B 16.57 4.103e-
		CDC25 family sign.	18 1089-1113
1185	BL00215	Mitochondrial energy	BL00215A 15.82 4.553e-
		transfer proteins.	13 204-229 BL00215A
		<u> </u>	15.82 1.429e-12 11-36
			BL00215A 15.82 9.809e-
1107	1,77,00000		11 104-129
1187	BL00983	Ly-6 / u-PAR domain	BL00983C 12.69 2.761e-
1188	BL00878	proteins. Orn/DAP/Arg	10 77-93
	5204876	decarboxylases family 2	BL00878B 10.95 6.000e- 16 189-204 BL00878C
		pyridoxal-P attachment	17.74 8.435e-15 225-
		si.	245 BL00878F 19.67
		1	3.625e-13 379-402
	i	[BL00878D 16.56 1.621e-
			09 270-289
1191	PD02939	PROTEIN GLUTATHIONE	PD02939B 10.10 2.723e-
		SYNTHETASE SY.	12 203-220 PD02939C
		1	20.01 1.000e-11 224-
1193	PR00345	CTATUMIN PARTY V	252
	1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 72-101 PR00345B
			20 /2-101 PRUU343B

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			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D 10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 108-137 PR00345B 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e- 28 137-161 PR00345D 10.97 1.964e-24 161- 185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e-
1196	ВЬ00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e- 11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959c- 09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e- 09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e- 37 184-229 BL01183D 27.71 8.535e-27 264- 307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e- 09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e- 14 227-241 PR00048A 10.52 4.316e-11 199- 213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 1.720e- 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e- 10 179-230
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 5.348e- 11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066 13.92 7.231e-15 406- 419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e- 12 434-447 PD00066 13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile.	BL50058 27.23 1.000e- 40 13-61
1226	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 8.439e- 09 279-330
1227	BL00437	Catalase proximal heme- ligand proteins.	BL00437A 18.82 1.000e- 40 49-101 BL00437B 16.28 1.000e-40 114- 168 BL00437C 21.86

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			1.000e-40 190-239 BL00437D 25.72 1.000e- 40 248-301 BL00437E 23.95 1.000e-40 327- 379
1230	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 8.297e- 10 6-60
1231	PR00735	GLYCOSYL HYDROLASE FAMILY 8 SIGNATURE	PR00735A 11.19 6.857e- 09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1233	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 5.553e- 10 158-176
1235	BL00866	Carbamoyl-phosphate synthase subdomain proteins.	BL00866B 36.29 2.776e- 09 75-121
1237	BL00027	Homeobox domain proteins.	BL00027 26.43 1.818e- 21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e- 11 10-25
1246	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168L 9.47 2.837e- 10 31-46 PD01168L 9.47 4.490e-10 174-189 PD01168L 9.47 7.612e- 10 183-198
1249	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.800e-10 183-196
1254	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 2.440e- 36 96-144
1255	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e- 11 8-52
1256	BL00373	Phosphoribosylglycinamid e formyltransferase proteins.	BL00373C 10.35 3.348e- 12 143-156
1258	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.217e- 10 174-193
1259	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 8.286e- 10 31-40
1261	PR00070	DIHYDROFOLATE REDUCTASE SIGNATURE	PR00070D 11.63 1.000e- 15 112-127 PR00070C 13.09 9.500e-15 51-63 PR00070A 12.92 5.500e- 12 16-27
1262	BL00462	Gamma- glutamyltranspeptidase proteins.	BL00462A 20.89 6.438e- 24 140-183 BL00462B 17.88 5.500e-20 230- 267 BL00462C 27.41 2.023e-11 292-347
1263	BL00038	Myc-typc, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 9.455e- 11 62-83
1264	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 5.670e-
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY SIGNATURE	PR00837C 17.21 2.714e- 18 165-182 PR00837A 14.77 4.512e-12 86-105 PR00837D 11.12 7.577e- 12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449C 17.27 9.308e- 22 40-63 PR00449E 13.50 1.000e-16 137- 160 PR00449D 10.79 3.520e-11 102-116
1270	BL00276	Channel forming colicins proteins.	BL00276A 8.87 1.500e- 09 17-29
1275	PD02327	GLYCOPROTEIN ANTIGEN PRECURSOR IMMUNOGLO.	PD02327C 15.47 9.769e- 09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-

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	NO.	SIGNATURE	10 170 125 00004400
	i	SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165-
	1		179 PR00412A 13.23
	1		3.400e-11 100-119
1277	PF00756	Putative esterase.	PF00756C 14.12 9.538e-
f			10 127-157
1279	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
		trypsin family,	13 128-145
L		histidine proteins.	
1280	BL01220	Phosphatidylethanolamine	BL01220C 14.75 9.348e-
		-binding protein family	15 248-276
1005	DY BOETO	proteins.	<u> </u>
1285	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 2.286e-
1287	PF00791	(RING finger), proteins. Domain present in ZO-1	10 33-42
1207	FEOUTSI	and Unc5-like netrin	PF00791B 28.49 7.182e- 11 288-343
		receptors.	11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY	PR00802B 16.51 1.610e-
[-	SIGNATURE	10 81-105
1297	PR00716	M-PHASE INDUCER	PR00716C 17.65 5.696e-
L	Ī	PHOSPHATASE SIGNATURE	09 23-44
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-
			14 268-283
1301	BL00127	Pancreatic ribonuclease	BL00127C 31.49 3.571e-
		family proteins.	28 82-126 BL00127B
1202	PD00000		26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR	PR00637B 11.27 4.250e-
1307	BL00215	SIGNATURE Mitochondrial energy	09 290-306
1307		transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A
		cranster processes.	15.82 1.000e-16 226-
			251 BL00215A 15.82
			2.658e-13 107-132
1308	PR00898	VASOPRESSIN V2 RECEPTOR	PR00898H 11.34 4.682e-
		SIGNATURE	09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE	PD00301B 5.49 2.731e-
1310	BL00983	Ly-6 / u-PAR domain	09 390-401
1310	BE00303	proteins.	BL00983C 12.69 9.654e-
	1	proteins.	13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family	BL00194 12.16 1.900e-
		proteins.	11 15-28
1314	BL00594	Aromatic amino acids	BL00594A 16.75 8.969e-
	<u></u>	permeases proteins.	10 53-97
1316	BL00134	Serine proteases,	BL00134A 11.96 9.325e-
	1	trypsin family,	13 128-145
1556	NY 0.000-	histidine proteins.	
1320	BL00783	Ribosomal protein L13	BL00783C 22.43 6.559e-
		proteins.	24 87-117 BL00783A
			14.55 1.600e-19 8-33 BL00783B 12.76 3.500e-
	1		12 74-86
1327	2F00514	Armadillo/beta-catenin-	PF00514A 31.30 7.268e-
		like repeat proteins.	11 82-120
1329	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 6.294e-
		region RNP-1 proteins.	11 129-148 ВЬОООЗОВ
		_	7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 7.239e-
		FACTOR P40 SIGNATURE	09 25-43
1332	PR00161	NICKEL-DEPENDENT	PR00161C 9.51 4.930e-
		HYDROGENASE/B-TYPE	09 317-337
1222	DD01066	CYTOCHROME SIGNATURE	
1333	PD01066	PROTRIN ZINC FINGER	PD01066 19.43 6.769e-
		ZINC-FINGER METAL-	33 10-49
1336	PR00700	BINDING NU.	Program to the
1220	***************************************	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PRO0700D 12.47 2.200e- 09 262-281
	L		
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

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	<u> </u>	PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193B 19.47 9.069e- 22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PRO0447E 9.73 1.554e- 15 299-319 PRO0447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e- 10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e- 26 45-82 BL00303B 26.15 1.000e-24 93-130
1355	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 5.950e- 29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162- 176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w Kinase Alpha Adhesion T-Cell.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

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			10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B 8.13 8.615e- 09 469-479
1372	PR00625	DNAJ PROTBIN FAMILY	PR00625B 13.48 7.353e-
1372	PR00625	SIGNATURE	19 46-67 PRO0625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding	
		domain proteins.	BL00434C 23.85 3.778e- 09 90-130
1374	PR00962	LETHAL (2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e- 09 505-526
1375	PD02475	MUCIN EPITHELIAL TUMOR- ASSOCIATE.	PD02475A 23.18 8.552e- 10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 9.571e-
		ZINC-FINGER METAL- BINDING NU.	32 24-63
1380	BL00194	Thioredoxin family proteins.	BLC0194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 1.458e-
		ENDOSOMAL III.	15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	ВL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 271-282
1385	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e- 10 95-132
1386	BL01160	Kinesin light chain	BL01160B 19.54 5.042e-
1387	DT AOSTO	repeat proteins.	09 1574-1628
	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 3.600e-
		BINDING NU.	30 10-43
1390	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 3.512e-
•		ZINC-FINGER METAL- BINDING NU.	31 32-71
1392	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 9.723e-
2002	***************************************	PROTEIN SIGNATURE	10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e- 25 88-110 PR00380D
		BIGWIOKE	9.93 2.406e-20 304-326
		•	PR00380B 12.64 4.414e-
		1 .	16 208-226 PR00380C
			13:18 6.538e-16 243-
1394	PD00066	PROTEIN ZINC-FINGER	PD00066 13.92 3.400e-
		METAL-BINDI.	14 462-475 PD00066
			13.92 8.800e-14 348-
		1	361 PD00066 13.92
			9.571e-12 405-418 · PD00066 13.92 6.087e-
		1	11 490~503 PD00066
		1	13.92 B.043e-11 320-
			333
1398	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 6.786c-
,		ZINC-FINGER METAL- BINDING NU.	32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 7.038e-
1405	7000030	PROTEIN.	09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e- 15 363-389
1407	BP00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e- 10 457-476
1408	PR00019	LBUCINE-RICH REPEAT	PRO0019A 11.19 9.550e-
		SIGNATURE	11 179-193 PR00019A
		.	11.19 8.826e-10 228-
	1		242 PR00019B 11.36
	1		1.360e-09 199-213
			PR00019B 11.36 4.960e-

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	NO.		
			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-
			12 182-202 PR00510B 12.96 8.767e-12 210-
			230 PR00510F 9.88
		·.	8.172e-10 58-75
]	}	PR00510D 9.21 2.367e-
۸.	j		09 251-267
1410	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.696e-
		NUCLEAR ANKYR.	09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.00Ce-
	İ	proteins.	40 57-103 BL00358C
			13.75 6.097e-14 122-
		١	136 BL00358D 14.26
	1		5.500e-13 143-158
			BL00358A 13.06 1.931e-
1414	BL00282	Kazal serine protease	BL00282 16.88 7.338e-
1414	BP00585	inhibitors family	10 511-534
	l '	proteins.	
1415	BL00023	Type II fibronectin	BL00023 24.31 4.300e-
~		collagen-binding domain	29 40-77
		proteins.	
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
	i	SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
		YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e- 40 142-196 PD01941B
•	ļ	COTRANSPORTER SYMP.	15.02 7.049e-30 400-
	'		447 PD01941E 15.92
	Į		2.475e-20 817-864
			PD01941C 19.96 3.118e-
	}		19 488-543 PD01941D
	j		27.18 9.614e-18 641-
			690 PD01941F 28.52
			5.382e-15 1038-1093
1422	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 8.043e-
	5540000	AT DUA (DEPENDENCE AND THE	12 199-217 PR00209B 4.88 5.318e-
1423	PR00209	ALPHA/BETA GLIADIN FAMILY SIGNATURE	11 1009-1028
1424	BL50002	Src homology 3 (SH3)	BL50002A 14.19 8.200e-
1143	Billous	domain proteins profile.	14 367-386 BL50002A
		Proceedings of the second	14.19 9.250e-12 298-
			317 BL50002A 14.19
	İ		4.462e-11 208-227
			ВЬ50002В 15.18 1.000е-
`			09 244-258
1425	PF00628	PHD-finger.	PF0062B 15.84 3.045e-
			12 330-345
1426	PP00628	PHD-finger.	PF00628 15.84 3.045e-
1402	<u></u>	HIV REV INTERACTING	12 377-392 PR00405B 11.83 5.114e-
1427			: PRUDADON 11.85 5.1140-
	PR00405		
	PR00405	PROTEIN SIGNATURE	16 281-299 PR00405A
	PR00405		16 281-299 PR00405A 17.71 4.306e-14 262-
1428		PROTEIN SIGNATURE	16 281-299 PR00405A 17.71 4.306e-14 262- 282
1428	PR00405	PROTEIN SIGNATURE DEAD-box subfamily ATP-	16 281-299 PR00405A 17.71 4.306e-14 262-
1428		PROTEIN SIGNATURE	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e-
1428		PROTEIN SIGNATURE DEAD-box subfamily ATP- dependent helicases	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e-
	BL00039	DEAD-box subfamily ATP-dependent helicases proteins.	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193
	BL00039	DEAD-box subfamily ATP-dependent helicases proteins. G-PROTEIN BETA WD-40	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e-
1429	BL00039	PROTEIN SIGNATURE DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPRAT SIGNATURE	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592
1429	BL00039	PROTEIN SIGNATURE DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPRAT SIGNATURE INOSITOL PHOSPHATASE	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592 PR00378D 16.86 7.563e-
1429	BL00039	PROTEIN SIGNATURE DEAD-box subfamily ATP- dependent helicases proteins. G-PROTEIN BETA WD-40 REPRAT SIGNATURE INOSITOL PHOSPHATASE	16 281-299 PR00405A 17.71 4.306e-14 262- 282 BL00039D 21.67 5.219e- 34 147-193 PR00320C 13.01 8.920e- 10 577-592 PR00378D 16.86 7.563e- 12 295-314 PR00378B

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		PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e- 15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 1.000e- 12 84-103
1438	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.500e- 09 250-268 BL00290A 20.89 4.000e-09 188- 211
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e- 09 38-52
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e- 09 88-102
1444	BL00422	Granins proteins.	BL00422D 19.48 1.000e- 08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL	PD01841A 21.71 1.000e- 40 73-123 PD01841B 14.35 1.000e-40 144- 185 PD01841D 17.87 1.000e-40 206-258 PD01841F 13.36 1.000e- 40 296-345 PD01841G 24.26 1.000e-40 349- 403 PD01841I 23.00 1.000e-40 494-536 PD01841J 14.94 1.000e- 40 895-932 PD01841L 18.42 1.000e-40 1083- 1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e- 35 1041-1071 PD01841H 21.30 3.189e-31 435- 472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-
1446	PF00816	H-NS histone family.	20 1175-1194 PF00816B 13.84 8.875e-
1447	PR00048	C2H2~TYPE ZINC FINGER	09 190-220 PR00048A 10.52 2.080e-
1448	DM00315	SIGNATURE 072 RIBONUCLEASE	09 402-416 DM00315D 18.40 7.393e-
1451	BL00030	INHIBITOR. Eukaryotic RNA-binding	09 23-67 BL00030B 7.03 2.800e-
1454	DM01688	region RNP-1 proteins. 2 POLY-IG RECEPTOR.	10 94-104 DM01688D 13.44 7.146e-
1455	PF00777	Sialyltransferase	09 382-405 PF00777C 18.60 2.929e-
1457	ВЪ00927	family. Trehalase proteins.	22 4-59 BL00927C 10.83 8.085e-
1460	BL00545	Aldose 1-epimerase proteins.	09 42-53 BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153
1466	PR00097	ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE	PR00097C 9.42 9.069e- 09 233-245
1472	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 5.250e- 22 170-195 BL01129C 25.56 9.526e-18 63-106
1473	BL00790	Receptor tyrosine kinase class V proteins.	BL007901 20.01 2.821e- 09 2114-2145
1475	PF00686	Starch binding domain proteins.	PF00686A 13.45 9.100e- 09 267-277

		I bridge Thank	
SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1477	PF00566	Probable rabGAP domain proteins.	PF00566A 12.64 7.333e- 10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53
1479	DM00406	GLIADIN.	DM00406 7.73 8.541e-10
1480	BL00290	Immunoglobulins and	292-305 BL00290B 13.17 2.385e-
1480	DD00230	major histocompatibility complex proteins.	15 69-87 BL00290A 20.89 5.091e-11 12-35
1461	PR00150	PHOSPHOENOLPYRUVATE	PR00150F 10.45 9.039e-
		CARBOXYLASE SIGNATURE Domain found in NIX1-	09 21-51 PF00780I 14.69 4.825e-
1492	PF00780	like kinases, mouse citron and yeast ROM.	09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 5.909e-
		ZINC-FINGER METAL- BINDING NU.	25 17-56
1486	BL00107	Protein kinases ATP-	BL00107B 13.31 1.529e-
1400	77.00030	binding region proteins. DEAD-box subfamily ATP-	09 34-50
1488	BL00039	dependent helicases	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	Bnoyl-CoA	BL00166D 22.87 2.607e-
		hydratase/isomerase	24 190-226 BL00166C 18.93 5.500e-14 140-
		proteins.	167 BL00166B 16.92
1491	BL00452	Guanylate cyclases	9.357e-11 93-115 BL00452D 28.59 3.700e-
1401	BDOV432	proteins.	31 63-106 BL00452E 11.92 3.045e-13 115-
1492	PR00019	LEUCINE-RICH REPEAT	131 PR00019A 11.19 3.667e-
		SIGNATURE	09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322-
			353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e- 10 107-117
1502	BL00027	'Homeobox' domain	BL00027 26.43 4.789e-
1503	BL00027	proteins. 'Homeobox' domain	24 112-155 BL00027 26.43 4.789e-
		proteins.	24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177R 20.64 5.800e 24 448-475 BL01177C
ļ		<u> </u>	17.39 5.333e-19 402-
		•	421 BL01177B 13.61 7.840e-16 155-171
			7.8408-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 5.500e-
		terminal hydrolases	14 311-336 BL00972A
		family 2 proteins.	11.93 7.429e-14 48-66 BL00972B 20.72 8.759e-
ļ			10 341-363
1512	BL00523	Sulfatases proteins.	BL00523R 19.27 4.536e- 22 76-106 BL00523D
			9.89 1.563e-11 40-52
			BL00523F 10.85 4.162e- 09 159-170 BL00523G
			9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class-	BL00600A 17.98 6.143e-
		III pyridoxal-phosphate	19 98-122 BL00600K
' . I		attachment si.	16.43 1.771e-17 302-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		331 BL006COG 12.43
			9.625e-17 377-396
			BL00600B 19.60 5.091e-
			15 160-186 BL00600C
		<u> </u>	16.18 6.04Ce-12 190-
			206 BL006COF 8.77
	{		1.000e-11 343-356
			BL00600D 8.71 1.000e-
			10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN	PD00930B 33.72 9.600e-
	<u> </u>	ACTIVATION.	18 41-82
1528	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 4.774e-
	i	REPEAT SIGNATURE	11 192-207 PR00320B 12.19 8.839e-11 272-
		ł	287 PR00320B 12.19
		1	9.743e-10 106-121
		1	PR00320A 16.74 1.878e-
	1 .		09 192-207 PR00320A
		1.	16.74 2.317e-09 106-
			121 PR00320A 16.74
	ľ		8.683e-09 272-287
	ļ	ŀ	PR00320C 13.01 8.800e-
			09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C	DM01970B 8.60 4.508e-
	1	ENDOSOMAL III.	15 171-184
1539	PF00781	Diacylglycerol kinase	PF00781D 11.11 7.593e-
	1	catalytic domain	10 103-127
		proteins (presumed).	
1540	PR00965	OCULAR ALBINISM TYPE 1	PR00965H 10.73 1.231e-
		PROTEIN SIGNATURE	29 312-334 PR00965E 12.93 5.846e-29 172-
		,	195 PR00965F 5.98
		į.	1.123e-28 209-231
			PR00965C 15.04 1.000e-
			27 131-151 PR00965D
	1		5.84 1.000e-27 150-170
		į.	PR00965G 8.52 2.440e~
			27 258-279 PR00965B
			4.80 8.650e-26 88-109
			PR00965A 12.52 1.000e-
	1		25 35-55 PR00965I
l			3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding	BL01013D 26.81 9.719e-
		protein family proteins.	17 163-207 PD02699C 24.84 1.000e-
1543	PD02699	PROTEIN DNA-BINDING	40 599-646 PD02699A
· ·	1	BINDING DNA.	8.91 2.286e-34 219-248
	1		PD02699B 18.28 6.143e-
l	· .	1	21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.857e-
		SIGNATURB	10 182-197 PR00049D
1	1		0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein	BL00951C 19.35 1.000e-
1		retaining receptor	40 93-142 BL00951D
1	1	proteins.	13.94 8.714e-40 142-
1	1		177 BL00951A 15.10
	1	1	1.000e-38 2-38 .
	1		BL00951B 14.23 6.250e-
L			33 38-69
1548	BL00536	Ubiquitin-activating	BL00536F 13.65 8.920e-
1		enzyme proteins.	30 279-318 BL00536D
1			22.91 5.737e-24 21-65 BL00536E 16.94 4.696e-
1		1	[
			18 248-279 PR00139C 11.72 9.679e-
1549	PR00139	ASPARAGINASE/GLUTAMINASE	09 550-569
15.50	222222	FAMILY SIGNATURE	PR00049D 0.00 5.119e-
1553	PR00049	WILM'S TUMOUR PROTEIN	09 58-73
1	1	STORWIONE	

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1556	BL00061	Short-chain	BL00061B 25.79 6.276e-
		dehydrogenases/reductase s family proteins.	13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1562	ВЬ00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B 27.30 1.738e-16 364- 410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e-
			14 502-532 BL00522F 14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.947c- 11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e- 10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e- 17 184-228 BL01013C 9.97 4.905e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e- 17 297-313 BL00479A 19.86 6.625e-15 271- 294 BL00479A 19.86 2.667e-14 147-170
			BL00479B 12.57 6.294e- 12 173-189
1576	PR00665	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e- 24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e- 10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e- 14 52-73
1580	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e- 16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e- 09 79-87
1584	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.000e- 10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e- 11 125-145
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354S 11.61 7.750e- 09 474-495

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1587	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUPL CHROMOSOMB.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL005591 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION	DESCRIPTION	RRSULTS*
	NO.		
			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
		polymerase II	09 152-201 BL00115Z
		heptapeptide repeat proteins.	3.12 9.603e-09 145-194
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
		binding protein.	32 51~88 BL00303A
1610	DY 010E4		21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e- 09 137-147
1619	PD01888	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
		PROTEIN METHI.	40 47-97 PD01888C
		Į	21.56 7.000e-30 125-
			155 PD01888A 12.84
1621	PR00239	MOLLUSCAN RHODOPSIN C-	8.800e-15 7-23 PR00239E 1.58 3.455e-
1021	PR00239	TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
	,	IERMINAL TALE SIGNATURE	1.58 4.580e-09 697-709
			PR00239E 1.58 4.580e-
			09 702-714 PR00239E
			1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
		METALLOTHIONEIN	18 27-41 PR00860C
		SIGNATURE	9.61 1.474e-14 41-51
		ļ	PR00860A 5.46 1.720e-
			14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
		UNCOUPLING PROTEIN	11 77-95
1626	BL00325	SIGNATURE Actin-depolymerizing	BL00325B 21.66 1.000e-
1020	D100323	proteins.	40 93-139 BL00325A
		protessis.	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
		proteins.	40 82-130 BL00064C
		ļ ⁻	17.28 1.000e-40 137-
		1	182 BL00064E 27.20
		· †	1.000e-40 223-275
			BL00064F 25.14 7.882e-
			36 286-331 BL00064A 21.16 1.000e-33 22-60
		<i>:</i>	BL00064D 14.19 6.500e-
	1	i	31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
	1	SIGNATURE	11 59-84 PR00063A
	<u> </u>		11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
		TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
1636	DY 01010		3.51 2.538e-09 37-45
1636	BL01210	Caveolins proteins.	BL01210B 13.92 9.531e-
1637	BL00982	Bacterial-type phytoene	10 133-183 BL00982A 18.41 5.388e-
2001	5500000	dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COO5	BL01183B 21.31 8.144e-
		methyltransferase family	12 132-177
		proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
		SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	<u> </u>
1641	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
		REPBAT SIGNATURE	11 364-379 PR00320A
			16.74 7.828e-11 364-
			379 PR00320C 13.01
			2.800e-10 279-294
			PR00320C 13.01 2.800e-
	1		10 364-379 PR00320B
	1		12.19 5.114e-10 279- 294 PR00320A 16.74
			1.659e-09 279-294
		_ 	

SBQ ID NO	ACCESSION NO.	DESCRIPTION	RESULTS*	
			PR00320A 16.74 2.098e- 09 229-244	
1642	PF00023	Ank repeat proteins.	PF00023A 16.03 6.464e; 09 114-130	
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e-	
1644	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 109-120 BL00678 9.67 5.737e-09 528-539	
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89	
1646	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.270e- 21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292- 310	
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540	
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34	
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485	
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472	
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115	
1654	BL00982	Bacterial-type:phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334	
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314	
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630	
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.93Be- 11 114-136	
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e- 10 442-455	
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972B 20.72 5.629e-09 446- 468	
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243	
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319	
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163	
1663	PR00319	BETA G-PROTRIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85	

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
1664	NO. BL00018	PP hand galaium hindi-	DI 00019 7 42 F 000- 10
T004	BEOOTS	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10 489-502
1667	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 8.500e- 38 7-46
1669	BL01153	NOL1/NOP2/sun family proteins.	BL01153D 19.69 1.188e- 17 115-141 BL01153C 13.67 8.977e-15 66-80 BL01153B 20.52 1.885e- 10 13-37
1671	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT SIGNATURE	PR00678H 9.13 3.100e- 10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e- 20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.329e-
1674	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PROG049D 0.00 7.580e- 11 343-358 PRO0049D 0.00 1.286e-10 342-357
1676	PROD747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e- 19 427-448 PR00747G 14.50 2.286e-18 368- 393 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747D 15.23 8.759e-17 163- 183 PR00747E 15.13 8.244e-15 254-272 PR00747B 7.65 5.355e- 13 75-90 PR00747F 13.56 8.714e-10 311- 328
1677	PR00747	GLYCOSYL HYDROLASE FAMILY 47 SIGNATURE	PR00747H 12.76 8.636e- 19 309-330 PR00747G 14.50 2.286e-18 250- 275 PR00747C 12.06 7.500e-18 112-131 PR00747A 14.05 4.600e- 17 42-63 PR00747B 7.65 5.355e-13 75-90 PR00747F 13.56 8.714e- 10 193-210
1680	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 406-417 BL00678 9.67 6.684e-09 320-331
1681	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67 6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 1.346e- 13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR SIGNATURE	PR00646H 6.32 4.188e- 09 755-771
1690	ВБ01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 75-129
1691	PR00456	RIBOSOMAL PROTBIN PZ SIGNATURE	PR00456E 3.06 7.281e- 10 418-433 PR00456E 3.06 7.281e-10 419-434 PR00456E 3.06 8.125e- 10 420-435
1692	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	PR00456E 3.06 7.281e- 10 487-502 PR00456B 3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504
1693	BL00674	AAA-protein family proteins.	BL00674C 22.60 8.043e- 24 274-317 BL00674B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	NO.		4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414-
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PRO0409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PRO0466C 10.17 3.443e- 13 187-20B PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-21B
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1714	PF00642	Zinc finger C-x8-C-x5-C- x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1715	BL01115 .	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e- 09 7-51 BL00353C 14.83 6.018e-
1718	BL00353	HMG1/2 proteins.	10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e- 09 432-483
1721	BP00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTBIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e- 09 418-428
1724	BL01279	Protein-L- isoaspartate(D- aspartate) 0- methyltransferase signa.	BL01279A 24.27 5.663c- 12 233-201
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e- 09 17-61

1731	ACCESSION	DESCRIPTION	RESULTS*
7/37	NO.	Kinesin light chain	BL01160B 19.54 9.676e~
	BL01160	repeat proteins.	10 296-350
1732	BL01160	Kinesin light chain	BL01160B 19.54 9.676e-
1733	DEPONICO	repeat proteins. Histone deacetylase	10 316-370 PF00850F 15.70 4.349e-
1/33	PF00850	family.	22 246-279 PF00850D
	1		14.76 6.850e-20 177-
	1		201 PF00850E 8.88
	ľ		8.691e-18 209-235 PF00850G 22.75 4.098e-
			14 281-323
1734	BL00354	HMG-I and HMG-Y DNA-	BL00354C 6.61 5.932e-
	İ	binding domain proteins (Abook)	09 292-307
1735	DM00179	w KINASE ALPHA ADHESION	DM00179 13.97 5.263e-
		T-CELL.	10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e-
		TOTAL STORATORS	10.79 2.241e-10 109-
			123 PR00449E 13.50
1744	PR00449	TRANSFORMING PROTEIN P21	9.289e-10 144-167 PR00449A 13.20 1.188e-
-/33	1200113	RAS SIGNATURE	11 5-27 PR00449D
			10.79 2.241e-10 109-
			123 PR00449E 13.50 9.289e-10 144-167
1745	ВЬ00720	Guanine-nucleotide	BL00720B 16.57 8.297e-
·		dissociation stimulators CDC25 family sign.	15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY	PR00081B 10.38 6.727e- 11 45-57 PR00081E
		SIGNATURE	17.54 3.935e-10 150-
	<u> </u>		168
1747	BL00439	Acyltransferases ChoActase / COT / CPT	BL00439H 18.24 8.435e- 14 65-91 BL00439G
•		family proteins.	13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY	PR00819B 10.83 7.158e-
1751	PD00066	SIGNATURE PROTEIN ZINC-FINGER	11 4-20 PD00066 13.92 3.400e-
1.01	1200000	METAL-BINDI.	14 33-46 PD00066
	1	· ·	13.92 1.000e-13 89-102
`	1		L The state of the
			PD00066 13.92 7.000e-
			PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117-
1752	DV01013	. Count and the desired	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117-
1753 1754	BL01013	protein family proteins. Receptor tyrosine kinase	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e-
		protein family proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I
		protein family proteins. Receptor tyrosine kinase	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e-
1754	BL00790	protein family proteins. Receptor tyrosine kinase class V proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
		protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e-
1754	BL00790	protein family proteins. Receptor tyrosine kinase class V proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1754	BL00790	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09
1754 1756	BL00790 PD01066 DM00406	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC FINGER ZINC-FINGER METALBUNDING NU. GLIADIN.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666
1754 1756 1759 1762	PD01066 DM00406 PD02929	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER ZINC-FINGER METALBUNDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278
1754 1756	BL00790 PD01066 DM00406	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OBG GTP-BINDING	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e-
1754 1756 1759 1762	PD01066 DM00406 PD02929	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278
1754 1756 1758 1762 1765	PD01066 DM00406 PD02929 PR00326 PF00023	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE Ank repeat proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539
1754 1756 1758 1762	PD01066 DM00406 PD02929 PR00326	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OEG GTP-BINDING PROTEIN FAMILY SIGNATURE ANK repeat proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539 BL00942F 15.07 4.343e-
1754 1756 1758 1762 1765	PD01066 DM00406 PD02929 PR00326 PF00023	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC FINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE Ank repeat proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539
1754 1756 1758 1762 1765	PD01066 DM00406 PD02929 PR00326 PF00023	protein family proteins. Receptor tyrosine kinase class V proteins. PROTEIN ZINC PINGER ZINC-FINGER METAL-BINDING NU. GLIADIN. ADHESION GLYCOPROTEIN PRECURSOR I. GTP1/OEG GTP-BINDING PROTEIN FAMILY SIGNATURE ANK repeat proteins.	PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130 BL01013D 26.81 6.516e- 18 33-77 BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318 PD01066 19.43 9.750e- 35 10-49 DM00406 7.73 7.600e-09 653-666 PD02929A 28.27 4.529e- 09 224-278 PR00326A 8.75 5.950e- 11 146-167 PF00023A 16.03 3.077e- 14 523-539 BL00942F 15.07 4.343e- 10 371-389 BL00942B

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.
TRADOCS:1416223.I(%CRJ0!!.DOC)

WO 01/53312

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
2	 		_	SCORE
3	ig pkinase	Immunoglobulin domain	2.le-32	109.5
	<u></u>	Bukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP_GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH_C	IMP dehydrogenase / GMP	1.6e-119	410.5
	,	reductase C terminus		j
21	IMPDH_C	IMP dehydrogenase / GMP	4.3e-102	352.6
		reductase C terminus	1	1
22	pkinase	Bukaryotic protein kinase domain	2.4e-79	277.0
23	pkinase	Rukaryotic protein kinase domain	8.4e-74	258.6
25	RNA_pol_A	RNA polymerase alpha subunit	10	1077.7
26	C1q	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal L2	Ribosomal protein L23	le-29	104.2
30	2f-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Bts-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	OCH-5	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase		
54	myb_DNA- binding	Myb-like DNA-binding domain	2.1e-65 0.096	230.7 15.2
55	voltage CLC	Voltage gated chloride channels	3.3e-186	631.9
56	sugar tr	Sugar (and other) transporter	0.00015	-64.3
57	TBC	TBC domain	2.2e-37	
58	ank	Ank repeat	5.9e-25	137.6 96.3
59	ank	Ank repeat	5.9e-25	96.3
67	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	7.9e-25	175.6
68	C2	C2 domain	7.9e-54	102 7
69	C2	C2 domain	7.9e-54 2.3e-54	192.2
		Kelch motif	2.3e-54 9.4e-99	194.0
70	retcu			241 5
70 72	Kelch ig	Immunoglobulin domain	8.2e-28	341.5 94.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	PRAM NAME	DESCRIPTION	p-varue	SCORE
MO:		domain		SCORE
74	pkinase	Rukaryotic protein kinase	2.8e-38	140.6
14	pkinase	domain	2.06-30	140.6
76	zf-	Topoisomerase DNA binding C4	5.4e-54	192.8
,,	C4 Topoisom	zinc fing	3.40 51	
83	Peptidase S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase	1.4e-59	211.4
93	pkinase	domain	1.46.33	211.2
96	pkinase	Eukaryotic protein kinase	2.6e-51	183.9
	PALIZISE	domain	7.00 52	
97	adh short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various	6.8e-05	-5.2
204	1	cellular act	****	
104	pkinase	Eukaryotic protein kinase	2.7e-73	256.9
		domain		1
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas	FAD/NAD-binding Cytochrome	7.7e-61	215.5
	e	reductase		1
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase	4e-88	306.2
		domain	ļ ·	į
116	PH	PH domain	3.1e~11	45.2
117	lipocalin	Lipocalin / cytosolic fatty-	2.4e-14	53.5
		acid binding pr	<u></u>	L
118	pkinase	Bukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IPS eIF4 eIF	eIF4-gamma/eIF5/eIF2-epsilon	le-32	122.2
	2			
124	iq	Immunoglobulin domain	6.5e-08	30.6
127	mito carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C	Protein phosphatase 2C	2.2e-71	250.6
129	ATPIGI PLM M	ATP1G1/PLM/MATS family	3.1e-20	80.6
	AT8	_		ļ
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	2,200	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATPIG1_PLM_M	ATPIGI/PLM/MAT8 family	9.3e-22	85.7
	AT8		·	
139	WH2	Wiskott Aldrich syndrome	0.0067	23.1
		homology region 2		
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S2	Signal peptidase I	5.7e-10	35.7
143	6	ADD will be for the first firs	1 2 20	145 3
143	arf KRAB	ADP-ribosylation factor family	1.2e-39	145.2
148	1 · · · · · · · · · · · · · · · · · · ·	KRAB box	7.3e-30	1
	DUFÉ	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide	3.8e-80	231.1
151	54	phosphodiesterase S4 domain	1 70 00	42.3
153			1.1e-08 3.8e-103	L
	tRNA-synt_1d	tRNA synthetases class I (R)	1	356.1
154	Cyt_reductas	FAD/NAD-binding Cytochrome	7.8e-60	212.2
155	e	reductase Ras family	3 60 00	107.0
157	ras actin	Actin	3.6e-28 3.8e-26	87.1
13/	Lacem	MCCTU	7.06-70	107.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn carbOpept	Zinc carboxypeptidase	5e-138	471.9
165	pkinase	Eukaryotic protein kinase	5.1e-67	236.1
	1	domain		27.0
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	
168	Ribosomal_Sl 5	Ribosomal protein S15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157:0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	qlobin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	le-31	118.8
178	ATPIG1_PLM_M AT8	ATP1G1/PLM/MAT8 family	2.5e-17	71.0
179	2F-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-38	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	VATP- synt AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ_con	Ubiquitin-conjugating enzyme	le-53	191.9
215	DEAD	DEAD/DRAH box helicase	1.8e-43	140.4
216	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans f_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD4 D	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
235	LRR	Leucine Rich Repeat	1.2e-30	115.3
236	LRR	Leucine Rich Repeat	6.7e-29	109.4
237	PDZ	PDZ domain (Also known as DHR	1.7e-09	45.0
	1	or GLGF).	1	1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	JCMD	Cabi di a a a A doom a bi a a a		SCORB
	dCMP_cyt_dea m	Cytidine and deoxycytidylate deaminase	2.5e-05	31.1
245	ig	Immunoglobulin domain	6.7e-08	30.5
248	wnt	wnt family of developmental signaling protei	9.1e-270	742.6
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu x	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekin ase	Adenylate kinase	2.le-110	380.2
259	HIT	HIT family	8.2e-07	25.3
260	Bacterial_PQ Q	PQQ enzyme repeat	1.6e-15	65.0
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	101.0
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina se	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_\$7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Bukaryotic protein kinase domain	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	2f-C2H2	Zinc finger, C2H2 type	2.2e~125	430.0
296	mito_carr	Mitochondrial carrier proteins	4.1e-59	205.5
302	HMG_box Glycos trans	HMG (high mobility group) box	6.7e-29	109.4
304	f_4	Glycosyl transferase	5e-87	302.5
	tRNA-synt_2	tRNA synthetases class II (D, K and N)		294.8
305 306	KRAB	KRAB box	2e-44	161.0
308	rrm 7tm 1	RNA recognition motif. 7 transmembrane receptor	2.7e-44 5.2e-39	160.6 126.1
309	_	(rhodopsin family)	<u> </u>	
311	DNA_polymera seX	DNA polymerase X family	2.4e-64	227.2
312	ig	Immunoglobulin domain	9.5e-08	39.2
313	Ets	Ets-domain	6.8e-19	65.9
315	Kelch	Kelch motif	8.1e-60 1.3e-106	192.3 367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Bukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
327	HMG_box	HMG (high mobility group) box	6.7e-29	109.4
328	cadherin	Cadherin domain	8.1e-81	281.9
331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7
		organization Fourtier/	· '	

PCT/US00/34263

SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM
335	vwa	von Willebrand factor type A	2.3e-07	37.9
		domain		
339	ras	Ras family	7.8e-07	-59.1
340	zf-C2H2	Zinc finger, C2H2 type	8.2e-64	225.4
342	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
343	ig	Immunoglobulin domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Rukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
354	TBC	TBC domain	5.1e-15	63.3
355	PHD	PHD-finger	3.2e-07	37.4
358	DUF6	Integral membrane protein DUP6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	BF hand	5.4c-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin G	Laminin G domain	1.5e-33	121.7
369	PP2C	Protein phosphatase 2C	5.3e-20	73.9
372	LIM	LIM domain containing proteins	9.9e-15	57.1
373	KRAB	krab box	4.8e-23	90.0 .
376	ion trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase	1.6e-94	327.5
	21-31	domain		<u> </u>
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank .	Ank repeat	2.5e-101	350.0
386	ig	Immunoglobulin domain	9.5e-05	23.6
388	zf-C2H2	Zinc finger, C2H2 type	1.7e-42	154.6
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.le-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
399	fn3	Pibronectin type III domain	4.1e-102	352.6
400	WD40	WD domain, G-beta repeat	0.00049	26.8
401	El_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	fn3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	P-box	F-box domain.	4.2e-06	33.7
412	SNF2 N	SNF2 and others N-terminal	5.8e-16	61.6
	_	domain		
415	CPSase_L_cha	domain Carbamoyl-phosphate synthase	1.5e-172	586.6
	CPSase L cha	Carbamoyl-phosphate synthase (CPSase)	<u> </u>	L
418	CPSase_L_cha in LRR	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat	3.8e-24	93.6
418 419	CPSase L cha in LRR DENN	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain	3.8e-24 2e-58	93.6
418 419 420	CPSase L cha in LRR DENN RasGEF	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	3.8e-24 2e-58 8.1e-43	93.6 207.5 155.7
418 419 420 421	CPSase L cha in LRR DENN RasGEF ank	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	3.8e-24 2e-58 8.1e-43 1.4e-153	93.6 207.5 155.7 523.7
418 419 420 421 424	CPSase L cha in LRR DENN RasGEF ank G-patch	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain	3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	93.6 207.5 155.7 523.7 78.9
418 419 420 421	CPSase L cha in LRR DENN RasGEF ank	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain	3.8e-24 2e-58 8.1e-43 1.4e-153	93.6 207.5 155.7 523.7
418 419 420 421 424	CPSase L cha in LRR DENN RasGEF ank G-patch	Carbamoyl-phosphate synthase (CPSase) Leucine Rich Repeat DENN (AEX-3) domain RasGEF domain Ank repeat G-patch domain Eukaryotic protein kinase	3.8e-24 2e-58 8.1e-43 1.4e-153 1e-19	93.6 207.5 155.7 523.7 78.9

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
	t			
429	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.2e-256	866.0
442	Alpha_adapti	Alpha adaptin carboxyl-terminal	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON)	0.00012	-17.1
446	İq	Immunoqlobulin domain	0.00011	20.1
451	sushi	Sushi domain (SCR repeat)	1.4e-18	75.2
452	fn3	Fibronectin type III domain	1.5e-06	35.2
454	pyridoxal de	Pyridoxal-dependent	8.3e-14	50.3
737	C pyridoxai_de	decarboxylase conse	3,50]
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur chan	Neurotransmitter-gated ion-	le-175	597.1
331	near_enan	channel		1
458	Josephin	Josephin	0.0002	18.7
468	bzip	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	le-31	118.8
481	ArfGap	Putative GTP-ase activating protein for Arf	8.4e-66	232.0
485	SH2	Src homology domain 2	0.011	11.4
486	Clq	Clg domain	4.3e-74	259.6
487	dsxm	Double-stranded RNA binding motif	1.1e-47	171.9
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti	Alpha adaptin carboxyl-terminal	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	KNV_polyprot	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain .	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	39.5
504	abhydrolase	alpha/beta hydrolase fold	0.045	-3.6
505	∧#9	von Willebrand factor type A domain	7.1e-62	219.0
508	Na_K_ATPase_	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201.5
		Glycosyl transferases group 1	2.9e-06	27.0
510	Glycos_trans f 1		\	1
511	Glycos_trans f_1 Glycos_trans f 1	Glycosyl transferases group 1	2.9e-06	27.0
	f_1 Glycos_trans		2.9e-06 1.9e-09	27.0

SEQ ID NO: PFAM NAME DESCRIPTION p-value 50: EGF EGF-like domain 1.9e-18 516 Surp Surp module 4.3e-38 523 ig Immunoglobulin domain 3.3e-06 526 UBX UBX domain 1.1e-34	PFAM SCORE 74.7 140.0
515 EGF EGF-like domain 1.9e-18 516 Surp Surp module 4.3e-38 523 ig Immunoglobulin domain 3.3e-06	74.7
516 Surp Surp module 4.3e-38 523 ig Immunoglobulin domain 3.3e-06	
523 ig Immunoglobulin domain 3.3e-06	1 1 4 0 n
3.56-00	
526 UBX UBX domain 1 1 1c-34	25.0
	128.6
528 adh_zinc Zinc-binding dehydrogenases 2.7e-34	127.4
530 SAM SAM domain (Sterile alpha 0.046	10.0
motif)	1
531 adh_short short chain denydrogenase 0.0025	-34.1
532 mito carr Mitochondrial carrier proteins 2.5e-81	281.7
533 mito_carr Mitochondrial carrier proteins 2e-61	213.5
534 thiolase Thiolase 3.5e-183	622.0
535 FMO-like Flavin-binding monooxygenase- 0	1
like	1153.7
	<u> </u>
	196.6
	466.0
M and V)	ı
538 tRNA-synt_1 tRNA synthetases class I (I, L, 3.1e-136	466.0
M and V)	1
539 tRNA-synt 1 tRNA synthetases class I (I, L, 1.9e-117	403.6
M and V)	
540 tRNA-synt_1 tRNA synthetases class I (I, L, 3.1e-136	466.0
M and V)	100.0
541 VATP-synt_E ATP synthase (E/31 kDa) subunit 5.9e-85	295.7
543 zf-C2H2 Zinc finger, C2H2 type 5.5e-69	242.6
5.5E-69	
DUF101 Protein of unknown function 8.5e-38	139.0
1.16-6/	238.2
ide	
547 WD40 WD domain, G-beta repeat 2.6e-32	120.8
548 RHD Rel homology domain (RHD) 1.6e-238	686.2
549 MMR HSR1 GTPase of unknown function 5.4e-67	236.0
551 HECT HECT-domain (ubiquitin- 4.3e-127	435.6
transferase).	
554 MHC_II_alpha Class II histocompatibility 3.5e-74	259.8
antigen, alp	
555 2f-UBR1 Putative zinc finger in N- 3.3e-16	67.3
recognin] 37.13
556 Kelch Kelch motif 5.5e-29	109.7
561 AMP-binding AMP-binding enzyme 2.8e-06	-163.7
562 PABP Poly-adenylate binding protein, 4.9e-38	1
unique domai	139.8
	
	238.2
5.1e-16	66.0
	238.9
1.3e-64	294.3
domain	1
570 pkinase Bukaryotic protein kinase 1.5e-84	294.3
domain	1 1
571 CN hydrolase Carbon-nitrogen hydrolase 0.00081	-79.7
572 myosin_head Myosin head (motor domain) 0	1495.2
573 myosin_head Myosin head (motor domain) 0	1490.4
575 Surp Surp module 1.7e-23	91.5
576 Surp Surp module 1.7e-23	91.5
577 DNA_pol_B DNA polymerase family B 0	i
rgo Polimento Zunily B	1138.6
PDZ domain (Also known as DHR 8.3e-09 or GLGP).	42.7
F.20	ļ. <u>.</u>
	83.3
	601.3
channel	1
503 sushi Sushi domain (SCR repeat) 0	1673.0
DRAD DRAD/DEAH box helicase 7.3e-36	116.3
586 KH-domain KH domain 2.9e-13	57.5
587 G-patch G-patch domain 2.3e-14	61.2
	133.4
589 LIM LIM domain containing proteins 2.3e-36	
589 LIM LIM domain containing proteins 2.3e-36	114.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase domain	5e-92	319.2
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_car=	Mitochondrial carrier proteins	6.3e-67	232.3 .
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20,1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin	Kinesin motor domain	1.1e-81	284.8
617	kinesin	Kinesin motor domain	8.4e-80	278.5
618	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.0098	13.1
620	MATH	MATH domain	7.8e-05	22.2
621	Y_phosphatas e	Protein-tyrosine phosphatase	1.4e-32	121.6
622	pkinase	Eukaryotic protein kinase domain	4.45-40	146.6
623	BNR	BNR repeat	2.1a-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632	rrm	RNA recognition motif.	4e-05	30.5
635	pkinase	Bukaryotic protein kinase domain	1.6e-104	360.7
636	Fork_head	Fork head domain ,	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
643	TPR	TPR Domain	4.8e-08	40.1
643	efhand SNF2 N	EF hand SNF2 and others N-terminal	1.9e-27	104.6
648	PseudoU synt	domain	1.2e-101	351.1
650	h_2 zf-C2H2	RNA pseudouridylate synthase Zinc finger, C2H2 type	1.9e-55	197.6
652	ank I LWEQ	Ank repeat	1.3e-17	71.9
653	neur_chan	I/LWEQ domain Neurotransmitter-gated ion- channel	9.5e-101 4.1e-171	341.0 581.8
654	tsp 1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
661		I	+	+
662	C2	C2 domain	6.7e-19	76.2
	C2 C2	C2 domain	6.7e-19	76.2
662	C2 C2	I		
662	C2	C2 domain	6.7e-19 6.7e-19	76.2
662 663 664	C2 C2	C2 domain C2 domain Glutathione S-transferases.	6.7e-19 6.7e-19 9.3e-34	76.2 76.2 114.4
662 663 664 667	C2 C2 GST LRR	C2 domain C2 domain Glutathione S-transferases. Leucine Rich Repeat	6.7e-19 6.7e-19 9.3e-34 9.3e-31	76.2 76.2 114.4 115.6
662 663 664 667 668	C2 C2 GST	C2 domain C2 domain Glutathione S-transferases. Leucine Rich Repeat Spectrin repeat	6.7e-19 6.7e-19 9.3e-34 9.3e-31 4e-57	76.2 76.2 114.4 115.6 203.2
662 663 664 667 668 670	C2 C2 GST LRR spectrin	C2 domain C2 domain Glutathione S-transferases. Leucine Rich Repeat	6.7e-19 6.7e-19 9.3e-34 9.3e-31	76.2 76.2 114.4 115.6

676 679 680 681 682 683 687 689 691 696	WD40 LRR zf-CCCH zf-C2H2 CH DSPC zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	WD domain, G-beta repeat Leucine Rich Repeat Zinc finger C-x8-C-x5-C-x3-H type Zinc finger, C2H2 type Calponin homology (CH) domain Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR Homeobox domain	4.8e-24 0.0015 2.6e-29 5.2e-05 2.4e-17 4.3e-43 0.051	93.3 25.2 107.7 30.1 71.1 156.6
676 679 680 681 682 683 687 689 691 696 697 698	LRR zf-CCH zf-C2H2 CH DSPC zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	Leucine Rich Repeat Zinc finger C-x8-C-x5-C-x3-H type Zinc finger, C2H2 type Calponin homology (CH) domain Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	0.0015 2.6e-29 5.2e-05 2.4e-17 4.3e-43 0.051	25.2 107.7 30.1 71.1 156.6
679 680 681 682 683 687 689 691 696 697 698	zf-CCH zf-C2H2 CH DSPc zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	Zinc finger C-x8-C-x3-H type Zinc finger, C2H2 type Calponin homology (CH) domain Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	2.6e-29 5.2e-05 2.4e-17 4.3e-43 0.051	30.1 71.1 156.6
680 681 682 683 687 689 691 696 697 698	zf-C2H2 CH DSPC zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	type Zinc finger, C2H2 type Calponin homology (CH) domain Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	5.2e-05 2.4e-17 4.3e-43 0.051	30.1 71.1 156.6
681 682 683 687 689 691 696 697 698	CH DSPc zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	Calponin homology (CH) domain Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	2.4e-17 4.3e-43 0.051	71.1 156.6
682 683 687 689 691 696 697 698	DSPc zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	Dual specificity phosphatase, catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	4.3e-43 0.051	156.6
683 687 689 691 696 697 698 701	zf-C3HC4 Synapsin PR55 homeobox Peptidase_M2	catalytic doma Zinc finger, C3HC4 type (RING finger) Synapsin Protein phosphatase 2A regulatory subunit PR	0.051	10.8
687 689 691 696 697 698 701	Synapsin PR55 homeobox Peptidase_M2	finger) Synapsin Protein phosphatase 2A regulatory subunit PR	0	1
689 691 696 697 698 701	PR55 homeobox Peptidase_M2	Protein phosphatase 2A regulatory subunit PR		1000
691 696 697 698 701	homeobox Peptidase_M2	regulatory subunit PR	0	1890.8
696 697 698 701	Peptidase_M2		ł	1038.8
696 697 698 701	Peptidase_M2	i Homeodox domain	8.5e-30	112.4
697 698 701		metallopeptidase family M24	2.6e-59	210.5
698 701	RhoGEF	RhoGEF domain	9.5e-35	128.9
701	PHD	PHD-finger	0.008	9.3
	zf-C2H2	Zinc finger, C2H2 type	5.5e-123	422.0
702	Sulfatase	Sulfatase	3e-231	781.6
	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
	Acyl transf	Acyl transferase domain	1.1e-22	88.8
	WD40	WD domain, G-beta repeat	1.1e-22 4.8e-19	76.7
	Ran BP1	RanBP1 domain.	8.4e-06	-7.3
	DEAD DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
	PH	l _ '	1.6e-09	39.0
	DSPC	PH domain	1.5e-37	138.2
		Dual specificity phosphatase, catalytic doma		
— · · · · · · · · · · · · · · · · · · ·	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
	ig	Immunoglobulin domain	1e-29	100.8
	integrin_B	Integrins, beta chain	0	1125.4
1	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
_ 1	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
	ig	Immunoglobulin domain	2.2e-05	22.4
	P-box	F-box domain.	0.007	23.0
	Nop	Putative snoRNA binding domain	8.1e-58	205.5
	Nop	Putative snoRNA binding domain	8.1e-58	205.5
	WD40	WD domain, G-beta repeat	7.5e-26	99.3
730	derm	Double-stranded RNA binding motif	0.027	12.1
	dynamin	Dynamin family	4.2e-16	66.9
733	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.8e-10	41.7
	CDP- OH_P_transf	CDP-alcohol phosphatidyltransferase	4.2e-26	100.1
	DEAD	DEAD/DEAH box helicase	8.6e-57	182.5
	TSC22	TSC-22/dip/bun family	6.5e-32	119.5
742	ras	Ras family	2.2e-100	346.9
	PMI_typeI	Phosphomannose isomerase type I	1.2e-243	822.9
	trypsin	Trypsin	6.4e-88	279.4
	kazal	Kazal-type serine protease inhibitor domain	2.2e-52	187.4
749	efhand	EF hand	6.3e-06	33.1
	PHD	PHD-finger	4.9e-16	66.7
	zf-C2H2	Zinc finger, C2H2 type	3.2e-21	83.9
	Hydrolase	haloacid dehalogenase-like hydrolase	6.le-11	49.8
	Ribosomal_L3	Ribosomal L39 protein	0.00018	26.7
	PH .	PH domain	3.6e-14	55.7
	SCAN			191.5
		SCAN domain	1.4e~53	23.1
	PA	PA domain	0.0065	
	arf CIDE-N	ADP-ribosylation factor family CIDE-N domain	2.2e-19 2.2e-40	17.8

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORB
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to	le-52	188.6
		homeobox domain	ŀ	1
767	VWC	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	BF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two domains)	2.4e-53	181.6
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.le-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD ·	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito_carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase_HII	Ribonuclease HII	2.5e-67	237.1
790	PI3_PI4_kina se	Phosphatidylinositol 3- and 4- kinases	5.4e-108	372.2
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal- bind_lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN_hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HM F	Histone-like transcription factor	6e-14	59.8
812	adh_short	short chain dehydrogenase	8.1e-20	79.3
614	IMP4	Domain of unknown function	3.3e-71	250.0
815	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
816	Pept_tRNA_hy dro	Peptidyl-tRNA hydrolase	1.6e-37	138.0
817	ARID	ARID DNA binding domain	2.5e-18	74.3
826	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1.6e-32	121.5
830	ArfGap	Putative GTP-ase activating protein for Arf	1.5e-53	191.3
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatas	Protein-tyrosinc phosphatase	2.60-119	409:8
841	pkinase	Bukaryotic protein kinase domain	3.4e-100	346.3
844	Ribosomal_L2	Ribosomal L22e protein family	1e-64	228.4
846	IBR	rnn A	1	
849		IBR domain	9e-15	62.5
	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.00016	18.9
851	SET	SET domain	5e-30	113.2
852	SRCR			

SCORE Scawenger receptor cysteine	SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
SRCR	NO.	 	rich domain	 -	SCORE
Superfamily	853	SRCR	Scavenger receptor cysteine-	0	1025.4
Section Sect		_	superfamily	0.012	-6.0
B61		COX6A	VIa	3.4e-58	206.7
Mito Carr Mitochondrial Carrier Proteins 2.9e-53 185.5		_1	RNA recognition motif.	5.4e-45	162.9
				5.1e-62	219.4
1966 19				2.9e-53	185.5
### 187				4.7e-158	538.5
					44.1
CPSase Cha Carbamoyl-phosphate synthase 2.1e-218 739.0					
In					1
Serpin Serpins (serine protease 2.5e-42 145.7 inhibitors)		in	(CPSase)	2.1e-218	739.0
Inhibitors Patatin Patatin Patatin Patatin Patatin RA RA Ras association (RalGDS/AF-6) 0.044 8.0 domain 1.2e-51 182.0 887 DUF92 Integral membrane protein DUF92 2.7e-12 54.3 889 Sugar tr Sugar (and other) transporter 8.2e-63 222.1 893 DUF28 Domain of unknown function 1.3e-43 158.3 DUF28 Domain of unknown function 1.3e-43 158.3 DUF28 Phosphatidylinositol transfer 6.5e-98 338.7 protein Pr		2e	1	2.1e-98	340.3
RA			inhibitors)	2.5e-42	145.7
B87 DUF92 Integral membrane protein DUF92 2.7e-12 54.3					
Sugar tr Sugar (and other) transportex 8.2e-63 222.1			domain	0.044	8.0
DUF28 DOMAIN of unknown function 1.3e-43 158.3			Integral membrane protein DUF92		
DUP28 DUP28 DUP28 Society					
Bead Dead Dead/DRAH box helicase 1.5e-48 156.5			DUF28		158.3
RE2 KE2 family protein 7e-61 215.7		_	protein	6.5e-98	338.7
NEC KE2 KE2 Family protein 4.3e-51 183.2					
901 zf-C2H2 Zinc finger, C2H2 type 2.7e-57 203.8 902 ras Ras family 2.3e-75 263.8 904 TPR TPR Domain 3.2e-22 87.2 906 GBP Guanylate-binding protein 6.9e-253 853.1 907 GBP Guanylate-binding protein 1.1e-239 809.6 908 WD40 WD domain, G-beta repeat 2.6e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5e-39 144.1 913 Epimerase NAD dependent 5e-07 -88.5 epimerase PED domain 1.5e-09 30.7 921 TBC TBC domain 1.5e-07 -88.5 921 TBC TBC domain 1.5e-09 30.7 922 WD40 WD domain, G-beta repeat 8.2e-07 36.1 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 926		1-1-1-1	KE2 family protein		1
902 ras Ras family 2.3e-75 263.8 904 TPR TPR Domain 3.2e-22 87.2 87.2 906 GBP Guanylate-binding protein 8.9e-253 853.1 907 GBP Guanylate-binding protein 1.1e-239 809.6 908 WD40 WD domain, G-beta repeat 2.6e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 2f-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent epimerase/dehydratase family 921 TBC TBC domain 5e-07 -88.5 98.2 WD40 WD domain, G-beta repeat 8.2e-07 36.1 15e-09 30.7 922 WD40 WD domain, G-beta repeat 8.2e-07 36.1 1ydrolase haloacid dehalogenase-like 2.9e-05 29.1 hydrolase haloacid dehalogenase-like 2.9e-05 29.1 hydrolase hydrolase hydrolase 1.3e-05 29.1 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 2f-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 finger) 2f-C3HC4 Finger) Ribulose-phosphate 3 epimerase 7.2e-105 361.8 16mily 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase family 932 C2 C2 domain Nucleosome assembly protein 1.1e-22 84.6 (NAP) Nucleosome assembly protein 1.1e-22 84.6 (NAP) 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase 3.4e-75 263.2 domain WD domain, G-beta repeat 1.6e-07 38.4		1	KB2 family protein		
904 TPR TPR Domain 3.2e-22 87.2 906 GBP Guanylate-binding protein 8.9e-253 853.1 907 GBP Guanylate-binding protein 1.1e-239 809.6 908 WD40 WD domain, G-beta repeat 2.6e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent 5e-07 -88.5 epimerase/dehydratase family 921 TBC TBC domain 1.5e-09 30.7 922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 hydrolase haloacid dehalogenase-like hydrolase 925 UO_con Ubiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 1mger) 930 Ribul P 3 ep Ribulose-phosphate 3 epimerase 7.2e-105 361.8 1mger) 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase 7.2e-105 361.8 1mger) 934 NAP_family Nucleosome assembly protein 1.1e-22 84.6 1mger) 940 abbydrolase Eukaryotic protein kinase 3.4e-75 263.2 1mger) 948 Pkinase Eukaryotic protein kinase 3.4e-75 263.2 2699 WD40 WD domain, G-beta repeat 1.8e-27 104.7 2650 Acyltransfer Acyltransferase 1.6e-07 38.4			Zinc linger, C2H2 type		
906 GBP Guanylate-binding protein 8.9e-253 853.1 907 GBP Guanylate-binding protein 1.1e-239 809.6 908 WD40 WD domain, G-beta repeat 2.6e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent 5e-07 -88.5 921 TBC TBC domain, G-beta repeat 1.6e-25 98.2 922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 1.6e-25 98.2 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 hydrolase haloacid dehalogenase-like 2.9e-05 29.1 hydrolase haloacid dehalogenase-like 3.3e-53 190.2 926 CH Calponin homology (CH) domain 3.3e-53 190.2 929 Zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 finger) 930 Ribul P 3 ep Ribulose-phosphate 3 epimerase family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase family 936 C2 C2 domain 9.2e-62 220.7 937 NAP family Nucleosome assembly protein 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 945 WD40 WD domain, G-beta repeat 3.4e-75 263.2 domain 947 WD40 WD domain, G-beta repeat 1.8e-27 104.7 948 Pkinase Eukaryotic protein kinase domain 3.4e-75 263.2					
907 GBP Guanylate-binding protein 1.1e-239 809.6 908 WD40 WD domain, G-beta repeat 2.5e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent epimerase/dehydratase family 5e-07 -88.5 921 TBC TBC domain 1.5e-09 30.7 922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 925 UQ_con Ubiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul_P_3_ep Ribulose-phosphate 3 epimerase family 931 Ribul_P_3_ep Ribulose-phosphate 3 epimerase 1.2e-96 334.4 936 C2 C2 domain 2.2e-62 220.7 NAP_family Nucleosome assembly protein 1.1e-22 84.6 937 NAP_family Nucleosome assembly protein (NAP) 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 949 WD40 WD domain, G-beta repeat 1.6e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4					
908 W040 WD domain, G-beta repeat 2.6e-26 100.8 909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent epimerase/dehydratase family 5e-07 -88.5 921 TBC TBC domain 1.5e-09 30.7 922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 925 UO_con Ubiquitin-conjugating enzyme 0.00033 -27.6 925 UO_con Ubiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul_P_3 ep Ribulose-phosphate 3 epimerase 7.2e-105 361.8 931	907	GBP	Guanylate-binding protein	1	1
909 PH PH domain 1.3e-09 39.4 910 zf-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1 913 Epimerase NAD dependent epimerase/dehydratase family 5e-07 -88.5 921 TBC TBC domain 1.5e-09 30.7 922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 925 UQ_con Ubiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul P 3 ep imacccccccccccccccccccccccccccccccccccc	908	WD40			1
2f-C2H2 Zinc finger, C2H2 type 2.5c-39 144.1	909	PH			1
epimerase/dehydratase family 921 TBC TBC domain 922 WD40 WD domain, G-beta repeat 923 WD40 WD domain, G-beta repeat 924 Hydrolase haloacid dehalogenase-like hydrolase 925 UO_con Ubiquitin-conjugating enzyme 926 CH Calponin homology (CH) domain 927 33 33 32 -27.6 928 WD40 WD domain, G-beta repeat 929 Zf-C3HC4 Zinc finger, C3HC4 type (RING finger) 930 Ribul P_3 ep Ribulose-phosphate 3 epimerase im family 931 Ribul P_3 ep Ribulose-phosphate 3 epimerase im family 936 C2 C2 domain 937 NAP_family Nucleosome assembly protein (NAP) 940 abhydrolase alpha/beta hydrolase fold 941 Tropomyosin Tropomyosins 942 Daloacid dehalogenase in separate im family 944 Tropomyosin Tropomyosins 945 Eukaryotic protein kinase domain 946 WD40 WD domain, G-beta repeat 1.8e-27 104.7 947 WD40 WD domain, G-beta repeat 1.6e-07 38.4		zf-C2H2	Zinc finger, C2H2 type	2.5e-39	144.1
922 WD40 WD domain, G-beta repeat 1.6e-25 98.2 923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 925 UO_con UDiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul P 3 ep im family Ribulose-phosphate 3 epimerase family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase 1.2e-96 334.4 936 C2 C2 domain 2.2e-62 220.7 937 NAP_family Nucleosome assembly protein 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4				5e-07	-88.5
923 WD40 WD domain, G-beta repeat 8.2e-07 36.1 924 Hydrolase haloacid dehalogenase-like 2.9e-05 29.1 925 UQ_con Ubiquitin-conjugating enzyme 0.00033 -27.6 926 CH Calponin homology (CH) domain 3.3e-53 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 finger) 930 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 936 C2 C2 domain 2.2e-62 220.7 937 NAP_family Nucleosome assembly protein 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4				1.5e-09	30.7
Hydrolase			WD domain, G-beta repeat	1.6e-25	98.2
hydrolase		1	WD domain, G-beta repeat	1	36.1
926 CH Calponin homology (CH) domain 3.3e-53 190.2 928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 936 C2 C2 domain 2.2e-62 220.7 937 NAP_family Nucleosome assembly protein 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4			hydrolase	2.9e-05	29.1
928 WD40 WD domain, G-beta repeat 5.9e-48 172.7 929 zf-C3HC4 Zinc finger, C3HC4 type (RING 3.1e-10 37.4 930 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 931 Ribul P 3 ep Ribulose-phosphate 3 epimerase im family 936 C2 C2 domain 2.2e-62 220.7 937 NAP_family Nucleosome assembly protein 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4			Ubiquitin-conjugating enzyme		
25					
im family 1.2e-96 334.4 931 Ribul_P_3_ep im Ribulose-phosphate 3 epimerase family 1.2e-96 334.4 936 C2 C2 domain 2.2e-62 220.7 937 NAP_family Nucleosome assembly protein (NAP) 1.1e-22 84.6 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4			finger)		37.4
im family		im	family	7.2e-105	361.8
937 NAP_family Nucleosome assembly protein 1.1e-22 84.6 (NAP) 940 abhydrolase alpha/beta hydrolase fold 0.011 3.1 944 Tropomyosin Tropomyosins 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase 3.4e-75 263.2 domain 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4		im		1.2e-96	334.4
(NAP)				2.2e-62	220.7
944 Tropomyosin 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4]	(NAP)	1.1e-22	84.6
944 Tropomyosin 3.2e-07 25.1 948 pkinase Eukaryotic protein kinase domain 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4		abhydrolase	alpha/beta hydrolase fold	0.011	3.1
948 pkinase Eukaryotic protein kinase domain 3.4e-75 263.2 949 WD40 WD domain, G-beta repeat 1.8e-27 104.7 950 Acyltransfer Acyltransferase 1.6e-07 38.4		Tropomyosin	Tropomyosins		
950 Acyltransfer Acyltransferase 1.6e-07 38.4	_	pkinase	domain		L
950 Acyltransfer Acyltransferase 1.6e-07 38.4		L	WD domain, G-beta repeat	1.8e-27	104.7
	950				}
		ase	l		

SEQ ID	PPAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MOCA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	OH P transf	phosphatidyltransferase	}	}
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IP-2B	Initiation factor 2 subunit	8.4e-193	653.9
	 	family	0- 34	92.4
970	RNase_PH	3' exoribonuclease family	9e-24	
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
989 993		tRNA intron endonuclease	0.0017	-34.2
- '	tRNA_int_end o			
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito_carr	Mitochondrial carrier proteins	9.7e-123	421.2
1001	RA	Ras association (RalGDS/AF-6) domain	1.2e-15	65.4
1004	DUF81	Domain of unknown function DUF81	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60 TCP1	TCP-1/cpn60 chaperonin family	3.7e-195	661.8
1008	TPR	TPR Domain	B.1e-44	159.0
1009	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	215.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	216.6
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.7e-15	53.1
1016	tRNA-synt 2c	finger) tRNA synthetases class II (A)	2.3e-15	55.2
1016	1 1 -		1.6e-78	274.3
1018	RhoGAP	RhoGAP domain Phosphoglycerate mutase family	3.8e-18	69.7
		i Phosphodivcerace mutase tamily	1 3 - 8E - 18	•
	PGAM			70.3
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1026 1027	HMG_box TBC	HMG (high mobility group) box TBC domain	8.4e-20 7.3e-45	162.5
1026 1027 1028	HMG_box	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR	8.4e-20	
1022 1026 1027 1028 1032	HMG_box TBC UQ_con	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme	8.4e-20 7.3e-45 1.4e-49	162.5 178.1
1026 1027 1028 1032	HMG_box TBC UQ_con PDZ Hydrolase	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). baloacid dehalogenase-like hydrolase	8.4e-20 7.3e-45 1.4e-49 0.028	162.5 178.1 16.3
1026 1027 1028 1032 1034	HMG_box TBC UQ_con PDZ Hydrolase	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). baloacid dehalogenase-like bydrolase KRAB box	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06	162.5 178.1 16.3 84.6
1026 1027 1028 1032	HMG_box TBC UQ_con PDZ Hydrolase	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). baloacid dehalogenase-like hydrolase	8.4e-20 7.3e-45 1.4e-49 0.028	162.5 178.1 16.3
1026 1027 1028 1032 1034 1037	HMG_box TBC UQ_con PDZ Hydrolase KRAB Cation_efflu	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). baloacid dehalogenase-like hydrolase KRAB box Cation efflux family NAD:arginine ADF-	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06	162.5 178.1 16.3 84.6
1026 1027 1028 1032 1034 1037 1038	HMG_box TBC UQ_con PDZ Hydrolase KRAB Cation_efflu x ART	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). baloacid dehalogenase-like hydrolase KRAB box Cation efflux family NAD:arginine ADF- ribosyltransferase	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06 7.1e-42	162.5 178.1 16.3 84.6 32.4 152.5
1026 1027 1028 1032 1034 1037 1038	HMG_box TBC UQ_con PDZ Hydrolase KRAB Cation_efflu x ART	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). haloacid dehalogenase-like bydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06 7.1e-42 4.7e-47	162.5 178.1 16.3 84.6 32.4 152.5 169.1
1026 1027 1028 1032 1034 1037 1038 1040	HMG_box TBC UQ_con PDZ Hydrolase KRAB Cation_efflu x ART WD40 zf-C2H2	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). haloacid dehalogenase-like bydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat Zinc finger, C2H2 type	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06 7.1e-42 4.7e-47 1.9e-18 3.7e-24	162.5 178.1 16.3 84.6 32.4 152.5 169.1 74.7 93.7
1026 1027 1028 1032 1034	HMG_box TBC UQ_con PDZ Hydrolase KRAB Cation_efflu x ART	HMG (high mobility group) box TBC domain Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR or GLGF). haloacid dehalogenase-like bydrolase KRAB box Cation efflux family NAD:arginine ADP- ribosyltransferase WD domain, G-beta repeat	8.4e-20 7.3e-45 1.4e-49 0.028 2e-21 4.8e-06 7.1e-42 4.7e-47	162.5 178.1 16.3 84.6 32.4 152.5 169.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal L2	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudi	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1 OBG	GTP1/OBG family	4.8e-41	141.8
1071	iq	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.8e-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1073	OLF	Olfactomedin-like domain	2.2e-66	234.0
•	1	Mitochondrial carrier proteins	1e-42	149.3
1078	mito_carr			1
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	.DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas e	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_su b	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_su b	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase 2	Asparaginase	6.4e-72	252.3
	1 4			
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3

NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
1163	linker histo	linker histone HI and H5 family	3.8e-14	60.4
	ne			
1164	DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha motif)	0.04	10.5
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	ND domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1 MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGRF	RasGEF domain	1.7e-88	307.4
1185	mito carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR LY6	u-PAR/Ly-6 domain	0.0042	15.6
	Orn DAP Arg	Pyridoxal-dependent	6.2e-128	430.6
1188	deC	decarboxylase	ŀ	
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Secl	Secl family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf _8	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie methylt	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm 3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	BF hand	3.2e-07	37.4
1213	efhand rrm	EF hand RNA recognition motif.		37.4
1219		RNA recognition motif.	3.2e-07	_L.'
1219 1220	rrm	<u> </u>	3.2e-07 2.1e-40	147.7
1219	DUP6	RNA recognition motif. Integral membrane protein DUF6	3.2e-07 2.1e-40 0.015	147.7 21.5
1219 1220 1222	rrm DUF6	RNA recognition motif. Integral membrane protein DUF6 SCAN domain	3.2e-07 2.1e-40 0.015 1.5e-71	147.7 21.5 251.1
1219 1220 1222 1223	DUF6 SCAN G-gamma	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36	147.7 21.5 251.1 129.5
1219 1220 1222 1223 1227	DUF6 SCAN G-gamma catalase	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36	147.7 21.5 251.1 129.5 1158.9
1219 1220 1222 1223 1227 1232 1233	DUF6 SCAN G-gamma catalase FX	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15	147.7 21.5 251.1 129.5 1158.9 64.5
1219 1220 1222 1223 1227 1232	DUF6 SCAN G-gamma catalase PX	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15	147.7 21.5 251.1 129.5 1158.9 64.5 64.5
1219 1220 1222 1223 1227 1232 1233 1236	DUF6 SCAN G-gamma catalase PX FCH Peptidase M2	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09	147.7 21.5 251.1 129.5 1158.9 64.5 64.5
1219 1220 1222 1223 1227 1232 1233 1236 1241	DUF6 SCAN G-gamma catalase FX FCH Peptidase_M2 0	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain PX domain Px domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1
1219 1220 1222 1223 1227 1232 1233 1236 1241	DUF6 SCAN G-gamma catalase FX PX FCH Peptidase_M2 0 WW UPF0006	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGI, domain Catalase PX domain PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1
1219 1220 1222 1223 1227 1232 1233 1236 1241 1243 1247	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Px domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8
1219 1220 1222 1223 1227 1232 1233 1236 1241 1243 1247 1248	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Px domain Pes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	147.7 21.5 251.1 129.5 1158.9 64.5 44.0 224.1 17.9 215.8
1219 1220 1222 1223 1227 1232 1233 1236 1241 1243 1247 1248	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Px domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73	147.7 21.5 251.1 129.5 1158.9 64.5 44.0 224.1 17.9 215.8 46.9
1219 1220 1222 1223 1227 1233 1236 1241 1243 1244 1244 1248	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Px domain Pes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10	147.7 21.5 251.1 129.5 1158.9 64.5 44.0 224.1 17.9 215.8
1219 1220 1222 1223 1227 1233 1236 1241 1243 1247 1248 1249 1254	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9
1219 1220 1222 1223 1227 1232 1233 1236 1241 1243 1247 1248	DUP6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1219 1220 1222 1223 1227 1233 1236 1241 1243 1247 1248 1249 1254 1255 1256	DUF6 SCAN G-gamma catalase FX FCH Peptidase M2 0 WW UPF0006 Glycos trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d G_glu_transp	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain PX domain Fes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger)	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3
1219 1220 1222 1223 1227 1232 1233 1236 1241 1243 1247 1248 1249 1254 1255 1256	DUF6 SCAN G-gamma catalase PX PX FCH Peptidase_M2 0 WW UPF0006 Glycos_trans f_2 efhand UQ_con ras formyl_trans f zf-C3HC4 DiHfolate_re d	RNA recognition motif. Integral membrane protein DUF6 SCAN domain GGL domain Catalase PX domain PX domain Px domain Pes/CIP4 homology domain Peptidase family M20/M25/M40 WW domain Metalloenzyme of unknown function UPF0006 Glycosyl transferases BF hand Ubiquitin-conjugating enzyme Ras family Formyl transferase Zinc finger, C3HC4 type (RING finger) Dihydrofolate reductase	3.2e-07 2.1e-40 0.015 1.5e-71 3.6e-36 0 2.2e-15 3.3e-09 2e-63 0.044 6.3e-61 4.5e-10 4e-11 2.1e-73 2.2e-62 4.9e-30 5.3e-13	147.7 21.5 251.1 129.5 1158.9 64.5 64.5 44.0 224.1 17.9 215.8 46.9 50.4 257.3 220.7 108.3

SEQ ID	PPAM NAME	DESCRIPTION	p-value	PEAM
NO:	1		Value	SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
1267	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	PIW	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.le-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1 3	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1335	UPP_syntheta	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
	UPP_syntheta 'se	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPC	Dual specificity phosphatase, catalytic doma	1,2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band_41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomera	0.086	-177.2
1348	BTB	BTB/POZ domain	5.3e-28	106.5
1349	DUP6	Integral membrane protein DUF6	0.033	15.8
1350	myosin_head	Myosin head (motor domain)	0	1088.7
1352	Nramp	Natural resistance-associated macrophage pro	1.2e-202	686.6
1353	S_100	S-100/ICaBP type calcium binding domain	5.3e-23	89.9
1355	DEAD	DEAD/DEAH box helicase	3.6e-65	209.0
1356	C2	C2 domain	2.4e-15	64.4
1357	RBD	Raf-like Ras-binding domain	4.2e-57	203.1
1360	zf-C2H2	Zinc finger, C2H2 type	7.4e-141	481.4
1361	HMG14_17	HMG14 and HMG17	7.9e-40	145.7

SEQ ID NO: 1362 1363 1364	SIS SIS	DESCRIPTION SIS domain	p-value 3.8e-30	PFAM SCORE 113.6
1362 1363 1364		<u></u>	3.8e-30	
1363 1364		<u></u>	3.8e-30	1113.6
1364	SIS			
		SIS domain	1.3e-28	108.5
	ig	Immunoglobulin domain	0.00026	19.0
1368	K_tetra	K+ channel tetramerisation	1.1e-16	68.9
l i	_	domain		1
1371	Collagen	Collagen triple helix repeat	2.2e-113	390,1
}		(20 copies)	2.20-113	330.1
1372	DnaJ	DnaJ domain	 	
1376	KRAB		6.6e-36	132.7
		KRAB box	2.1e-38	141.0
1378	EPW5	RLM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	BTB	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
	WD40			
	zf-C3HC4	WD domain, G-beta repeat	6.3e-24	92.9
130/	ZI-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	35.6
		finger)	į .	ļ
	zf-C2H2	Zinc finger, C2H2 type	5.5e-50	179.5
1390	zf-C2H2	Zinc finger, C2H2 type	2.5e-85	296.9
1393	kinesin	Kinesin motor domain	7.8e-188	637.4
1394	zf-C2H2	Zinc finger, C2H2 type	1.2e-49	178.4
	KRAB	KRAB box	5.1e-22	86.6
	bZIP	bZIP transcription factor		
<u> </u>		DZIP transcription factor	0.035	13.1
	sugar_tr	Sugar (and other) transporter	0.003	-101.5
	RhoGAP	RhoGAP domain	8.9e-47	168.8
	rrm	RNA recognition motif.	1e-35	132.1
	LRR	Leucine Rich Repeat	2.le-13	58.0
1409	Nebulin_repe	Nebulin repeat	6e-54	192.6
	at _ ·			1 - 2 - 3
1410	ank	Ank repeat	1.6e-17	71.6
	Ribosomal L5	ribosomal L5P family C-terminus	8.2e-58	
	C	LIBOSOMAL DSF LAMILLY C-CERMINUS	8.2e-58	205.5
1415				l
	trypsin	Trypsin	4.7e-85	270.4
	aminotran_1	Aminotransferases class-I	4.4e-05	-91.2
	S1	S1 RNA binding domain	1.6e-07	33.1
	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger		1
	ArfGap		3.2e-17	70.6
172/	AL LOAD	Putative GTP-ase activating	1e-37	138.8
		protein for Arf		
1428	helicase_C	Helicases conserved C-terminal	le-26	102.2
		domain		ŀ
	WD40	WD domain, G-beta repeat	3.9e-07	37.2
	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431 r	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433 (Clq	Clq domain	2.9e-16	66.2
	WD40	WD domain, G-beta repeat	1.6e-13	58.3
	Inos-1-	Myo-inositol-1-phosphate		
			7e-228	770.4
	P_synth	synthase		
	rrm	RNA recognition motif.	1.4e-34	128.3
	ig	Immunoglobulin domain	1.3e-12	45.6
1440	Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441 (Adapt CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
	Kelch	Kelch motif	0.00013	28.7
	ARID	ARID DNA binding domain		
	zf-C2H2	Zine finance Cour	1.8e-21	84.7
		Zinc finger, C2H2 type	9.4e-28	105.6
	MP-binding	AMP-binding enzyme	2.6e-07	-145.1
	crm	RNA recognition motif.	6.5e-21	82.9
	g	Immunoglobulin domain	5.6e-44	146.7
	Sialyltransf	Sialyltransferase family	5.4e-21	83.2
1455 S				
	Aldose enim	Aldoge 1_enimerace	7 00 2	
1460 A	ldose_epim	Aldose 1-epimerase	1.9e-35	131.2
1460 A	.2	C2 domain	4e-18	73.6
1460 A 1461 C 1470 T				

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
	h 2	 		† - · · · ·
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflu	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	Be-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_al	Telomere-binding protein alpha	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cy c	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Bukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain	0.084	13.8
1505	EGF	EGF-like domain	2.7e-23	90.8
1506	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.7e-21	
1508	Peptidase_M2 0	Peptidase family M20/M25/M40	2,8e-28	101.8
1511	PX	PX domain	1.9e-11	130.7
1512	Sulfatase	Sulfatase	2.8e-35 0.011	-62.3
1516 1518	Syntaxin aminotran_3	Syntaxin Aminotransferases class-III	9.7e-106	305.6
1520	+ 	pyridoxal-pho Immunoglobulin domain	0.075	11.0
1521	ig RA	Ras association (RalGDS/AF-6)	0.013	13.3
	1	domain		1 .
1521]	domain RhoGAP domain	2.5e-05	18.7
	RhoGAP	RhoGAP domain	2.5e-05 5.4e-24	18.7
1528	RhoGAP WD40	RhoGAP domain WD domain, G-beta repeat	2.5e-05 5.4e-24 7.8e-95	
1528 1535	RhoGAP WD40 IMS	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family	5.4e-24	93.1
1528 1535 1538 1539	RhoGAP WD40	RhoGAP domain WD domain, G-beta repeat	5.4e-24 7.8e-95 3.2e-27 6e-07	93.1 328.5 101.5 36.5
1528 1535 1538 1539	Rhogap WD40 IMS	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family fYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein	5.4e-24 7.8e-95 3.2e-27 6e-07	93.1 328.5 101.5 36.5
1528 1535 1538 1539	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family PYVE zinc finger Diacylglycerol kinase catalytic domain	5.4e-24 7.8e-95 3.2e-27 6e-07	93.1 328.5 101.5 36.5
1528 1535 1538 1539 1540 1653 1654	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e Amino_oxidas	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06	93.1 328.5 101.5 36.5 1184.7
1528 1535 1538 1539 1540 1653 1654	RhoGAP WD40 IMS FYVB DAGKC Ocular_alb SAP Amino_oxidas e Amino_oxidas	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family PYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43	93.1 328.5 101.5 36.5 1184.7 33.2 157.0
1528 1535 1538 1539 1540 1653 1654 1655	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e RhoGEF	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Dlacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24	93.1 328.5 101.5 36.5 1184.7 33.2 157.0
1528 1535 1538 1539 1540 1653 1654 1655	RhoGAP WD40 IMS FYVB DAGKC Ocular_alb SAP Amino_oxidas e Amino_oxidas	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43	93.1 328.5 101.5 36.5 1184.7 33.2 157.0
1528 1535 1538 1539 1540 1653 1654 1655 1656 1657 1659	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e Amino_oxidas e RhoGEF MMK HSRI UCH-2	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24 0.0011 2.5e-11	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 157.0 95.1 -45.5 51.1
1528 1535 1538 1539 1540 1653 1654 1655 1656 1657 1659	RhoGAP WD40 IMS FYVE DAGKC Ocular alb SAP Amino_oxidas e Amino_oxidas e RhoGEF MMK_HSR1 UCH-2 actin	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal bydrolase family Actin	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 3.2e-43 1.4e-24 0.0011 2.5e-11 6.6e-21	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 157.0 95.1 -45.5 51.1
1528 1535 1538 1539 1540 1653 1654 1655 1656 1657 1659	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e Amino_oxidas e RhoGEF MMK HSRI UCH-2	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24 0.0011 2.5e-11	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 157.0 95.1 -45.5 51.1
1528 1535 1538 1539 1540 1653 1654 1655 1656 1657 1659	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e RhoGEY MMK_HSR1 UCH-2 actin BAH VWa	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family fYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal bydrolase family Actin BAH domain von Willebrand factor type A domain	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24 0.0011 2.5e-11 6.6e-21 1.7e-82	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 95.1 -45.5 51.1 69.9 287.5 1909.4
1654 1655 1656 1657 1659 1660 1661 1662	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e RhoGEY MMR_HSRI UCH-2 actin BAH VWa	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family FYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal hydrolase family Actin BAH domain von Willebrand factor type A domain WD domain, G-beta repeat	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24 0.0011 2.5e-11 6.6e-21 1.7e-82 0	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 157.0 95.1 -45.5 51.1 69.9 287.5 1909.4
1528 1535 1538 1539 1540 1653 1654 1655 1656 1657 1659	RhoGAP WD40 IMS FYVE DAGKC Ocular_alb SAP Amino_oxidas e RhoGEY MMK_HSR1 UCH-2 actin BAH VWa	RhoGAP domain WD domain, G-beta repeat impB/mucB/samB family fYVE zinc finger Diacylglycerol kinase catalytic domain Ocular albinism type 1 protein SAP domain Flavin containing amine oxidase Flavin containing amine oxidase RhoGEF domain GTPase of unknown function Ubiquitin carboxyl-terminal bydrolase family Actin BAH domain von Willebrand factor type A domain	5.4e-24 7.8e-95 3.2e-27 6e-07 0 6e-06 3.2e-43 1.4e-24 0.0011 2.5e-11 6.6e-21 1.7e-82	93.1 328.5 101.5 36.5 1184.7 33.2 157.0 95.1 -45.5 51.1 69.9 287.5 1909.4

SRO ID	PFAM NAME	DESCRIPTION	p-value	PPAM
NO:	TOTAL MANS	DESCRIPTION	p-varue	SCORE
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
<u></u>	<u></u>	Organization MOdifier)) !	
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
1676	Glyco_hydro_	type Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.le-27	105.5
1681	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	B.3e-21	82.6
1719	TBC	TBC domain	1.le-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	darm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EP hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735				
	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	LRR PI-PLC-X	Phosphatidylinositol-specific phospholipase	4.6e-34 0.0023	126.6 16.1
1743	PI-PLC-X	Phosphatidylinositol-specific phospholipase Ras family	0.0023 3.7e-10	16.1 -21.3
1743 1744	PI-PLC-X ras ras	Phosphatidylinositol-specific phospholipase Ras family Ras family	0.0023 3.7e-10 3.7e-10	16.1 -21.3 -21.3
1743 1744 1745	PI-PLC-X ras ras RasGEP	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain	0.0023 3.7e-10 3.7e-10 3.2e-49	-21.3 -21.3 176.9
1743 1744 1745 1746	PI-PLC-X ras ras RasGEF adh_short	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase	3.7e-10 3.7e-10 3.2e-49 7.1e-08	16.1 -21.3 -21.3 176.9 34.6
1743 1744 1745 1746 1751	PI-PLC-X ras ras RasGEP adh_short zf-C2H2	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type	3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39	16.1 -21.3 -21.3 176.9 34.6 142.2
1743 1744 1745 1746 1751 1754	PI-FLC-X ras ras RasGEF adh_short zf-C2H2 fn3	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain	3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9
1743 1744 1745 1746 1751 1754 1756	PI-FLC-X ras ras RasGEF adh_short zf-C2H2 fn3 zf-C2H2	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type	3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1
1743 1744 1745 1746 1751 1754 1756 1758	PI-PLC-X ras ras RasGEP adh_short xf-C2H2 fn3 zf-C2H2	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif.	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2
1743 1744 1745 1746 1751 1754 1756 1758 1760	PI-FLC-X ras ras RasGRF adh_short zf-C2H2 fm3 zf-C2H2	Phosphatidylinositol-specific phospholipase Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Richard dehydrogenase Zinc finger, C2H2 type Fibronectin type III domain Zinc finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8
1743 1744 1745 1746 1751 1754 1756 1758 1760 1761	PI-FLC-X ras ras RasGRF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop	Phosphatidylinositol-specific phospholipase Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ras family Ris finger, C2H2 type Ris finger, C2H2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain	3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8
1743 1744 1745 1746 1751 1754 1756 1758 1760 1761	PI-PLC-X ras ras RasGRF adh short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop MMR_HSR1	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, CZH2 type Fibronectin type III domain Zinc finger, CZH2 type RNA recognition motif. Putative snoRNA binding domain GTPase of unknown function	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4
1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765 1769	PI-PLC-X ras ras RasGRF adh short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop Nop MMR HSR1 CN hydrolase	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, CZH2 type Fibronectin type III domain Zinc finger, CZH2 type RNA recognition motif. Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9
1743 1744 1745 1746 1751 1754 1756 1758 1760 1761	ras ras RasGRF adh_short zf-C2H2 fn3 zf-C2H2 rrm Nop Mop Mor HSR1 CN_hydrolase ank	Phosphatidylinositol-specific phospholipase Ras family Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, CZH2 type Fibronectin type III domain Zinc finger, CZH2 type RNA recognition motif. Putative snoRNA binding domain Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase Ank repeat	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.4e-41 3e-06 4.1e-07	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9 37.1
1743 1744 1745 1746 1751 1754 1756 1758 1760 1761 1765 1765 1769 1775	PI-PLC-X ras ras RasGRF adh short zf-C2H2 fn3 zf-C2H2 rrm Nop Nop Nop MMR HSR1 CN hydrolase	Phosphatidylinositol-specific phospholipase Ras family Ras family RasGEF domain short chain dehydrogenase Zinc finger, CZH2 type Fibronectin type III domain Zinc finger, CZH2 type RNA recognition motif. Putative snoRNA binding domain GTPase of unknown function Carbon-nitrogen hydrolase	0.0023 3.7e-10 3.7e-10 3.2e-49 7.1e-08 9e-39 5.5e-101 6.3e-93 0.017 6.1e-95 6.1e-95 6.4e-41 3e-06	16.1 -21.3 -21.3 176.9 34.6 142.2 348.9 322.1 21.2 328.8 328.8 149.4 -43.9

SEQ ID	PFAM NAME	DESCRIPTION .	p-value	PFAM
NO:				SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

1 2 3 3 4 5 6 6 7 7 8 8 9 100 11 1 12 13 14 15 16 17 18 19 20 21 1 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	ACID SEQUENCE 1-21 1-31 1-33 1-19 1-26 1-26 1-26 1-26 1-27 1-18 1-19 1-25 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-33 1-19 1-31 1-22 1-24	0.991 0.995 0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.989 0.989 0.932 0.938 0.941 0.972 0.964 0.973 0.964 0.953 0.935 0.935 0.936 0.937 0.964	0.955 0.944 0.736 0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-31 1-33 1-19 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-20 1-22 1-31	0.995 0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.974 0.974 0.991 0.991	0.944 0.736 0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-33 1-19 1-26 1-26 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-20 1-22 1-31 1-22 1-31	0.949 0.970 0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.941 0.953 0.961 0.995	0.736 0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-19 1-26 1-26 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.970 0.971 0.971 0.971 0.971 0.982 0.995 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935 0.935 0.935 0.974 0.961 0.995	0.951 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.959
5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-26 1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-37 1-27	0.971 0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.863 0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.995
6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-26 1-26 1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-19 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27 1-24	0.971 0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.935 0.935	0.863 0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-26 1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-32 1-22 1-27 1-24	0.971 0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.974 0.991 0.995	0.863 0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
8 9 10 11 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-26 1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-32 1-32	0.971 0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.863 0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-46 1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-32	0.982 0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.901 0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.0850 0.895
10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-21 1-23 1-25 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-32	0.991 0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.955 0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-23 1-25 1-18 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.989 0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.995	0.899 0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-25 1-18 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.955 0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.803 0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-18 1-18 1-18 1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.932 0.938 0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.625 0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.095
14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-18 1-25 1-17 1-27 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-31 1-22 1-27	0.938 0.941 0.972 0.964 0.914 0.953 0.973 0.974 0.961 0.991	0.876 0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.095
15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-25 1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.941 0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.811 0.939 0.777 0.657 0.840 0.701 0.850 0.895
16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-17 1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.972 0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.939 0.777 0.657 0.840 0.701 0.850 0.895
17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-27 1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.964 0.914 0.953 0.935 0.974 0.961 0.991	0.777 0.657 0.840 0.701 0.850 0.895 0.959
18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-16 1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.914 0.953 0.935 0.974 0.961 0.991 0.995	0.657 0.840 0.701 0.850 0.895 0.959
19 20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67	1-19 1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.953 0.935 0.974 0.961 0.991	0.840 0.701 0.850 0.895 0.959
20 21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-20 1-22 1-33 1-19 1-31 1-22 1-27	0.935 0.974 0.961 0.991 0.995	0.701 0.850 0.895 0.959
21 22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-22 1-33 1-19 1-31 1-22 1-27	0.974 0.961 0.991 0.995	0.850 0.895 0.959
22 23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-33 1-19 1-31 1-22 1-27	0.961 0.991 0.995	0.895 0.959
23 24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-19 1-3: 1-22 1-27 1-24	0.991	0.959
24 25 26 27 28 29 30 31 32 35 36 46 67 71	1-31 1-22 1-27 1-24	0.995	
25 26 27 28 29 30 31 32 35 36 46 67 71	1-22 1-27 1-24		
26 27 28 29 30 31 32 35 36 46 67 71	1-27 1-24	0.976	0.944
27 28 29 30 31 32 35 36 46 67 71	1-24		0.935
28 29 30 31 32 35 36 46 67		0.996	0.928
29 30 31 32 35 36 46 67	1-21	0.953	0.739
30 31 32 35 36 46 67 71		0.906	0.688
31 32 35 36 46 67 71	1-31	0.986	0.841
32 35 36 46 67 71	1-28	0.980	0.893
35 36 46 67 71	1-19	0.993	0.976
36 46 67 71	1-22	0.998	0.909
46 67 71	1-33	0.949	0.736
67 71	1-33	0.949	0.736
71	119	0.970	0.951
	1-25	0.968	0.848
22	1-18	0.949	0.845
	1-30	D.991	0.919
75	1-29	0.958	0.854
88.	1-20	0.986	0.945
	1~33	0.994	0.943
	1-46	0.964	0.595
	1-49	0.983	0.570
	1-26	0.978	0.885
	1-23	0.989	0.899
	1-25	0.955	0.803
	1-19	0.963	0.918
138	1-29	0.971	0.844
	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
	1-25	0.937	0.729
	1-16	0.939	0.826
	1-27	0.964	0.777
	1-21	0.945	0.825
	1-27	0.981	0.941
		0.982	0.936
		0.953	0.840
	1-28	0.975	0.916
197			u.,,10

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
199	1-20	0.935	0.701
200	1-23	0.977	0.773
206	1-30	0.984	0.890
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	
216	1-24	0.986	0.849
218	1-33	0.961	0.956
219		1	0.895
	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976 -	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
272	1-24	0,953	0.739
283	1-21	0.906	0.688
284	1-29	0.997	0.854
290	1-31	0.986	0.841
302	1-28	0.980	L
304	1-16	0.907	0.893
312	1-19		0.635
313	1-17	0.993	0.976
323	1-22	0.930	0.753
324		0.998	0.909
328	1-17	0.982	0.954
329	1-19	0.971	0.865
	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
344	1-22	0.994	0.928
345	1-17	0.966	0.687
346	1-19	0.936	0.822
347	1-22	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29		
356	1-15	0.932	0.632
357		0.994	0.969
350	1-33	0.935	0.726
	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841
		<u></u>	

7 TO 170		1	
SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
Ì	SIGNAL IN AMINO ACID SEQUENCE	SCORE)	SCORE)
366	1-21	0.916	0.820
367	1-19	0.936	0.822
368	1-29	0.972	0.874
370	1-24	0.920	0.712
371	1-24	0.961	0.773
372	1-27	0.919	0.768
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
	1-29	0.941	0.672
418	1-20	0.952	0.850
419 420	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-48	0.889	0.785
424	1-19	0.982	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.783
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27	0.888	0.597
462	1-16	0.925	0.681
486	1-27	0.972	0.845
495	1-24	0.917	0.636
498	1-26	0.993	0.890
505	1-20	0.976	0.926
507	1-17	0.966	0.687
510	1-23	0.930	0.593
	1		1

SEQ ID NO:	POSITION OF	Maxs (MAXIMUM	Monne /MIZEM
SEQ ID NO:	SIGNAL IN AMINO	SCORE)	MeanS (MEAN SCORE)
1	ACID SEQUENCE	SWAD,	SCOKE)
511	1-23	0.930	0.593
512	1-23	0.930	0.593
515	1-18	0.978	0.956
523	1-19	0.936	0.822
529	1-22	0.963	0.924
545	1-24	0.982	0.966
550	1-30	0.933	0.713
552	1-21	0.973	0.912
554	1-23	0.969	0.784
571	1-21	0.918	0.815
574	1-31	0.988	0.912
580	1-39	0.925	0,556
594	1-31	0.974	0.839
608	1-29	0.932	0.632
609	1-29	0.932	0.632
610	1-21	0.990	0.948
621	1-15	0.994	0.969
623	1-33	0.935	0.726
653	1-27	0.938	0.827
668	1-22	0.929	0.788
677	1-16	0.948	0,807
685	1-21	0.861	0.715
699	1-22	0.975	0.816
702	1-31	0.968	0.898
707	1-16	0.860	0.562
713	1-25	0.966	0.743
718	1-19	0.936	0.822
719	1-20	0.961	0.824
729	1-29	0.972	0.874
735	1-46	0.903	0.598
746	1-14	0.916	0.730
747	1-22	0.965	0.876
748	1-29	0.968	0.785
759	1-24	0.961	0.773
767	1-27	0.919	0.768
768	1-33	0.900	0.585
773	1-42	0.959	0.702
779	1-19	0.986	0.945
797	1-19	0.944	0.759
798	1-19	0.900	0.568
820	1-17	0.995	0.950
827	1-49	0.971	0.749
848	1-20	0.968	0.874
864 866	1-20	0.928	0.782
873	1-19 1-23	0.986	0.934
881	1-23	0.948	0.886
887	1-39		0.829
927	1-39	0.970	0.551
934	1-48		0.868
939		0.988	0.777
944	1-39	0.994	0.889
950	1-26	0.971	0.782
963	1-29	0.957	0.845
964	1-20		0.900
973		0.886	0.558
980	1-16	0.968	0.890
981	1-34	0.961	0.749
984	1-20	0.953	0.822
	1-12	0.938	0.780
1015	1-22	0.985	0.854
1052	1-46	0.977	0.698
1052	1-18	0.969	0.842
1065	1-20	0.927	0.867
1069	1-33	0.983	0.918
1003	1-22	0.993	0.935

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	Means (MEAN SCORE)
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1~19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-39	0.989	0.789
1142	1-33	0.897	0.570
1152	1-35	0.990	0.962
1170			0.827
	1-38	0.977	
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.967
1258	1-29	0.965	0.861
1265	1-22	0.889	0.785
1266	1-20	0.944	0.809
1276	1-48	0.982	0,862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.703
1397	1-26	0.962	
			0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	0.863
1424	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.831
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.881	0.561
1518	1-17	0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
	1-25 1-17	0.967	0.899

SEQ ID NO:	POSITION OF SIGNAL IN AMINO	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE	SCOKE)	SCORE
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 0		_			_
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	1
	sequence		l	application	
1	1787	3573	5359	784CIP2_1	1103
2	1.788	3574	5360	784CIP2_2	2673
3	1789	357,5	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562
6	1792	3578	5364	784CIP2 6	5562
7	1793	3579	5365	784CIP2 7	5562
8	1794	3580	5366	784CIP2 8	5562
9	1795	3581	5367	784CIP2 9	5563
10	1796	3582	5368	784CIP2 10	5564
11	1797	3583	5369	784CIP2 11	5565
12	1798	3584	5370	784CIP2 12	5689
13	1799	3585	5371	784CIP2 13	5729
14	1800	3586	5372	784CIP2 14	5745
15	1801	3587	5373	784CIP2 15	5777
16	1802	3588	5374	784CIP2 16	5777
17	1803	3589	5375	784CIP2 17	5789
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19	1805	3591	5377	784CIP2_19	5804
20	1806	3592	5378	784CIP2 20	5805
21	1807	3593	5379	784CIP2 21	5805
22	1808	3594	5380	784CIP2 22	5844
23	1809	3595	5381	784CIP2 23	5844
24	1810	3596	5382	784CIP2 24	5850
25	1811	3597	5383	784CIP2 25	5867
26	1812	3598	5384	784CIP2_25	5973
27	1812	3599	5385	784CIP2_28	5995
28	1814	3600	5386	784CIP2_27	5995
28	1814	3601	5387	784CIP2_28	6005
30	1815	3602	5388	784CIP2_29	6007
30		3603	5389	784CIP2 30	6007
32	1817	3604	5390	784CIP2_31	6009
	1818	·	5391	784CIP2_32	6012
33	1819	3605	5392	•••	
34	1820	3606			6015
35	1821	3607	5393	784CIP2_35	6016
36	1822	3608	5394	784CIP2_36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2 42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2 51 -	6204
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53	1839	3625	5411	784CIP2 53	6367
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55	1841	3627	5413	784CIP2 55	6442
56	1842	3628	5414	784CIP2 56	6445
57	1843	3629	5415	784CIP2_56	6457
58			5416	784CIP2_57	6458
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length nucleotide	full-	nucleotide	of contig	corresponding	U.S.S.N.
sequence	length peptide	sequence	peptide sequence	SEQ ID NO: in priority	09/488,725
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62	1848	3634	5420	784CIP2 62	6499
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64	1850	3636	5422	784CIP2 64	6505
65	1851	3637	5423	784CIP2 65	6534
66	1852	3638	5424	784CIP2 66	6534
67	1853	3639	5425	784CIP2 67	6540
68	1854	3640	5426	784CIP2 68	6550
69	1855	3641	5427	784CIP2 69	6550
70	1856	3642	5428	784CIP2 70	6592
71	1857	3643	5429	784CIP2 71	6645
72	1858	3644	5430	784CIP2 72	6671
73	1859	3645	5431	784CIP2 73	6763
74	1860	3646	5432	784CIP2 74	6763
75	1861	3647	5433	784CIP2 75	6786
76	1862	3648	5434	784CIP2 76	6824
77	1863	3649	5435	784CIP2 77	6830
78	1864	3650	5436	784CIP2 78	6831
79	1865	3651	5437	784CIP2 79	6832
80	1866	3652	5438	784CIP2 80	6834
81	1857	3653	5439	784CIP2 81	6834
82	186B	3654	5440	784CIP2 82	6835
83	1869	3655	5441	784CIP2 83	6837
84	1870	3656	5442	784CIP2 84	6843
85	1871	3657	5443	784C1P2_85	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_88	6957
89	1875	3661	5417	784CIP2_89	6961
90	1876	3662	5448	784C1P2_90	6973
91	1877	3663	5449	784CIP2_91	6973
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93	. 1879	3665	5451	784CIP2_94	7018
94	1880	3666	5452	784CIP2_95	7019
95	1881	3667	5453	784CIP2_96	7020
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102	1887 1888	3673	5459	784CIP2_102	7029
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105	1891	3677	5463	784CIP2_105 784CIP2_106	7033
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107	1893	3679	5465	784CIP2_107 784CIP2_108	7036 7039
108	1894	3680	5466	784CIP2_108 784CIP2_109	7043
109	1895	3681	5467	784CIP2_109 784CIP2_110	7043
110	1896				
111	1897	3682	5468	784CIP2_111	7046
112	1897	3683	5469	784CIP2_112	7054
113	1899	3684	5470	784CIP2_113	7061
114	1999	3685	5471	784CIP2_114	7077
		3686	5472	784CIP2_115	7092
115	1901	3687	5473	784CIP2_116	7094
116	1902	3688	5474	784CIP2_117	7106
117	1903	3689	5475	784CIP2_118	7107
118	1904	3690	5476	784CIP2_119	7111
119	1905	3691	5477	784CIP2_120	7123
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127		<u> </u>			J	7185
128					J →	7197
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131	L			L		I
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133 1919 3705 5491 784CIP2 134 7238 134 1920 3706 5492 784CIP2 135 7247 135 1921 3707 5493 784CIP2 136 7261 136 1922 3708 5494 784CIP2 137 7262 137 1923 3709 5495 784CIP2 137 7262 137 1923 3709 5495 784CIP2 139 7272 138 1924 3710 5496 784CIP2 139 7272 138 1925 3711 5497 784CIP2 140 7273 140 1926 3712 5498 784CIP2 140 7273 140 1926 3712 5498 784CIP2 141 7282 141 1927 3713 5499 784CIP2 142 7288 142 1928 3714 5550 784CIP2 143 7291 143 1929 3715 5501 784CIP2 144 7229 144 1930 3716 5502 784CIP2 145 7294 145 1931 3717 5503 784CIP2 146 7229 146 1932 3718 5504 784CIP2 147 7300 147 1933 3719 5505 784CIP2 148 7312 148 1934 3720 5506 784CIP2 149 7313 149 1935 3721 5507 784CIP2 149 7313 149 1935 3722 5508 784CIP2 149 7313 150 1936 3722 5508 784CIP2 150 7315 150 1936 3722 5508 784CIP2 150 7318 151 1937 3723 5509 784CIP2 151 73318 152 1938 3724 5510 784CIP2 153 7330 153 1599 3725 5511 784CIP2 153 7331 155 1941 3727 5513 784CIP2 154 7331 155 1941 3727 5513 784CIP2 156 7350 156 1942 3728 5514 784CIP2 156 7350 156 1944 3730 5516 784CIP2 157 7352 156 1944 3730 5516 784CIP2 156 7350 156 1944 3730 5516 784CIP2 157 7352 157 1943 3729 5511 784CIP2 157 7352 156 1944 3730 5516 784CIP2 157 7352 157 1943 3729 5511 784CIP2 157 7352 156 1944 3730 5516 784CIP2 157 7352 156 1944 3730 5516 784CIP2 157 7352 157 1943 3729 5513 784CIP2 156 7350 156 1944 3733 5519 784CIP2 157 7453 156 1948 3734 5520 784CIP2 167 7453 166 1946 3735 5521 784CIP2 167 7453 166 1953 3734 5526 784CIP2 167						
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167 1953 3739 5525 784CIP2_168 7514 168 1954 3740 5526 784CIP2_169 7520 169 1955 3741 5527 784CIP2_170 7541 170 1956 3742 5528 784CIP2_171 7570 171 1957 3743 5529 784CIP2_172 7578 172 1958 3744 5530 784CIP2_173 7583 173 1959 3745 5531 784CIP2_174 7592 174 1960 3746 5532 784CIP2_175 7601 175 1961 3747 5533 784CIP2_176 7602 176 1962 3748 5534 784CIP2_177 7608 177 1963 3749 5535 784CIP2_179 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624						
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197	1973	3759	5545	784CIP2_189	7656
188	1974	3760	5546	784CIP2_190	7657
189	1975	3761	5547	784CIP2_191	7657
190	1976	3762	5548	784CIP2_192	7662
191	1977	3763	5549	784CIP2_193	766B
192	1978	3764	5550	784CIP2_194	7673
193	1979	3765	5551	784CIP2_195	7690
194	1980	3766	5552	7040112_120	7700
195	1981	3767	5553	1 '04CIEZ_17'	7709
196	1982	3768	5554	784CIP2_198	7736
197	1983	3769	5555	784CIP2_199	7737
198	1984	3770	5556	784CIP2_200	7744
199	1985	3771	5557	784CIP2_201	7771
200	1986	3772	5558	784CIP2_202	7786
201	1987	3773	5559	784C1P2_203	7791
202	1988	3774	5560	784CIP2_204	7797
203	1989	3775	5561	784CIP2_205	7806
204	1990	3776	5562	784CIP2_206	7812
205	1991	3777	5563	784CIP2_207	7812
206	1992	3778	5564	784CIP2_208 784CIP2 209	7818 7822
207	1993 1994	3779 3780	5565 5566	784CIP2_209 784CIP2_210	7827
209	1994	3781	5567	784CIP2_210 784CIP2_211	7830
210	1995	3782	5568	784CIP2_211 784CIP2_212	7835
211	1997	3783	5569	784CIP2_212 784CIP2_214	7840
212	1998	3784	5570	784CIP2_214 784CIP2_215	7858
213	1999	3785	5571	784CIP2 216	7858
214	2000	3786	5572	784CIP2 217	7861
215	2001	3787	5573	784CIP2 218	7866
216	2002	3788	5574	784CIP2 219	7868
217	2003	3789	5575	784CIP2 220	7896
218	2004	3790	5576	784CIP2 221	7898
219	2005	3791	5577	784CIP2 222	7900
220	2006	3792	5578	784CIP2 223	7906
221	2007	3793	5579	784CYP2 224	7908
222	2008	3794	5580	784CIP2 225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2_242	8132
240	2026	3812	5598	784CIP2_243	8137
241	2027	3813	5599	784CIP2_244	8137
242	2028	3814	5600	784CIP2_245	8159
243	2029	3815	5501	784CIP2_246	8159
244	2030	3816	5602	784CIP2_247	8161
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247	2033	3819	5605	784CIP2_250	8200
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249	2035	3821	5607	784CIP2 252	8220
250	2036	3822	5608	784CIP2 253	8238
251	2037	3823	5609	784CIP2 254	8254
252	2038	3824	5610	784CIP2 255	8255
253	2039	3825	5611	784CIP2 256	8288
254	2040	3826	5612	784CIP2 257	
255	2041	3827		. —	8296
256	2041		5613	784CIP2_258	8329
	1	3828	5614	784CIP2_259	8362
257	2043	3829	5615	784CIP2_260	8429
258	2044	3830	5616	784CIP2_261	8436
259	2045	3831	5617	784CIP2_262	8448
260	2046	3832	5618	784CIP2 263	8472
261	2047	3833	5619	784CIP2 264	8502
262	2048	3834	5620	784CIP2 265	8504
263	2049	3835	5621	784CIP2 266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_268	
266	2052			L ~	8515
		3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
270	2056	3842	5628	784CIP2_274	8539
271	2057	3843	5629	784CIP2 275	8541
272	2058	3844	5630	784CIP2 276	8543
273	2059	3845	5631	784CIP2 277	8593
274	2060	3846	5632	784CIP2 278	8595
275	2061	3847	5633	784CIP2 279	8615
276	2062	3848	5634	784CIP2_279	8620
277	2063	3849	5635	784CIP2_280	
278	2064	3850	5636		8621
279				784CIP2_282	8623
	2065	3851	5637	784CIP2_283	8625
280	2066	3852	5638	784CIP2_284	8628
281	2067	3853	5639	784CIP2_285	8628
282	2068	3854	5640	784CIP2_286	8629
283	2069	3855	5641	784CIP2_287	8630
284	2070	3856	5642	784CIP2 288	8631
285	2071	3857	5643	784CIP2 289	8633
286	2072	3858	5644	784CIP2 290	8634
287	2073	3859	5645	784CIP2 291	8635
288	2074	3860	5646	784CIP2 292	8636
289	2075	3861	5647	784CIP2 293	8659
290	2076	3862	5648	784CIP2_293 784CIP2_294	8660
291	2077	3863			L
292	2077		5649	784CIP2_295	9667
		3864	5650	784CIP2_296	8667
293	2079	3865	5651	784CIP2_297	8685
294	2080	3866	5652	784CIP2_298	8805
295	2081	3867	5653	784CIP2_299	8896
296	2082	3868	5654	784CIP2 300	8978
297	2083	3869	5655	784CIP2 301	9046
298	2084	3870	5656	784CIP2 302	9048
299	2085	3871	5657	784CIP2 303	9116
300	2086	3872	5658		
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	2087	3873	5659	784CIP2_305	9201
302	2088	3874	5660	784CIP2_306	9307
	2089	3875	5661	784CIP2_307	9321
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303 304	2090	3876	5662	784CIP2 308	9397
		3876 3877	5662 5663	784CIP2_308 784CIP2_309	9397 9405
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310	2096	3882	5668	784CIP2_314	9632
311	2097	3883	5669	784CIP2_315	9661
312	2098	3884	5670	784CIP2_316	9664
313	2099	3885	5671	784CIP2_317	9691
314	2100	3886	5672	784CIP2_318	9700
315	2101	3887	5673	784CIP2_319	9716
316	2102	3888	5674	784CIP2_320	9721
317	2103	3889	5675	784CIP2_321	9870
318	2104	3890	5677	784CIP2_322	9887
319	2105	3891 3892	5678	784CIP2_323 784CIP2_324	9923
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321	2107	3894	5680	784CIP2_325 784CIP2_326	10007
323	2109	3895	5681	784CIP2_326 784CIP2_327	10007
324	2110	3896	5682	784CIP2 327	10046
325	2111	3897	5683	784CIP2 329	10156
326	2112	3898	5684	784CIP2 330	10276
327	2113	3899	5685	784CIP2_330	10283
328	2114	3900	5606	784CIP2B 1	152
329	2115	3901	5687	784CIP2B 2	167
330	2116	3902	5688	784CIP2B 3	205
331	2117	3903	5689	784CIP2B 4	210
332	2118	3904	5690	784CIP2B 5	225
333	2119	3905	5691	784CIP2B 6	226
334	2120	3906	5692	784CIP2B 7	264
335	2121	3907	5693	784CIP2B 8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342	2128	3914	5700	784CIP2B_15	358
343	2129	3915	5701	784CIP2B_16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	. 5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919 3920	5705	784CIP2B_20	508
348	2134		5706	784CIP2B_21	515
349 350	2135	3921 3922	5707 5708	784CIP2B_22 784CIP2B_23	578 588
350	2136	3922	5709	784CIP2B_23 784CIP2B 24	588
352	2137	3923	5710	784CIP2B_24 784CIP2B_25	593
353	2138	3925	5711	784CIP2B_25	594
354	2140	3926	5712	784CIP2B_20 784CIP2B_27	619
355	2141	3927	5713	784CIP2B 28	620
356	2142	3928	5714	784CIP2B 29	654
357	2143	3929	5715	784CIP2B_29	692
358	2144	3930	5716	784CIP2B 31	753
359	2145	3931	5717	784CIP2B 32	758
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361	2147	3933	5719	784CIP2B_33	833
362	2148	3934	5720	784CIP2B 35	838
363	2149	3935	5721	784CIP2B_33	870
364	2150	3936	5722	784CIP2B_30	891
365	2151	3937	5723	784CIP2B_37	891
366	2152	3938	5724	784CIP2B 39	921
367	2153	3939	5725	784CIP2B_33	924
368	2154	3940	5726	784CIP2B 41	932
369	2155	3941	5727	784CIP2B 42	942
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	length	full-	nucleotide	of contig	corresponding	U.S.S.N.
Sequence	nucleotide	length	sequence	peptide	SEQ ID No: in	09/488,725
370 2156 3942 5728 794CIP2B 43 958 371 2157 3943 5729 794CIP2B 44 968 372 2158 3944 5736 794CIP2B 45 992 373 2159 3945 5731 784CIP2B 46 969 373 2159 3945 5731 784CIP2B 47 1074 375 2160 3946 5732 784CIP2B 48 1104 376 2162 3948 5734 784CIP2B 48 1104 377 2163 3949 5735 784CIP2B 49 1114 377 2163 3949 5735 784CIP2B 50 1144 377 2163 3949 5735 784CIP2B 50 1144 378 2164 3950 5736 784CIP2B 50 1144 379 2165 3951 5737 784CIP2B 52 1318 380 2166 3952 5738 784CIP2B 52 1318 381 2167 3953 5739 784CIP2B 52 1318 382 2168 3954 5740 784CIP2B 54 1328 383 2168 3955 5740 784CIP2B 54 1328 384 2170 3955 5741 784CIP2B 55 1436 385 2171 3957 5743 784CIP2B 56 1464 386 2172 3958 5740 784CIP2B 56 1464 386 2173 3959 5740 784CIP2B 57 1584 386 2173 3955 5741 784CIP2B 58 1617 386 2171 3957 5743 784CIP2B 58 1617 386 2171 3957 5743 784CIP2B 58 1617 386 2174 3956 5746 784CIP2B 57 1584 387 2173 3959 5745 784CIP2B 58 1617 388 2174 3960 5746 784CIP2B 56 1728 399 2176 3962 5748 784CIP2B 61 1772 399 2176 3962 5748 784CIP2B 61 1772 399 2176 3962 5748 784CIP2B 63 1668 393 2179 3964 5750 784CIP2B 63 1668 393 2179 3964 5750 784CIP2B 63 1668 393 2179 3966 5751 784CIP2B 63 1668 393 2179 3966 5751 784CIP2B 63 1668 393 2181 3967 5753 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2176 3962 5748 784CIP2B 67 1967 399 2178 3996 5751 784CIP2B 68 1952 400 2198 3997 5758 784CIP2B 67 1967 399 310 310 3966 5757 784CIP2B 67 1967 399 310 310 3966 5757 784CIP2B 67 1967 399 310 310 3966 5757 784CIP2B 67 1967 399 318 319 3965 5751 784CIP2B 67 1967 399 319 319 3965 5751 784CIP2B 67 1967 399 319 319 3965 5751 784CIP2B 67 1967 399 319 319 3965 5751 784CIP2B 67 1967 399 319 319 3965 5751 784CIP2B 67 1967 399 319 319 399 379 5768 784CIP2B 67 2256 400 219 399 399 5765 784CIP2B 97 2250 401 219 399 399 5765 784CIP2B 98 2447 411 2197 3983 5779 784CIP2B 99 2467 411 2197 3983 5779 784CIP2B 99 2467 411 2197 3983 5779 784CIP2B 99 2467	sequence	l	j	sequence	priority	ļ
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424 2210 3996 5782 784CIP2B 98 2819 425 2211 3997 5783 784CIP2B 99 2943 426 2212 3998 5784 784CIP2B 100 3137 427 2213 3999 5785 784CIP2B 101 3137 428 2214 4000 5786 784CIP2B 102 3160 429 2215 4001 5787 784CIP2B 103 3323 430 2216 4002 5788 784CIP2B 104 3360	422	2208	3994	5780	784CIP2B_96	2816
425 2211 3997 5783 784CIP2B 99 2943 426 2212 3998 5784 784CIP2B 100 3137 427 2213 3999 5785 784CIP2B 101 3137 428 2214 4000 5786 784CIP2B 102 3160 429 2215 4001 5787 784CIP2B 103 3323 430 2216 4002 5788 784CIP2B 104 3360	423	2209	3995	5781	784C1P2B_97	2818
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426 2212 3998 5784 784CIP2B 100 3137 427 2213 3999 5785 784CIP2B 101 3137 428 2214 4000 5786 784CIP2B 102 3160 429 2215 4001 5787 784CIP2B 103 3323 430 2216 4002 5788 784CIP2B 104 3360	425	2211	3997	5783	784CIP2B 99	
427 2213 3999 5785 784CIP2B 101 3137 428 2214 4000 5786 784CIP2B 102 3160 429 2215 4001 5787 784CIP2B 103 3323 430 2216 4002 5788 784CIP2B 104 3360	426	2212	3998			
428 2214 4000 5786 784CIP2B_102 3160 429 2215 4001 5787 784CIP2B_103 3323 430 2216 4002 5788 784CIP2B_104 3360	427	2213	3999			
429 2215 4001 5787 784CIP2B_103 3323 430 2216 4002 5788 784CIP2B_104 3360	428	2214				
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1 100 1 100	431	2217	4003	5789	784CIP2B 105	3362

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491					Erno -
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of full- length nucleotide sequence 494 2280 496 495 2281 4067 496 2282 4068 497 2283 4069 498 2284 4070 499 2285 4071 500 2286 4072 501 2287 504 2290 4076 505 2291 4077 506 2292 4078 507 2293 4079 508 2294 4080	NO: of contig peptide sequence 5852 5853 5854 5855 5856 5857 5858 5859 5860 5861 5862 5863 5864 5865 5866 5867	Priority docket number corresponding SEQ ID NO: in priority application 784CIP2B 168 784CIP2B 170 784CIP2B 171 784CIP2B 172 784CIP2B 173 784CIP2B 174 784CIP2B 175 784CIP2B 177 784CIP2B 177 784CIP2B 177 784CIP2B 177 784CIP2B 177 784CIP2B 177 784CIP2B 178 784CIP2B 179 784CIP2B 180 784CIP2B 180	SEQ ID NO: in U.S.S.N. 09/488,725 5686 5694 5698 5699 5712 5719 5720 5727 5730 5734 5738 5738
nucleotide sequence length peptide sequence sequence 494 2280 4066 495 2281 4067 496 2282 4068 497 2283 4069 498 2284 4070 499 2285 4071 500 2286 4072 501 2287 4073 502 2288 4074 503 2289 4075 504 2290 4076 505 2291 4077 506 2292 4078 507 2293 4079 508 2294 4080	peptide sequence 5852 5853 5854 5855 5856 5857 5858 5859 5860 5861 5862 5863 5864 5865 5866	SEQ ID NO: in priority application 784CIP2B 168 784CIP2B 170 784CIP2B 171 784CIP2B 171 784CIP2B 173 784CIP2B 175 784CIP2B 176 784CIP2B 176 784CIP2B 176 784CIP2B 177 784CIP2B 177 784CIP2B 178 784CIP2B 178 784CIP2B 178 784CIP2B 178 784CIP2B 180 784CIP2B 180 784CIP2B 181 784CIP2B 181	5686 5694 5698 5699 5712 5719 5720 5727 5730 5734 5738 5738 5739 5740
sequence peptide sequence 494 2280 4066 495 2281 4067 496 2282 4068 497 2283 4069 498 2284 4070 499 2265 4071 500 2286 4072 501 2287 4073 502 2288 4074 503 2289 4075 504 2290 4076 505 2291 4077 506 2292 4078 507 2293 4079 508 2294 4080	5852 5853 5854 5855 5856 5857 5858 5859 5860 5861 5862 5863 5864 5865 5866	priority application 784CIP2B 168 784CIP2B 169 784CIP2B 170 784CIP2B 171 784CIP2B 172 784CIP2B 173 784CIP2B 175 784CIP2B 176 784CIP2B 176 784CIP2B 177 784CIP2B 177 784CIP2B 179 784CIP2B 180 784CIP2B 180 784CIP2B 180	5686 5694 5698 5699 5712 5719 5720 5727 5730 5734 5738 5738 5739 5740
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504 2290 4076 505 2291 4077 506 2292 4078 507 2293 4079 508 2294 4080	5862 5863 5864 5865 5866 5867	784CIP2B 178 784CIP2B 179 784CIP2B 180 784CIP2B 181 784CIP2B 182	5738 5739 5740 5744
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553 2339 4125	5911	784CIP2B 228	5947
554 2340 4126	5912	784CIP2B 229	5956
555 2341 4127	5913	784CIP2B 230	5967

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of full- length nucleotide sequence	SEQ ID NO: of full- length peptide sequence 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361	SEQ ID NO: of contig nucleotide sequence 4128 4129 4130 4131 4132 4133 4134 4135 4136 4137 4138 4139 4140 4141 4142 4143 4144	SEQ ID NO: of contig peptide sequence 5914 5915 5916 5917 5918 5919 5920 5921 5922 5923 5924 5925 5926 5927 5928 5929	Priority docket number_ corresponding SBQ ID NO: in priority application 784CIP2B_232 784CIP2B_233 784CIP2B_235 784CIP2B_236 784CIP2B_236 784CIP2B_236 784CIP2B_239 784CIP2B_239 784CIP2B_240 784CIP2B_240 784CIP2B_241 784CIP2B_242 784CIP2B_243 784CIP2B_243 784CIP2B_244 784CIP2B_244 784CIP2B_244 784CIP2B_244 784CIP2B_245 784CIP2B_244 784CIP2B_244 784CIP2B_244	NO:in U.S.S.N. 09/488,725 5975 5977 5978 5979 5980 5988 5989 5991 5997 5998 6003 6004 6013 6028 6028
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696	2482	4268	6054	784CIP2B_378	6410
697	2483	4269	6055	784CIP2B_379	. 6422
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734	2520	4306	6092	784CIP2B_418	6573
735	2521	4307	6093	784CIP2B_419	6575
736	2522	4308	6094	784CIP2B_420	6577
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747	2532	4319	6105	784CIP2B 431	6634
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793	2579	4365	6151	784CIP2B 477	6825
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795	2581	4367	6153	784CIP2B 479	6839
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798	2584	4370	6156	784CIP2B 483	6854
799	2585	4371	6157	784CIP2B 484	6857
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800					

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812	259B	4384	6170	784CIP2B_497	6914
813	2599	4385	6171	784CIP2B_498	6917
814	2600	4386	6172	784CIP2B_499	6923
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816	2602	4388	6174	784CIP2B_501	6931
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863	2649	4435	6221	784CIP2B_548	7144
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913	2699	4485	6271	784CIP2B_600	7381
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923	2709	4495	6281	784CIP2B_610	7406
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927	2713	4499	6285	784CIP2B 614	

of full-length length peptide sequence Polymer Polym	SEQ ID NO:	SEO ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
Longth Roughest	_				· -	1
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932 2718 4505 6291 784CIP28 619 7423 934 2720 4506 6292 784CIP28 621 7428 934 2720 4506 6292 784CIP28 621 7428 935 2721 4507 6223 784CIP28 621 7428 936 2722 4508 6294 784CIP28 622 7427 937 2723 4508 6294 784CIP28 623 7428 938 2724 4510 6296 784CIP28 624 7430 938 2724 4510 6296 784CIP28 624 7430 939 2725 4511 6297 784CIP28 627 7439 940 2726 4512 6298 784CIP28 626 7437 940 2726 4512 6298 784CIP28 628 7439 941 2727 4513 6298 784CIP28 628 7440 942 2728 4514 6300 784CIP28 628 7440 942 2728 4514 6300 784CIP28 628 7440 942 2728 4515 6301 784CIP28 628 7440 943 2729 4515 6301 784CIP28 629 7459 944 2730 4516 6302 784CIP28 632 7459 946 2732 4518 6304 784CIP28 632 7459 947 2733 4519 6305 784CIP28 632 7459 948 2734 4520 6306 784CIP28 632 7459 949 2735 4521 6307 784CIP28 633 7454 950 2736 4522 6308 784CIP28 634 7457 950 2736 4522 6308 784CIP28 634 7457 951 2737 4523 6309 784CIP28 634 7457 952 2738 4524 6310 784CIP28 635 7459 953 2739 4525 6311 784CIP28 637 7463 952 2738 4524 6310 784CIP28 637 7463 953 2739 4526 6312 784CIP28 633 7466 953 2739 4526 6312 784CIP28 633 7466 953 2739 4526 6312 784CIP28 633 7469 954 2741 4527 6313 784CIP28 641 7481 955 2741 4527 6313 784CIP28 641 7481 955 2741 4528 6310 784CIP28 643 7482 959 2745 4534 6530 784CIP28 643 7482 959 2745 4534 6310 784CIP28 641 7481 956 2742 4528 6311 784CIP28 641 7481 957 2743 4529 6315 784CIP28 641 7481 958 2748 4530 6316 784CIP28 643 7482 959 2745 4531 6317 784CIP28 641 7481 958 2748 4530 6316 784CIP28 645 7485 959 2745 4531 6317 784CIP28 646 7485 959 2745 4531 6317 784CIP28 647 7483 968 2748 4530 6316 784CIP28 646 7485 959 2745 4533 6319 784CIP28 646 7485 959 2745 4533 6319 784CIP28 646 7485 959 2745 4533 6319 784CIP28 646 7485 968 2752 4538 634 784CIP28 646 7485 968 2754 4530 6326 784CIP28 657 7551 968 2758 4544 6330 784CIP28 656 7559 979 2756 4542 6338 784CIP28 657 7551 971 2767 4553 633 784CIP28 657 7551 972 2768 4544 6330 784CIP28 657 7551 973 2758 4544 6330 784CIP28 657 7551 974 2756 4555 6338 784CIP28 657 7551 975 2766 4552 638 784CIP28 657 7552 977 2765 4558	930		4502	6288	784CIP2B_617	7422
933 2719 4505 6291 784CIP23 620 7424 934 2720 4506 6292 784CIP23 620 7428 935 2721 4507 6293 784CIP23 622 7427 936 2722 4508 6294 784CIP23 622 7428 937 2723 4509 6295 784CIP23 622 7428 938 2724 4510 6295 784CIP23 623 7428 939 2725 4511 6297 784CIP23 625 7435 939 2725 4511 6297 784CIP23 625 7435 940 2726 4512 6298 784CIP23 627 7439 941 2727 4513 6299 784CIP23 627 7439 941 2727 4513 6299 784CIP23 628 7440 942 2728 4514 6300 784CIP23 629 7440 942 2728 4515 6301 784CIP23 629 7450 944 2730 4516 6302 784CIP23 631 7450 945 2731 4517 6303 784CIP23 632 7452 946 2732 6518 6304 784CIP23 631 7451 947 2733 4519 6306 784CIP23 632 7452 948 2734 4520 6306 784CIP23 632 7452 949 2735 4521 6307 784CIP23 636 7461 950 2736 4522 6308 784CIP23 636 7461 950 2736 4522 6309 784CIP23 637 7463 951 2737 4523 6309 784CIP23 636 7461 950 2736 4522 6308 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4522 6309 784CIP23 636 7461 950 2736 4525 6311 784CIP23 636 7461 950 2736 4525 6311 784CIP23 637 7463 951 2737 4523 6309 784CIP23 638 7466 953 2738 4526 6312 784CIP23 638 7466 953 2738 4527 6313 784CIP23 639 7469 953 2738 4526 6312 784CIP23 639 7469 953 2738 4527 6311 784CIP23 630 7469 954 2740 4526 6312 784CIP23 630 7469 955 2744 4530 6316 784CIP23 630 7469 956 2742 4528 631 784CIP23 630 7469 957 2743 4529 6315 784CIP23 630 7469 958 2744 4530 6316 784CIP23 630 7469 959 2755 4541 4527 6313 784CIP23 640 7473 958 2744 4530 6316 784CIP23 640 7473 958 2744 4530 6316 784CIP23 640 7473 959 2755 4541 6327 634CIP23 640 7473 959 2756 4542 6328 784CIP23 640 7459 966 2752 4538 634 784CIP23 640 7559 979 2756 4541 6327 784CIP23 640 7559 979 2756 4546 6332 784CIP23 660 7559 979 2756 4546 6332 784CIP23 660 7559 979 2756 4546 6332 784CIP23 660 7559 979 2756 4546 6332 784CIP23 660 7559 979 2756	931	2717	4503	6289	784CIP23_618	7422
934 2720 4506 6392 784CIP2B 631 7426 935 2721 4507 6293 784CIP2B 631 7426 936 2722 4508 6394 784CIP2B 632 7427 937 2723 4509 6295 784CIP2B 624 7430 938 2724 4510 6296 784CIP2B 624 7430 939 2725 4511 6297 784CIP2B 626 7437 940 2726 4512 6298 784CIP2B 626 7437 940 2726 4512 6298 784CIP2B 626 7437 941 2727 4513 6299 784CIP2B 626 7437 941 2727 4513 6299 784CIP2B 626 7439 942 2728 4514 6300 784CIP2B 629 7440 943 2729 4515 6301 784CIP2B 629 7440 944 2730 4516 6302 784CIP2B 630 7450 945 2731 4517 6303 784CIP2B 632 7459 946 2732 4518 6304 784CIP2B 632 7459 947 2733 4519 6305 784CIP2B 632 7459 948 2734 4520 6306 784CIP2B 632 7459 949 2735 4511 6307 784CIP2B 632 7459 949 2735 4521 6307 784CIP2B 634 7457 948 2734 4520 6306 784CIP2B 634 7457 949 2735 4521 6307 784CIP2B 634 7457 950 2736 4522 6308 784CIP2B 634 7465 951 2737 4523 6309 784CIP2B 637 7463 952 2738 4524 6310 784CIP2B 639 7466 953 2739 4526 6312 784CIP2B 639 7466 953 2739 4526 6312 784CIP2B 639 7466 953 2739 4526 6312 784CIP2B 639 7466 955 2741 4520 6309 784CIP2B 639 7466 955 2742 4528 6314 784CIP2B 631 7463 955 2741 4520 6306 784CIP2B 633 7469 956 2742 4528 6314 784CIP2B 641 7481 957 2743 4529 6315 784CIP2B 642 7482 957 2743 4529 6315 784CIP2B 642 7482 959 2745 4531 6317 784CIP2B 643 7463 959 2745 4531 6317 784CIP2B 647 7481 964 2757 448 4530 6316 784CIP2B 647 7482 956 2742 4528 6314 784CIP2B 647 7482 957 2743 4529 6315 784CIP2B 647 7482 958 2741 4530 6316 784CIP2B 647 7482 966 2752 4538 6324 784CIP2B 656 7485 968 2745 4531 6317 784CIP2B 646 7485 969 2755 4544 4530 6316 784CIP2B 646 7485 960 2746 4532 6313 784CIP2B 656 7482 961 2747 4533 6319 784CIP2B 656 7559 962 2758 4544 6330 784CIP2B 656 7559 963 2745 4538 6324 784CIP2B 656 7559 979 2756 4541 6327 784CIP2B 656 7559 979 2756 4541 6327 784CIP2B 656 7559 979 2756 4544 6530 784CIP2B 656 7559 979 2756 4544 6530 784CIP2B 656 7559 979 2756 4546 6332 784CIP2B 656 7559 979 2756 4546 6352 784CIP2B 656 7559 979 2756 4551 6337 784CIP2B 656 7559 984 2770 4555 634 784CIP2B 666 7557 984 2770 4556 634 784CIP2B 667 7559 986		1	4504	6290	784CIP2B_619	7423
935 2721 4507 6293 784CIP2B 622 7427 936 2722 4508 6294 784CIP2B 622 7428 937 2723 4509 6295 784CIP2B 624 7430 938 2724 4510 6296 784CIP2B 624 7430 938 2724 4510 6296 784CIP2B 626 7437 940 2726 4511 6297 784CIP2B 626 7437 940 2726 4512 6299 784CIP2B 626 7437 941 2727 4513 6299 784CIP2B 627 7439 941 2727 4513 6299 784CIP2B 627 7439 942 2728 4514 6500 784CIP2B 629 7442 943 2729 4515 6301 784CIP2B 639 7442 943 2729 4515 6301 784CIP2B 630 7450 944 2730 4516 6302 784CIP2B 631 7451 945 2731 4517 6303 784CIP2B 632 7452 946 2732 4518 6304 784CIP2B 631 7451 946 2732 4518 6304 784CIP2B 631 7451 947 2733 4519 6305 784CIP2B 634 7457 948 2734 4520 6306 784CIP2B 636 7461 949 2735 4521 6307 784CIP2B 637 7463 951 2737 4523 6306 784CIP2B 637 7463 951 2737 4523 6309 784CIP2B 637 7463 951 2737 4523 6309 784CIP2B 637 7463 952 2738 4524 6310 784CIP2B 637 7463 953 2739 4525 6311 784CIP2B 637 7463 954 2740 4526 6312 784CIP2B 637 7463 955 2744 4520 6306 784CIP2B 637 7463 955 2744 4520 6312 784CIP2B 641 7481 956 2742 4528 6310 784CIP2B 641 7481 957 2743 4529 6315 784CIP2B 641 7481 958 2744 4530 6316 784CIP2B 641 7481 958 2744 4530 6316 784CIP2B 641 7481 958 2744 4530 6316 784CIP2B 647 743 958 2745 4531 6317 784CIP2B 647 743 959 2746 4532 6318 784CIP2B 647 7482 956 2746 4532 6318 784CIP2B 647 7482 957 2743 4529 6315 784CIP2B 647 7482 958 2744 4530 6316 784CIP2B 646 7473 961 2747 4533 6319 784CIP2B 646 7485 961 2747 4533 6329 784CIP2B 645 7485 962 2748 4530 6316 784CIP2B 645 7485 963 2746 4532 6318 784CIP2B 646 7491 964 2753 4536 6322 784CIP2B 656 7519 970 2756 4542 638 784CIP2B 656 7559 971 2753 4538 6324 784CIP2B 656 7559 971 2753 4538 6324 784CIP2B 656 7559 972 2758 4544 630 6326 784CIP2B 656 7559 973 2758 4554 6336 6324 784CIP2B 656 7559 974 2753 4539 6325 784CIP2B 656 7559 975 2754 4556 6332 784CIP2B 656 7559 977 2756 4546 6332 784CIP2B 656 7559 979 2756 4546 6332 784CIP2B 656 7559 979 2756 4546 6332 784CIP2B 656 7559 979 2756 4546 6332 784CIP2B 656 7559 980 2756 4556 6351 784CIP2B 667 7559 980 2756 4558 6344 784CIP2B 677 7559 980 2	933	2719	4505	6291	784CIP23_620	7424
9316 2722 4508 6294 784CIP2B 623 7428 937 2723 4509 6295 784CIP2B 624 7430 938 2724 4510 6296 784CIP2B 624 7430 938 2725 4511 6297 784CIP2B 626 7437 939 2725 4511 6297 784CIP2B 626 7437 940 2726 4512 6298 784CIP2B 626 7437 941 2727 4513 6299 784CIP2B 628 7430 941 2727 4513 6299 784CIP2B 628 7430 942 2728 4514 6500 784CIP2B 628 7430 942 2728 4515 6301 784CIP2B 630 7450 944 2730 4516 6302 784CIP2B 630 7450 944 2730 4516 6302 784CIP2B 632 7452 945 2731 4517 6303 784CIP2B 632 7452 946 2732 4518 6304 784CIP2B 632 7452 947 2733 4519 6305 784CIP2B 634 7457 948 2734 4520 6306 784CIP2B 634 7457 948 2734 4520 6306 784CIP2B 636 7461 950 2736 4522 6308 784CIP2B 637 7463 951 2737 4523 6309 784CIP2B 638 7466 952 2738 4524 6310 784CIP2B 639 74669 953 2739 4526 6311 784CIP2B 639 7469 953 2739 4526 6311 784CIP2B 639 7469 954 2744 4530 6314 784CIP2B 644 7483 955 2741 4529 6314 784CIP2B 644 7483 956 2742 4528 6314 784CIP2B 644 7483 958 2744 4530 6316 784CIP2B 647 7482 958 2744 4530 6316 784CIP2B 647 7482 958 2745 4531 6317 784CIP2B 647 7482 958 2746 4532 6318 784CIP2B 647 7482 958 2746 4532 6318 784CIP2B 647 7482 958 2745 4531 6317 784CIP2B 647 7481 956 2746 4532 6315 784CIP2B 647 7481 960 2746 4532 6315 784CIP2B 647 7487 961 2746 4533 6319 784CIP2B 647 7487 962 2748 633 6320 784CIP2B 648 7482 963 2749 4536 6312 784CIP2B 647 7487 964 2750 4536 6322 784CIP2B 648 7482 965 2751 4531 6317 784CIP2B 647 7487 966 2746 4532 6318 784CIP2B 647 7487 967 2733 4529 6315 784CIP2B 647 7487 968 2745 4531 6317 784CIP2B 647 7487 969 2755 4541 6327 784CIP2B 656 7518 969 2755 4541 6327 784CIP2B 656 7518 969 2755 4541 6337 6321 784CIP2B 657 7581 969 2755 4541 6337 6321 784CIP2B 657 7581 969 2755 4541 6337 6321 784CIP2B 657 7581 969 2755 4541 6327 784CIP2B 656 7519 970 2756 4545 6336 784CIP2B 657 7581 971 2757 4543 6559 6342 784CIP2B 656 7519 972 2758 4545 6331 784CIP2B 657 7551 973 2759 4545 6331 784CIP2B 656 7557 974 2763 4553 6339 784CIP2B 666 7557 975 2751 4547 6533 6339 784CIP2B 667 7559 981 2765 4554 6554 6340 784CIP2B 667 7557 982 2768 4555 634	934	2720	4506	6292	784CIP2B_621	7426
937	935	2721	4507	6293	784CIP29_622	7427
938		2722	4508	6294	784CIP2B_623	7428
939 2725 4511 6297 784CIP2B 626 7437 940 2726 4512 6298 784CIP2B 627 7439 941 2727 4513 6299 784CIP2B 628 7440 942 2728 4514 6300 784CIP2B 629 7442 943 2729 4515 6301 784CIP2B 630 7455 944 2730 4516 6302 784CIP2B 631 7451 945 2731 4517 6303 784CIP2B 631 7451 946 2732 4518 6304 784CIP2B 631 7452 947 2733 4518 6304 784CIP2B 633 7455 948 2734 4520 6306 784CIP2B 635 7459 949 2735 4521 6307 784CIP2B 635 7459 949 2735 4521 6307 784CIP2B 636 7461 955 2731 452 6308 784CIP2B 637 7463 951 2737 4523 6309 784CIP2B 638 7466 952 2738 4524 6310 784CIP2B 638 7466 953 2739 4525 6311 784CIP2B 639 7469 954 2730 4526 6312 784CIP2B 641 7481 955 2742 4528 6314 784CIP2B 641 7481 955 2742 4528 6314 784CIP2B 643 7482 956 2742 4528 6314 784CIP2B 643 7483 957 2743 4529 6316 784CIP2B 640 7473 958 2744 4530 6316 784CIP2B 640 7473 958 2744 4530 6316 784CIP2B 640 7482 959 2746 4532 6316 784CIP2B 645 7482 956 2742 4528 6314 784CIP2B 641 7481 958 2744 4530 6316 784CIP2B 645 7482 959 2746 4532 6318 784CIP2B 645 7485 959 2746 4532 6318 784CIP2B 645 7485 959 2746 4532 6318 784CIP2B 645 7485 960 2746 4532 6318 784CIP2B 645 7485 961 2747 4533 6319 784CIP2B 645 7485 964 2730 4536 6322 784CIP2B 645 7485 965 2754 4530 6316 784CIP2B 645 7485 965 2754 4530 6316 784CIP2B 645 7485 965 2764 4532 6318 784CIP2B 645 7485 966 2752 4534 4537 6320 784CIP2B 645 7485 969 2756 4542 6330 784CIP2B 656 7594 964 2730 4536 6322 784CIP2B 657 7587 964 2750 4534 6330 784CIP2B 656 7594 964 2750 4534 6330 784CIP2B 656 7594 965 2751 4537 6322 784CIP2B 656 7594 966 2752 4534 6536 6322 784CIP2B 656 7594 967 2753 453 6326 784CIP2B 656 7552 971 2756 4542 6330 784CIP2B 656 7552 973 2758 4544 6330 784CIP2B 656 7552 971 2756 4542 6330 784CIP2B 656 7552 971 2757 4543 6330 784CIP2B 656 7552 973 2758 4544 6330 784CIP2B 656 7552 973 2758 4544 6330 784CIP2B 656 7552 973 2759 4545 6337 784CIP2B 656 7552 973 2758 4546 6332 784CIP2B 656 7552 973 2759 4545 6337 784CIP2B 656 7552 973 2759 4545 6337 784CIP2B 666 7557 978 2766 4552 6338 784CIP2B 666 7557 979 2765 4554 6364 784CIP2B 666 7557 988		1		6295	784CIP2B_624	7430
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973 2759 4545 6331 784CIP29_660 7533 974 2760 4546 6332 784CIP2B_661 7535 975 2761 4547 6333 784CIP2B_662 7545 976 2762 4548 6334 784CIP2B_663 7546 977 2763 4549 6335 784CIP2B_664 7552 978 2764 4550 6336 784CIP2B_665 7554 979 2765 4551 6337 784CIP2B_666 7567 980 2766 4552 6338 784CIP2B_666 7567 981 2767 4553 6339 784CIP2B_668 7575 982 2768 4554 6340 784CIP2B_669 7576 983 2769 4555 6341 784CIP2B_669 7577 984 2770 4556 6342 784CIP2B_671 7579 985 2771 4557 6343 784CIP2B_672 7582	972	2758	4544	6330	784CIP2B 659	
974 2760 4546 6332 784CIP2B_661 7535 975 2761 4547 6333 784CIP2B_662 7545 976 2762 4548 6334 784CIP2B_663 7546 977 2763 4549 6335 784CIP2B_664 7552 978 2764 4550 6336 784CIP2B_665 7554 979 2765 4551 6337 784CIP2B_666 7567 980 2766 4552 6338 784CIP2B_668 7575 981 2767 4553 6339 784CIP2B_668 7575 982 2768 4554 6340 784CIP2B_669 7576 983 2769 4555 6341 784CIP2B_669 7577 984 2770 4556 6342 784CIP2B_671 7579 985 2771 4557 6343 784CIP2B_672 7582 986 2772 4558 6344 784CIP2B_674 7587	973	2759	4545	6331		7533
976 2762 4548 6334 784CIP2B_663 7546 977 2763 4549 6335 784CIP2B_664 7552 978 2764 4550 6336 784CIP2B_665 7554 979 2765 4551 6337 784CIP2B_666 7567 980 2766 4552 6338 784CIP2B_667 7569 981 2767 4553 6339 784CIP2B_668 7575 982 2768 4554 6340 784CIP2B_669 7576 983 2769 4555 6341 784CIP2B_670 7577 984 2770 4556 6342 784CIP2B_671 7579 985 2771 4557 6343 784CIP2B_672 7582 986 2772 4558 6344 784CIP2B_673 7567 987 2773 4559 6345 784CIP2B_675 7597	974	2760	4546	6332		
977 2763 4549 6335 784CIP2B 664 7552 978 2764 4550 6336 784CIP2B 665 7554 979 2765 4551 6337 784CIP2B 666 7567 980 2766 4552 6338 784CIP2B 667 7569 981 2767 4553 6339 784CIP2B 668 7575 982 2768 4554 6340 784CIP2B 669 7576 983 2769 4555 6341 784CIP2B 670 7577 984 2770 4556 6342 784CIP2B 671 7579 985 2771 4557 6343 784CIP2B 672 7582 986 2772 4558 6344 784CIP2B 673 7567 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	975	2751	4547	6333	784CIP2B_662	7545
978 2764 4550 6336 784CIP2B_665 7554 979 2765 4551 6337 784CIP2B_666 7567 980 2766 4552 6338 784CIP2B_667 7569 981 2767 4553 6339 784CIP2B_668 7575 982 2768 4554 6340 784CIP2B_669 7576 983 2769 4555 6341 784CIP2B_670 7577 984 2770 4556 6342 784CIP2B_671 7579 985 2771 4557 6343 784CIP2B_672 7582 986 2772 4558 6344 784CIP2B_673 7567 987 2773 4559 6345 784CIP2B_675 7597 988 2774 4560 6346 784CIP2B_675 7597	976	2762	4548	6334	784C1P2B_663	7546
979 2765 4551 6337 784CIP2B 666 7567 980 2766 4552 6338 784CIP2B 667 7569 981 2767 4553 6339 784CIP2B 668 7575 982 2768 4554 6340 784CIP2B 669 7576 983 2769 4555 6341 784CIP2B 670 7577 984 2770 4556 6342 784CIP2B 671 7579 985 2771 4557 6343 784CIP2B 672 7582 986 2772 4558 6344 784CIP2B 673 7567 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	977	2763	4549	6335	784CIP2B 664	7552
980 2766 4552 6338 784CIP2B_667 7569 981 2767 4553 6339 784CIP2B_668 7575 982 2768 4554 6340 784CIP2B_669 7576 983 2769 4555 6341 784CIP2B_670 7577 984 2770 4556 6342 784CIP2B_671 7579 985 2771 4557 6343 784CIP2B_672 7582 986 2772 4558 6344 784CIP2B_673 7567 987 2773 4559 6345 784CIP2B_674 7589 988 2774 4560 6346 784CIP2B_675 7597	978	2764	4550	6336	784CIP2B_665	7554
981 2767 4553 6339 784CIP2B 668 7575 982 2768 4554 6340 784CIP2B 669 7576 983 2769 4555 6341 784CIP2B 670 7577 984 2770 4556 6342 784CIP2B 671 7579 985 2771 4557 6343 784CIP2B 672 7582 986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	979	2765	4551	6337	784CIP2B 666	7567
982 2768 4554 6340 784CIP23 669 7576 983 2769 4555 6341 784CIP23 670 7577 984 2770 4556 6342 784CIP28 671 7579 985 2771 4557 6343 784CIP23 672 7582 986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	980	2766	4552	6338	784CIP23_667	7569
983 2769 4555 6341 784CIP2B 670 7577 984 2770 4556 6342 784CIP2B 671 7579 985 2771 4557 6343 784CIP2B 672 7582 986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	981	2767	4553	6339	784CIP2B 668	7575
984 2770 4556 6342 784CIP2B 671 7579 985 2771 4557 6343 784CIP23 672 7582 986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	982	2768	4554	6340	784CIP23_669	7576
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986 2772 4558 6344 784CIP2B 673 7587 987 2773 4559 6345 784CIP2B 674 7589 988 2774 4560 6346 784CIP2B 675 7597	984	2770	4556		784CIP2B 671	
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995	2781	4567	6353	784CIP2B_682	7629
996	2782	4568	6354	784CIP2B_683	7630
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1008	2794	4580	6366	784CIP2B 696	7675
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1019	2805	4591	6377	784CIP2B_706	7723
1020	2806	4592	6378	784CIP2B_707	7729
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	2812	4598	6384	784CIP2B_714	7750
1027	2813	4599	6385	784CIP2B_715	7757
	2814	4600	6386	784CIP2B_716	7759
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1056	2842	4628	6414	784CIP2B_745	7853
1057	2843	1629	6415	784CIP2B_746	7854
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	2845	4631	6417	784CIP2B_748	7862
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	2851	4637	6423	784CIP2B_754	7884
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1089	2875	4661	6447	784CIP2B 778	7957
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	2895	4681	6467	784CIP2B_798	8020
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1120	2906	4692	6478	784CIP2B_809	8051
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1126	2912	4698	6484 6485	784CIP2B_815 784CIP2B_816	8079
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1132	2918	4704	6490	784CIP2B 821	8099
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1148	2934	4720	6506	784CIP2B_837	8154
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1161	2947	4733	6519	784CIP2B 850	8190
1162	2948	4734	6520	784CIP2B 851	8190
1163	2949	4735	6521	784CIP2B 852	8192
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1165	2951	4737	6523	784CIP2B 854	8197
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1173	2959	4745	6531	784CIP2B 862	8214
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	sequence			application	
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1179	2965	4751	6537	784CIP2B_868	8229
1180	2966	4752	6538	784CIP2B_869	8232
1181	2967	4753	6539	784CIP2B_870	8236
1182	2968	4754	6540	784CIP2B_871	8239
1183	2969	4755	6541	784CIP2B_872	8244
1184	2970	4756	6542	784CIP2B_873	8245
1185	2971	4757	6543	784CIP2B_874	8248
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1187	2973	4759	6545	784CIP2B_876	8253
1188	2974	4760	6546	784CIP2B_877	8260
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1190	2976	4762	6548	784CIP2B_879	8268
1191	2977	4763	6549	784CIP2B_BB0	8270
1192	2978	4764	6550	784CIP2B_881	8272
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1194	2980	4766	6552	784CIP2B_883	8274
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nucleotide sequence length peptide sequence sequence sequence sequence peptide sequence SEQ ID NO: in priority application 1300 3086 4872 6658 784CIP2B_990 1301 3087 4873 6659 784CIP2B_991 1302 3088 4874 6660 784CIP2B_991 1303 3089 4875 6661 784CIP2B_993 1304 3090 4876 6662 784CIP2B_994 1305 3091 4877 6663 784CIP2B_995 1306 3092 4878 6664 784CIP2B_996 1307 3093 4879 6665 784CIP2B_997 1308 3094 4880 6666 784CIP2B_998 1309 3095 4881 6667 784CIP2B_999 1310 3096 4882 6668 784CIP2B_1000 1311 3097 4883 6669 784CIP2B_1001 1312 3098 4884 6670 784CIP2B_1003	8640 8643 8645 8650 8651 8654 8655 8665 8665 8668 8671 8672 8692 8706 8716
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1365	3151	4937	6723	784CIP2B 1055	9556
1366	3152	4938	6724	784CIP2B 1056	9556
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1372	3158	4944	6730	784CIP2B_1061	9622
1373	3159	4945	6731	784CIP2B 1063	9623
1374	3150	4946	6732	784CIP2B_1063	9646
1375	3161	4947	6733	784CIP2B_1064 784CIP2B_1065	9747
1376	3161	4948	6734	784CIP2B 1065	
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1377	3164	4949	6735		9785
1378	3164	4950 4951	6736	784CIP2B_1068 784CIP2B_1069	9801 9811
1380	L		6738		
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1381	3167	14953	6739	784CIP2B_1071	9854
1383	3168	4954	6740	784CIP2B_1072	9854
1383	3169 3170	4955	6741	784CIP2B_1073	9864
1385		4956	6742	784CIP2B_1074	9864
	3171	4957	6743	784CIP2B_1075	9871
1386	3172	4958	6744	784C1P2B_1076	9879
1388	3173 3174	4959	6745	784CIP2B_1077	9881
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	3175	4961	6747	784CIP2B_1079	9901
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1391	3177	4963	6749	784CIP2B_1081	9916
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	3196	4982	6768	784CTP2B_1101	10226
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1412	3198	4984	6770	784CIP2B_1103	10237
	3199	4985	6771	784CIP2B_1104	10279
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1415	3201	4987	6773	784CIP2C_2	271
1416	3202	4988	6774	784CIP2C_3	848
1417	3203	4989	6775	784CIP2C_4	849
1418	3204	4990	6776	784CIP2C_5	864
1419	3205	4991	6777	784CIP2C_6	953
2400				704GTD0G 2	980
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of full- length nucleotide sequence seq	SEQ ID NO:	SBO ID	SEQ ID NO:	SBO ID	Priority	SEQ ID
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1424 3210	nucleotide	length	sequence			
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1431 3217 5003 6789 784CIPZC 18 2905 1432 3218 5004 6790 784CIPZC 19 2948 1433 3219 5005 6791 784CIPZC 20 2956 1434 3220 5006 6792 784CIPZC 21 2959 1435 3221 5007 6793 784CIPZC 21 2959 1435 3222 5008 6793 784CIPZC 21 2959 1435 3222 5008 6794 784CIPZC 22 2966 1437 3223 5009 6795 784CIPZC 24 2979 1438 3224 5010 6795 784CIPZC 24 2979 1439 3225 5011 6797 784CIPZC 25 2985 1439 3225 5011 6797 784CIPZC 26 2987 1440 3226 5012 5798 784CIPZC 27 2993 1441 3227 5013 6799 784CIPZC 28 2993 1442 3228 5014 6800 784CIPZC 28 2993 1444 3229 5015 6801 784CIPZC 28 2993 1444 3320 5016 6802 784CIPZC 31 3056 1446 3222 5018 6804 784CIPZC 31 3056 1446 3222 5018 6804 784CIPZC 31 3056 1446 3223 5018 6804 784CIPZC 31 3357 1446 3223 5018 6804 784CIPZC 34 3432 1448 3234 5020 6806 784CIPZC 34 3432 1449 3235 5021 6807 784CIPZC 34 3432 1449 3235 5021 6807 784CIPZC 35 3438 1450 3236 5022 6808 784CIPZC 37 3466 1451 3237 5023 6809 784CIPZC 39 3466 1452 3238 5024 6810 784CIPZC 39 3466 1453 3239 5025 6811 784CIPZC 39 3466 1455 3238 5024 6810 784CIPZC 39 3466 1455 3238 5024 6810 784CIPZC 39 3466 1457 3233 5026 6807 784CIPZC 39 3466 1458 3234 5020 6808 784CIPZC 39 3466 1459 3236 5022 6808 784CIPZC 39 3466 1451 3237 5023 6809 784CIPZC 39 3463 1450 3236 5022 6808 784CIPZC 39 3466 1451 3237 5023 6809 784CIPZC 39 3466 1452 3238 5024 6810 784CIPZC 39 3466 1453 3239 5025 6811 784CIPZC 41 3466 1458 3244 5030 6816 784CIPZC 47 3491 1460 3246 5032 6808 784CIPZC 47 3491 1461 3247 5033 6819 784CIPZC 48 3488 1459 3245 5031 6807 784CIPZC 55 3468 1459 3245 5031 6807 784CIPZC 59 3564 1468 3254 5030 6816 784CIPZC 59 3581 1468 3255 5041 6827 784CIPZC 50 3553 1468 3254 5030 6816 784CIPZC 50 3553 1469 3245 5031 6807 784CIPZC 50 3553 1469 3245 5031 6807 784CIPZC 50 3553 1468 3256 5051 6807 784CIPZC 50 3553 1469 3255 5041 6827 784CIPZC 50 3553 1469 3255 5041 6827 784CIPZC 50 3553 1469 3255 5041 6827 784CIPZC 50 3553 1470 3256 5044 6830 784CIPZC 50 3553 1471 3257 5033 6039 6835 784CIPZC 50 3553 1471 3257 5036 6839 784CIPZC 60 3551 1470 3256 5044 6830 784CIPZC 57 3536 1471 3	1429	3215	5001	6787	784CIP2C_16	2901
1432 3218 5004 6790 784CIPZC 29 2948 1433 3219 5005 6791 784CIPZC 20 2956 1434 3220 5006 6792 784CIPZC 21 2959 1435 3221 5007 6793 784CIPZC 21 2959 1435 3221 5007 6793 784CIPZC 22 2966 1436 3222 5008 6794 784CIPZC 22 2966 1437 3223 5009 6795 784CIPZC 23 2966 1437 3223 5009 6795 784CIPZC 24 2970 1438 3224 5010 6796 784CIPZC 26 2987 1440 3226 5011 6797 784CIPZC 26 2987 1440 3226 5012 6799 784CIPZC 26 2987 1441 3227 5013 6799 784CIPZC 27 2993 1441 3227 5013 6799 784CIPZC 27 2993 1441 3228 5014 6600 784CIPZC 28 2993 1442 3228 5015 6801 784CIPZC 29 3017 1443 3229 5015 6801 784CIPZC 29 3017 1443 3220 5016 6802 784CIPZC 21 3050 1444 3230 5016 6802 784CIPZC 31 3357 1446 3231 5017 6803 784CIPZC 31 3357 1446 3231 5017 6803 784CIPZC 33 3357 1447 3233 5019 6805 784CIPZC 33 3351 1448 3234 5020 6806 784CIPZC 33 3359 1449 3233 5019 6805 784CIPZC 33 3359 1449 3233 5019 6805 784CIPZC 34 3432 1449 3235 5020 6806 784CIPZC 36 3439 1450 3236 5022 6806 784CIPZC 36 3439 1450 3236 5022 6806 784CIPZC 36 3439 1450 3236 5022 6808 784CIPZC 36 3439 1450 3236 5022 6808 784CIPZC 36 3439 1450 3236 5022 6808 784CIPZC 36 3439 1450 3236 5022 6808 784CIPZC 36 3439 1450 3236 5022 6808 784CIPZC 34 3432 1450 3234 5020 6806 784CIPZC 34 3432 1450 3234 5020 6806 784CIPZC 34 3434 1450 3231 5017 6807 784CIPZC 42 3467 1455 3238 5024 6807 784CIPZC 42 3467 1455 3238 5024 6807 784CIPZC 43 3466 1455 3234 5026 6801 784CIPZC 41 3466 3454 3240 5026 6801 784CIPZC 41 3466 3454 3240 5026 6801 784CIPZC 49 3494 1456 3242 5028 6804 784CIPZC 47 3491 1459 3245 5028 6801 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 47 3491 1459 3245 5034 6802 784CIPZC 56 3531 1468 3249 5035 6801 784CIPZC 56 3531 1468 3254 5040 6802 784CIPZC 56 3531 1468 3254 5040 6802 784CIPZC 56 3531 1468 3254 5040 6802 784CIPZC 56 3531 1468 3255 5041 6807 784CIPZC 56 3531 1469 3255 5	1430	3216	5002	6788	784CIP2C_17	2902
1433 3219 5005 6791 784CIP2C_20 2956 1434 3220 5006 6792 784CIP2C_21 2959 1435 3221 5007 6793 784CIP2C_22 2965 1436 3222 5008 6794 784CIP2C_22 2965 1437 3223 5009 6795 784CIP2C_24 2970 1438 3224 5010 6795 784CIP2C_25 2985 1439 3225 5011 6797 784CIP2C_25 2985 1439 3225 5011 6797 784CIP2C_25 2985 1439 3225 5011 6797 784CIP2C_26 2987 1440 3226 5012 6798 784CIP2C_27 2993 1441 3227 5013 6799 784CIP2C_27 2993 1442 3228 5014 6800 784CIP2C_28 2993 1442 3228 5014 6800 784CIP2C_28 2993 1443 3229 5015 6801 784CIP2C_30 3046 1443 3230 5616 6802 784CIP2C_31 3050 1444 3231 5017 6803 784CIP2C_32 3357 1446 3221 5018 6804 784CIP2C_32 3357 1447 3233 5019 6805 784CIP2C_33 3359 1448 3234 5020 6806 784CIP2C_34 3431 1448 3234 5020 6806 784CIP2C_34 3432 1448 3234 5020 6806 784CIP2C_34 3432 1449 3235 5021 6807 784CIP2C_34 3432 1449 3235 5021 6807 784CIP2C_34 3432 1448 3234 5020 6806 784CIP2C_34 3432 1448 3234 5020 6806 784CIP2C_34 3432 1450 3236 5022 6808 784CIP2C_36 3438 1451 3237 5023 6809 784CIP2C_36 3439 1453 3239 5025 6811 784CIP2C_36 3439 1453 3239 5025 6811 784CIP2C_40 3466 1453 3239 5025 6811 784CIP2C_41 3467 1454 3240 5026 6810 784CIP2C_47 3467 1455 3243 5029 6815 784CIP2C_47 3491 1458 3244 5030 6816 784CIP2C_47 3491 1459 3245 5031 6817 784CIP2C_48 3467 1459 3245 5031 6817 784CIP2C_48 3467 1459 3245 5031 6817 784CIP2C_48 3467 1459 3245 5031 6817 784CIP2C_48 3467 1459 3245 5031 6817 784CIP2C_48 3493 1460 3246 5032 6818 784CIP2C_55 3511 1467 3253 5049 6825 784CIP2C_56 3551 1468 3254 5031 6827 784CIP2C_56 3551 1468 3254 5031 6817 784CIP2C_56 3551 1469 3255 5041 6827 784CIP2C_56 3551 1469 3266 5052 6831 784CIP2C_56 3551 1469 3255 5041 6827 784CIP2C_56 3551 1470 3256 5046 6831 784CIP2C_56 3551 1469 3256 5051 6831 784CIP2C_56 3551 1469 3255 5041 6827 784CIP2C_56 3551 1469 3255 5041 6827 784CIP2C_56 3551 1471 3257 5043 6839 784CIP2C_56 3551 1473 3258 5044 6830 784CIP2C_56 3551 1479 3256 5051 6837 784CIP2C_56 3551 1479 3256 5052 6838 784CIP2C_56 3551 1479 3256 5054 6837 784CIP2C_56 3551 1479 3256 5054 6837 784CIP2C_56 3551 1479 3265 5	1431	3217	5003	6789	784CIP2C_18	2905
1414 3220 5006 6792 784CIP2C 21 2959 1435 3221 5007 6793 784CIP2C 21 2959 1436 3222 5008 6794 784CIP2C 23 2966 1437 3223 5009 6795 784CIP2C 24 2970 1438 3224 5010 6795 784CIP2C 24 2970 1439 3224 5011 6797 784CIP2C 26 2985 1439 3225 5011 6797 784CIP2C 26 2987 1440 3226 5012 6799 784CIP2C 27 2993 1441 3227 5013 6799 784CIP2C 28 2993 1442 3228 5014 6800 784CIP2C 28 2993 1443 3229 5015 6800 784CIP2C 29 3017 1444 3230 5016 6800 784CIP2C 30 3046 1445 3231 5017 6803 784CIP2C 31 3050 1445 3231 5017 6803 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 32 3357 1448 3234 5020 6805 784CIP2C 33 3359 1449 3235 5021 6807 784CIP2C 35 3438 1449 3235 5021 6807 784CIP2C 35 3438 1449 3235 5021 6807 784CIP2C 35 3438 1450 3236 5022 6808 784CIP2C 35 3438 1451 3237 5023 6809 784CIP2C 35 3438 1452 3238 5024 6810 784CIP2C 39 3465 1453 3239 5025 6811 784CIP2C 40 3466 1452 3234 5020 6808 784CIP2C 39 3467 1456 3242 5028 6814 784CIP2C 43 3466 1457 3243 5029 6813 784CIP2C 44 3466 1458 3244 5030 6816 784CIP2C 45 3488 1458 3244 5030 6816 784CIP2C 47 3491 1460 3246 5032 6818 784CIP2C 55 3496 1461 3247 5033 6819 784CIP2C 55 3531 1468 3255 5031 6817 784CIP2C 55 3531 1468 3255 5036 6822 784CIP2C 55 3531 1468 3255 5036 6822 784CIP2C 56 3551 1469 3255 5041 6820 784CIP2C 56 3551 1469 3255 5041 6820 784CIP2C 56 3551 1469 3255 5041 6820 784CIP2C 56 3551 1470 3256 5042 6834 784CIP2C 56 3551 1470 3256 5042 6832 784CIP2C 56 3551 1470 3256 5042 6832 784CIP2C 56 3551 1476 3255 5045 6831 784CIP2C 66 3551 1477		1	5004	6790	784CIP2C_19	2948
1415 3221 5008 6794 784CIP2C 22 2965 1416 3222 5008 6794 784CIP2C 23 2966 1417 3223 5009 6795 784CIP2C 24 2970 1418 3224 5010 6796 784CIP2C 25 2965 1419 3225 5011 6796 784CIP2C 25 2965 1419 3226 5012 6799 784CIP2C 27 2987 1440 3226 5013 6799 784CIP2C 27 2993 1441 3227 5013 6799 784CIP2C 27 2993 1442 3228 5014 6800 784CIP2C 29 2093 1443 3229 5015 6801 784CIP2C 29 3017 1444 3230 5016 6800 784CIP2C 29 3017 1444 3230 5016 6800 784CIP2C 31 3050 1444 3231 5016 6802 784CIP2C 31 3050 1444 3231 5016 6802 784CIP2C 31 3050 1445 3231 5017 6803 784CIP2C 31 3050 1446 3232 5018 6804 784CIP2C 33 3357 1446 3232 5018 6804 784CIP2C 33 3357 1447 3233 5019 6805 784CIP2C 34 3432 1448 3234 5020 6806 784CIP2C 33 3438 1449 3235 5021 6807 784CIP2C 36 3439 1449 3235 5021 6807 784CIP2C 36 3439 1450 3236 5022 6808 784CIP2C 36 3439 1451 3237 5023 6809 784CIP2C 40 3466 1452 3238 5024 6810 784CIP2C 40 3466 1453 3239 5025 6811 784CIP2C 41 3467 1454 3240 5026 6812 784CIP2C 41 3467 1455 3241 5027 6813 784CIP2C 41 3467 1457 3243 5029 6815 784CIP2C 43 3467 1458 3244 5030 6816 784CIP2C 47 3481 1459 3245 5031 6809 784CIP2C 40 3466 1457 3243 5029 6815 784CIP2C 47 3481 1459 3245 5031 6810 784CIP2C 47 3461 1457 3243 5029 6815 784CIP2C 47 3491 1460 3246 5032 6818 784CIP2C 47 3491 1460 3246 5032 6818 784CIP2C 48 3488 1457 3241 5027 6813 784CIP2C 49 3494 1460 3246 5032 6818 784CIP2C 49 3494 1460 3246 5032 6818 784CIP2C 50 3494 1460 3246 5032 6818 784CIP2C 50 3494 1460 3246 5032 6818 784CIP2C 50 3494 1460 3246 5032 6818 784CIP2C 50 3531 1468 3259 5036 6822 784CIP2C 55 3531 1469 3255 5041 6827 784CIP2C 55 3531 1469 3255 5041 6827 784CIP2C 56 3531 1469 3255 5041 6827 784CIP2C 56 3551 1470 3256 5046 6830 784CIP2C 56 3551 1471 3257 5043 6839 784CIP2C 56 3551 1479 3255 5041 6827 784CIP2C 56 3551 1479 3256 5046 6830 784CIP2C 56 3551 1479 3256 5046 6830 784CIP2C 66 3551 1479 3256 5046 6830 784CIP2C 66 3551 1479 3256 5051 6837 784CIP2C 66 3551 1479 3265 5051 6837 784CIP2C 67 3583 1479 3265 5051 6837 784CIP2C 67 3583 1479 3265 5055 6841 784CIP2C 73 3506			5005	6791	784CIP2C_20	2956
1436 3222 5008 6794 784CIP2C_23 2966 1437 3223 5009 6795 784CIP2C_24 2970 1438 3224 5010 6796 784CIP2C_25 2985 1439 3225 5011 6797 784CIP2C_26 2987 1440 3226 5012 6798 784CIP2C_26 2987 1441 3227 5013 6799 784CIP2C_28 2993 1441 3227 5013 6799 784CIP2C_28 2993 1442 3228 5014 6800 784CIP2C_28 2993 1443 3229 5015 6801 784CIP2C_28 3017 1443 3229 5015 6801 784CIP2C_30 3046 1444 3230 5016 6802 784CIP2C_31 3050 1445 3231 5017 6803 784CIP2C_31 3050 1446 3232 5018 6804 784CIP2C_31 3055 1446 3232 5018 6804 784CIP2C_32 3357 1448 3233 5019 6805 784CIP2C_33 3359 1449 3235 5020 6806 784CIP2C_35 3439 1449 3235 5020 6806 784CIP2C_35 3439 1449 3235 5020 6806 784CIP2C_35 3439 1449 3235 5020 6806 784CIP2C_36 3439 1450 3236 5022 6808 784CIP2C_39 3463 1451 3237 5023 6809 784CIP2C_40 3466 1453 3239 5025 6811 784CIP2C_41 3466 1453 3239 5025 6811 784CIP2C_41 3466 1454 3240 5026 6812 784CIP2C_41 3466 1455 3243 5028 6814 784CIP2C_42 3467 1456 3242 5028 6814 784CIP2C_43 3481 1457 3243 5029 6815 784CIP2C_44 3485 1458 3244 5030 6816 784CIP2C_45 3481 1459 3244 5030 6816 784CIP2C_45 3481 1459 3245 5031 6817 784CIP2C_45 3481 1459 3244 5030 6816 784CIP2C_45 3481 1459 3245 5031 6817 784CIP2C_45 3481 1460 3246 5032 6818 784CIP2C_48 3493 1461 3247 5033 6819 784CIP2C_55 3496 1462 3248 5030 6816 784CIP2C_55 3496 1463 3249 5035 6821 784CIP2C_55 3496 1464 3250 5036 6822 784CIP2C_55 3531 1468 3255 5041 6827 784CIP2C_55 3531 1469 3255 5041 6827 784CIP2C_55 3531 1469 3255 5041 6827 784CIP2C_56 3531 1470 3255 5041 6827 784CIP2C_56 3531 1471 3257 5043 6829 784CIP2C_56 3531 1473 3259 5045 6831 784CIP2C_56 3551 1473 3259 5045 6831 784CIP2C_56 3551 1479 3256 5046 6832 784CIP2C_56 3551 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3256 5046 6830 784CIP2C_56 3553 1479 3265 5051 6837 784CIP2C_56 3553 1479 3266 5052 6838 784CIP2C_56 3553 1479 3266 5052 6838 784CIP2C_56 3553 1479 3266 5	1434	3220	5006	6792	784CIP2C_21	2959
1437 3223 5009 6795 784CIP2C 24 2970 1438 3224 5010 6796 784CIP2C 25 2985 1439 3225 5011 6797 784CIP2C 26 2987 1440 3226 5012 6798 784CIP2C 27 2993 1441 3227 5013 6799 784CIP2C 27 2993 1441 3228 5014 6800 784CIP2C 28 2993 1442 3228 5014 6800 784CIP2C 29 3017 1443 3229 5015 6801 788CIP2C 31 3050 1444 3230 5016 6802 784CIP2C 31 3055 1445 3231 5017 6803 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 33 3353 1447 3233 5019 6805 784CIP2C 33 3353 1449 3235 5020 6806 784CIP2C 35 3438 1449 3235 5021 6807 784CIP2C 36 3439 1450 3236 5022 6808 784CIP2C 36 3439 1451 3237 5023 6809 784CIP2C 39 3463 1452 3238 5024 6810 784CIP2C 41 3466 1453 3239 5025 6811 784CIP2C 42 3467 1454 3240 5026 6812 784CIP2C 41 3466 1455 3241 5027 6813 784CIP2C 43 3483 1456 3242 5028 6814 784CIP2C 44 3483 1457 3243 5029 6815 784CIP2C 43 3469 1459 3245 5031 6817 784CIP2C 49 3494 1460 3246 5032 6818 784CIP2C 49 3494 1461 3247 5033 6819 784CIP2C 49 3494 1462 3248 5034 6820 784CIP2C 53 3493 1463 3249 5035 6821 784CIP2C 53 3495 1464 3250 5036 6822 784CIP2C 53 3503 1465 3251 5037 6823 784CIP2C 59 3494 1467 3253 5039 6825 784CIP2C 59 3494 1468 3254 5040 6826 784CIP2C 59 3541 1469 3255 5041 6827 784CIP2C 59 3541 1469 3255 5041 6827 784CIP2C 59 3551 1469 3255 5041 6827 784CIP2C 66 3551 1470 3256 5042 6828 784CIP2C 59 3548 1471 3257 5043 6835 784CIP2C 66 3574 1476 3263 5045 6831 784CIP2C 69 3623 1479 3265 5046 6832 784CIP2C 66 3573 1479 3265 5046 6832 784CIP2C 69 3623 1479			5007	6793	784CIP2C_22	2965
1438 3224 5010 6796 784CIP2C 25 2985 1439 3225 5011 6797 784CIP2C 26 2987 1440 3226 5012 6798 784CIP2C 27 2993 1441 3227 5013 6799 784CIP2C 28 2993 1441 3227 5013 6799 784CIP2C 28 2993 1442 3228 5014 6800 784CIP2C 29 3017 1443 3229 5015 6801 784CIP2C 30 3046 1444 3230 5016 6802 784CIP2C 31 3050 1445 3231 5017 6803 784CIP2C 31 3051 1446 3232 5018 6804 784CIP2C 31 3357 1446 3232 5018 6804 784CIP2C 33 3357 1447 3233 5019 6805 784CIP2C 34 3432 1449 3233 5019 6805 784CIP2C 34 3432 1449 3235 5021 6807 784CIP2C 36 3439 1450 3236 5022 6808 784CIP2C 36 3439 1450 3236 5022 6808 784CIP2C 39 3466 1451 3237 5023 6809 784CIP2C 40 3466 1452 3238 5024 6810 784CIP2C 41 3466 1453 3239 5025 6811 784CIP2C 43 3466 1454 3240 5026 6812 784CIP2C 43 3466 1455 3241 5027 6813 784CIP2C 43 3468 1456 3242 5028 6814 784CIP2C 43 3468 1457 3243 5029 6815 784CIP2C 43 3468 1458 3244 5030 6816 784CIP2C 48 3493 1460 3246 5032 6818 784CIP2C 43 3468 1459 3245 5031 6807 784CIP2C 43 3468 1457 3243 5029 6815 784CIP2C 43 3468 1458 3244 5030 6816 784CIP2C 45 3488 1459 3245 5031 6817 784CIP2C 46 3488 1459 3245 5031 6817 784CIP2C 47 3491 1461 3247 5033 6819 784CIP2C 48 3493 1460 3246 5032 6818 784CIP2C 50 3494 1461 3247 5033 6819 784CIP2C 51 3496 1463 3249 5035 6821 784CIP2C 51 3494 1464 3250 5036 6822 784CIP2C 51 3494 1466 3247 5033 6819 784CIP2C 51 3494 1467 3253 5039 6827 784CIP2C 50 3495 1468 3255 5041 6827 784CIP2C 53 3503 1468 3255 5041 6827 784CIP2C 56 3531 1469 3255 5041 6827 784CIP2C 56 3531 1467 3253 5039 6825 784CIP2C 56 3531 1468 3254 5040 6826 784CIP2C 57 3536 1470 3255 5041 6827 784CIP2C 60 3551 1471 3257 5043 6829 784CIP2C 60 3551 1472 3258 5044 6830 784CIP2C 60 3551 1473 3259 5045 6831 784CIP2C 66 3551 1479 3256 5047 6833 784CIP2C 66 3551 1479 3256 5046 6832 784CIP2C 66 3551 1479 3256 5046 6830 784CIP2C 66 3551 1479 3256 5046 6830 784CIP2C 66 3557 1479 3263 5049 6835 784CIP2C 66 3557 1479 3265 5051 6837 784CIP2C 68 3566 1479 3265 5051 6837 784CIP2C 66 3573 1479 3265 5055 6841 784CIP2C 77 3586			5008	6794	784CIP2C_23	2966
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1441 3227 5013 6799 784CIP2C 28 2993 1442 3228 5014 6800 784CIP2C 29 3017 1443 3229 5015 6800 784CIP2C 29 3017 1444 3230 5016 6802 784CIP2C 31 3050 1445 3231 5017 6803 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 34 3432 1449 3233 5019 6805 784CIP2C 34 3432 1449 3233 5019 6805 784CIP2C 34 3432 1449 3235 5020 6806 784CIP2C 35 3438 1449 3235 5021 6807 784CIP2C 39 3463 1451 3237 5023 6809 784CIP2C 39 3463 1451 3237 5023 6809 784CIP2C 39 3466 1452 3238 5024 6810 784CIP2C 41 3466 1453 3239 5025 6811 784CIP2C 41 3466 1454 3240 5026 6812 784CIP2C 43 3468 1455 3241 5027 6813 784CIP2C 44 3483 1456 3242 5028 6814 784CIP2C 47 3491 1457 3243 5029 6815 784CIP2C 48 3488 1458 3244 5030 6816 784CIP2C 47 3491 1459 3245 5031 6817 784CIP2C 47 3491 1460 3246 5032 6818 784CIP2C 49 3494 1461 3247 5033 6819 784CIP2C 53 3503 1464 3229 5036 6821 784CIP2C 51 3496 1463 3249 5035 6821 784CIP2C 52 3503 1465 3225 5036 6822 784CIP2C 53 3503 1466 3259 5036 6822 784CIP2C 53 3503 1467 3253 5039 6823 784CIP2C 53 3503 1468 3259 5036 6822 784CIP2C 53 3503 1469 3255 5031 6827 784CIP2C 53 3503 1467 3253 5039 6823 784CIP2C 53 3503 1468 3259 5036 6822 784CIP2C 53 3503 1469 3255 5036 6822 784CIP2C 53 3503 1469 3255 5036 6822 784CIP2C 53 3503 1469 3255 5041 6827 784CIP2C 55 3511 1469 3255 5046 6826 784CIP2C 57 3536 1470 3256 5042 6828 784CIP2C 53 3503 1467 3253 5049 6825 784CIP2C 58 3536 1470 3256 5046 6826 784CIP2C 60 3551 1471 3257 5043 6829 784CIP2C 66 3551 1472 3258 5044 6830 784CIP2C 66 3551 1473 3259 5045 6831 784CIP2C 66 3551 1476 3265 5051 6837 784CIP2C 66 3551 1477 3266 5042 6838 784CIP2C 66 3551 1479 3266 5046 6834 784CIP2C 66 3551 1479 3266 5046 6834 784CIP2C 67 35366 1479 3266 5046 6834 784CIP2C 66 3551 1479 3266 5047 6837 784CIP2C 66 3551 1479 3266 5048 6834 784CIP2C 66 3551 1479 3266 5052 6838 784CIP2C 66 3551 1479 3266 5052 6838 784CIP2C 66 3574 1479 3266 5052 6838 784CIP2C 66 3567 1479 3266 5055 6846 6840 784CIP2C 72 36667			5011	6797	784CIP2C_26	2987
1442 3228 5014 6800 784CIP2C 29 3017 1443 3229 5015 6801 784CIP2C 30 3046 1444 3230 5016 6802 784CIP2C 31 3050 1445 3231 5017 6803 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 32 3357 1446 3232 5018 6804 784CIP2C 33 3359 1447 3233 5019 6805 784CIP2C 35 3439 1449 3234 5020 6806 784CIP2C 35 3439 1449 3235 5021 6807 784CIP2C 36 3439 1450 3236 5022 6808 784CIP2C 36 3439 1451 3237 5023 6809 784CIP2C 30 3466 1452 3238 5024 6810 784CIP2C 30 3466 1453 3239 5024 6810 784CIP2C 40 3466 1453 3239 5025 6911 784CIP2C 41 3466 1454 3240 5026 6912 784CIP2C 41 3466 1455 3241 5027 6813 784CIP2C 43 3468 1455 3241 5027 6813 784CIP2C 43 3468 1455 3241 5027 6813 784CIP2C 43 3468 1455 3244 5030 6816 784CIP2C 45 3484 1457 3243 5029 6815 784CIP2C 46 3488 1458 3244 5030 6816 784CIP2C 47 3491 1460 3246 5032 6818 784CIP2C 48 3493 1460 3246 5032 6818 784CIP2C 49 3491 1461 3247 5033 6819 784CIP2C 50 3495 1462 3248 5034 6820 784CIP2C 51 3496 1463 3249 5035 6821 784CIP2C 51 3496 1464 3250 5036 6822 784CIP2C 51 3496 1465 3251 5031 6817 784CIP2C 51 3496 1465 3251 5031 6817 784CIP2C 53 3503 1466 3252 5038 6821 784CIP2C 55 3503 1467 3253 5039 6825 784CIP2C 55 3503 1468 3259 5036 6821 784CIP2C 55 3503 1469 3255 5041 6827 784CIP2C 55 3503 1469 3255 5041 6827 784CIP2C 55 3503 1469 3255 5041 6827 784CIP2C 56 3531 1469 3250 5036 6822 784CIP2C 57 3536 1469 3255 5041 6827 784CIP2C 57 3536 1469 3255 5041 6827 784CIP2C 56 3531 1467 3253 5039 6825 784CIP2C 57 3536 1470 3256 5042 6828 784CIP2C 57 3536 1470 3256 5046 6832 784CIP2C 57 3536 1470 3256 5046 6832 784CIP2C 56 3551 1471 3257 5043 6829 784CIP2C 66 3551 1472 3258 5044 6830 784CIP2C 66 3551 1473 3259 5045 6831 784CIP2C 66 3551 1479 3265 5046 6832 784CIP2C 66 3551 1479 3265 5046 6832 784CIP2C 66 3551 1479 3265 5046 6837 784CIP2C 67 3583 1479 3265 5046 6830 784CIP2C 67 3583 1479 3265 5046 6831 784CIP2C 67 3583 1479 3265 5046 6837 784CIP2C 67 3583 1479 3265 5046 6837 784CIP2C 69 3663 1479 3266 5055 6838 784CIP2C 67 3583						2993
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1594	3380	5166	6952	784CIP2C_186	5793
1595	3381	5167	6953	784CIP2C_187	5806
1596	3382	5168	6954	784CIP2C_188	5852
1597	3383	5169	6955	784CIP2C_189	5892
1598	3384	5170	6956	784CIP2C_190	6057
1599	3385	5171	6957	784CIP2C_191	6061
1600	3386	5172	6958	784CIP2C 192	6109
1601	3387	5173	6959	784CIP2C_193	6160
1602	3388	5174	6960	784CIP2C_194	6297
1603	3389	5175	6961	784CIP2C_195	6398
1604	3390	5176	6962	784CIP2C_196	6398
	3391	5177	6963	784CIP2C_197	6415
1605					6448
1605	3392	5178	6964	784CIP2C 198	0440
	3392 3393	5178 5179	6964 6965	784CIP2C_198 784CIP2C_199	6469
1606			L		

SEQ ID NO:	SEO ID	SEO ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	i	sequence	priority	ļ
	sequence	l		application	
1610	3396	5182	6968	784CIP2C_202	6574
1611	3397	5183	6969	784CIP2C_203	6578
1612	3398	5184	6970	784C1P2C_204	6662
1613	3399	5185	6971	784CIP2C_205	6572
1614	3400	5186	6972	784C1P2C_206	6691
1615	3401	5187	6973	784CIP2C_207	6695
1616	3402	5188	6974	784CIP2C_208	6746
1617	3403	5189	6975	784CIP2C_209	6898
1618	3404	5190	6976	784CIP2C_210	6938
1619	3405	5191	6977	784CIP2C_211	6943
1620	3406	5192	6978	784CIP2C_212	7110
1621	3407	5193	6979	784CIP2C_213	7200
1622	3408	5194	6980	784CIP2C_214	7212
1623	3409	5195	6981	784CIP2C_215	7218
1624	3410	5196	6982	784CIP2C_216	7249
1625	3411	5197	6983	784CIP2C 217	7500
1626	3412	5198	6984	784CIP2C 218	7509
1627	3413	5199	6985	784CIP2C 219	7523
1628	3414	5200	6986	784CIP2C 220	7544
1629	3415	5201	6987	784CIP2C 221	7564
1630	3416	5202	6988	784CIP2C 222	7568
1631	3417	5203	6989	784CIP2C 223	7631
1632	3418	5204	6990	784CIP2C 224	7813
1633	3419	5205	6991	784CIP2C 225	7831
1634	3420	5206	6992	784CIP2C 226	7843
1635	3421	5207	6993	784CIP2C 227	7907
1636	3422	5208	6994	784CIP2C 228	7943
1637	3423	5209	6995	784CIP2C 229	8175
1638	3424	5210	6996	784CIP2C 230	8216
1639	3425	5211	6997	784CIP2C 231	8225
1640	3426	5212	6998	784CIP2C 232	8271
1641	3427	5213	6999	784CIP2C 233	8397
1642	3428	5214	7000	784CIP2C 234	8466
1643	3429	5215	7001	784CIP2C 235	8503
1644	3430	5216	7002	784CIP2C 236	8953
1645	3431	5217	7003	784CIP2C 237	9106
1646	3432	5218	7004	784CIP2C 238	9139
1647	3433	5219	7005	784CIP2C 239	9555
1648	3434	5220	7006	784CIP2C 240	9650
1649	3435	5221	7007	784CIP2C 241	9889
1650	3436	5222	7008	784CIP2C 242	9933
1651	3437	5223	7009	784CIP2C 243	9953
1652	3438	5224	7010	784CIP2C 244	9981
1653	3439	5225	7011	784CIP2D 1	746
1654	3440	5226	7012	784CIP2D 2	3558
1655	3441	5227	7013	784CIP2D 3	3558
1656	3442	522B	7014	784CIP2D 4	3633
1657	3443	5229	7014	784CIP2D 5	3658
1658	3444	5230	7016	784CIP2D 6	3732
	3445	5231	7017	784CIP2D_6	4004
1659		5232	7017	784CIP2D 7	4700
1660 1661	3446	5232	·	784CIP2D_8 784CIP2D_9	4703
	3447		7019		4774
1662	3448	5234	7020	784CIP2D 10	4894
1663	3449	5235	7021	784CIP2D 11	
1664	3450	· 5236	7022	784CIP2D_12	4918
1665	3451	5237	7023	784CIP2D_13	5159
1666	3452	5238	7024	784CIP2D_14	7443
1667	3453	5239	7025	784CIP2D_15	8673
1668	3454	5240	7026	784CIP2D_16	8679
1669	3455	5241	7027	784CIP2D_17	8727
1670	3456	5242	7028	784CIP2D_18	8734
1671	3457	5243	7029	784CIP2D_19	8756
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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1	веquence	priority	1
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1672	3458	5244	7030	784CIP2D_20	8818
1673	3459	5245	7031	784C1P2D_21	8844
1674	3460	5246	7032	784CIP2D_22	8846
1675	3461	5247	7033	784CIP2D_23	8912
1676	3462	5248	7034	784CIP2D_24 784CIP2D_25	8918
1677	3463	5249	7035 7036	784CIP2D_25 784CIP2D_26	8918 8941
1678	3464	5250 5251	7037	784CIP2D_26	8941
1679	3465	5251	7037	784C1P2D_27	8951
1680 1681	3466 3467	5252	7039	784C1P2D_28	8951
1682	3468	5254	7040	784CIP2D_29	9007
1683	3469	5255	7041	784CIP2D 31	9012
1684	3470	5256	7042	784CIP2D 32	9013
1685	3471	5257	7043	784CIP2D_32	9025
1686	3472	5258	7044	784CIP2D 34	9053
1687	3473	5259	7045	784CIP2D 35	9054
1688	3474	5260	7046	784CIP2D 36	9054
1689	3475	5261	7047	784CIP2D 37	9113
1690	3476	5262	7048	784CIP2D 38	9134
1691	3477	5263	7049	784CIP2D 39	9152
1692	3478	5264	7050	784CIP2D 40	9152
1693	3479	5265	7051	784CIP2D 41	9211
1694	3480	5266	7052	784CIP2D 42	9223
1695	3481	5267	7053	784CIP2D 43	9223
1696	3482	5268	7054	784CIP2D_44	9231
1697	3483	5269	7055	784CIP2D_45	9236
1698	3484	5270	7056	784CIP2D_46	9236
1699	3485	5271	7057	784CIP2D_47	9303
1700	3486	5272	7058	784CIP2D_48	9309
1701	3487	5273	7059	784CIP2D_49	9314
1702	3498	5274	7060	784CIP2D_50	9326
1703	3489	5275	7061	784CIP2D_51	9339
1704	3490	5276	7062	784CIP2D_52	9348
1705	3491	5277	7063	784CIP2D 53 784CIP2D 54	9376
1706	3492	5278 5279	7064 7065	784CIP2D_54 784CIP2D_55	9382
1707 1708	3493 3494	5280	7066	784CIP2D_55	9414
1709	3494	5281	7067	784CIP2D_56	9439
1710	3496	5282	7068	784CIP2D 58	9485
1711	3497	5283	7069	784CIP2D 59	9493
1712	3498	5284	7070	784CIP2D 60	9501
1713	3499	5285	7071	784CIP2D 61	9526
1714	3500	5286	7072	784CIP2D 62	9526
1715	3501	5287	7073	784CIP2D_63	9551
1716	3502	5288	7074	784CIP2D_64	9557
1717	3503	5289	7075	784CIP2D_65	9568
1718	3504	5290	7076	784CIP2D 66	9588
1719	3505	5291	7077	784CIP2D_67	9597
1720	3506	5292	7078	784CIP2D_68	9615
1721	3507	5293	7079	784CIP2D_69	9628
1722	3508	5294	7080	784CIP2D_70	9649
1723	3509	5295	7081	784CIP2D_71	9652
1724	3510	5296	7082	784CIP2D_72	9660
1725	3511	5297	7083	784CIP2D_73	9662
1726	3512	5298	7084	784CIP2D_74	9725
1727	3513	5299	7085	784CIP2D_75	9746
1728	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D_78	9790
1731	3517	5303	7089	784CIP2D_79	9842
1732	3518	5304	7090	784CIP2D_80	9842
1733	3519	5305	7091	784CIP2D_81	9848

SEO ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEO ID
of full-	NO: of	of contig	NO:	docket number	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide	1 -	sequence	priority	1 , ,
1	sequence	ľ	-	application	
1734	3520	5306	7092	784CIP2D 82	9867
1735	3521	5307	7093	784CIP2D 83	, 10010
1736	3522	5308	7094	784CIP2D 84	10011
1737	3523	5309	7095	784CIP2D 85	10052
1738	3524	5310	7096	784CIP2D 86	10057
1739	3525	5311	7097	784CIP2D 87	10085
1740	3526	5312	7098	784CIP2D 89	10139
1741	3527	5313	7099	784CIP2D 90	10142
1742	3528	5314	7100	784CIP2D 92	10165
1743	3529	5315	7101	784CIP2D 93	10173
1744	3530	5316	7102	784CIP2D 94	10173
1745	3531	5317	7103	784CIP2D 95	10273
1746	3532	5318	7104	784CIP2B 1	3121
1747	3533	5319	7105	784CIP2B 2	3628
1748	3534	5320	7105	784CIP2B_2	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIP2B 6	4467
1751	3537	5323	7108	784CIP2E 7	4865
1752	3538	5324	7110	784CIP2E 8	4916
1753	3539	5325	7111	784CIP2B_8	i 4923
1754	3540	5326	7112	784CIP2B 10	4926
1755	3541	5327	7113	784CIP2B_10	4962
1756	3542	5328	7114	784CIP2E 11 784CIP2E 12	4962
1757	3543	5329	7115	784CIP2B 13	4964
1758	3544	5330	7116	784CIP2B 13	4988
1759	3545	5331	7117	784CIP2B_14	5835
1760	3546	5332	7118	784CIP2B 15	7682
1761	3547	5333	7119	784CIP2B_17	7682
1762	3548	5334	7120	784CIP2B_17	7699
1763	3549	5335	7121	784CIP2E 19	7707
1764	3550	5336	7122	784CIP2E 20	7707
1765	3551	5337	7123	784CIP2E 21	7752
1766	3552	5338	7124	784CIP2E_21	8357
1767	3553	5339	7125	784CIP2E_22	9065
1768	3554	5340	7126	784CIP2B_23	9324
1769	3555	5341	7127	784CIP2B_24 784CIP2F 1	2976
1770	3556	5342	7128	784CIP2F 2	3559
1771	3557	5343	7128	784CIP2F_2	4021
1772	3558	5344	7130	784CIP2F_3	4474
1773	3559	5345	7131	784CIP2F_4	4566
1774	3560	5346	7132	784CIP2F 6	4705
1775	3561	5347	7132	784CIP2F 7	4705
1776	3562	5348	7133	784CIP2F_7	4707
1777	3563	5348	7134	784CIP2F 9	
1778	3564	5349	7135	784CIP2F_9 784CIP2F_10	5008
1779	3565	5350	7136		5009
1780	3566	5351		784CIP2F_11	5015
1781	3567		7138	784CIP2F_12	5015
1782		5353	7139	784CIP2F_13	7724
	3568	5354	7140	784CIP2F_14	7725
1783	3569	5355	7141	784CIP2F_15	8828
1784	3570	5356	7142	784CIP2F_16	8830
1785	3571	5357	7143	784CIP2F_17	9739
1786	3572	5358	7144	784CIP2F 18	9896

TRADOCS:1416247.1(%CS7011.DOC)

TABLE 7

	Tree Street	T 62 - 37 - 1 - 5 - 5 - 5	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
!	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	
Į.		2	L-Leucine; M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		h '	
ſ	amino acid	sequence	Codon, /=possible mucleotide deletion,
1	sequence		\=possible nucleotide insertion)
5359	337	1131	AHLSARISALILDEVAILPAPONLSVLSTNMKHLLMWSPVIAPG
ł	1	1	BTVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
1	i e	1	
Į.	į.	1	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	1	l .	TKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSGGIP
1		i	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
1	Í	ſ	VLALFAFVGPMLILVVVPLFVWKNGRLLQ/YLLLPRGGSSQTPW
1	1 .	1	· · · · · · · · · · · · · · · · · · ·
!	· .		KITQF
5360	2	1115	PRVRSSGGQBDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
1	1	J	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
I	l .	j	
1	1	İ	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
1	1	ľ	FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
1	ł	}	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYS
ı	í	1	FRSAFLTVLPDPKPPCPPVASSSSATSLPWPVVIGIPAGAVFIL
1	l	1 -	GTLLLWLCQAQKKPCTPAPAPPLPGHR>PGTARDRSGDKDLPSL
1	1	1	1
1		!	AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
ı	}]	TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDQFQPKLTDFAMAHFRSHLEHQSCTINMTSS
1	i -	}	SSKELWYMPEBYIRQGKLSIXTDVYSFGIVIMEVLTGCRVVLDD
1			
1			PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
ł	ł		AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
ł	ľ	•	PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
ſ			SQSEVMFLSLDKKPESKRNEBACNMPSSSCEESWFPKYIVPSQD
ł	l	ŀ	1 "
L			LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
5362	2	4879	SCQVEGCTRTYNSSQSIGKHMKTAHPDQYAAFKMQRKSKKGQXA
	1	1	NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
1	İ		VSPPIPPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
í	ſ	ſ	MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSL?AESSSIDL
ł	1	l	•
	1	1	PPSPADSGTNSVPSQLENNTNHYSSQIEGNTNSSFLKGGNGENA
	1		VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1	ļ	ž	RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
	ì	1	EIAQBLLQ9NGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
	1 .	i '	PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
1	•		
1	1		ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
1	1	[TVCHPNTLLINQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
İ	}	1	GLCSSSPPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
			ASKRRKKVAPPLIAPNASONLVTSDLTTMGLIAKSVEIPTTNLH
1	i	l	SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
1			
1			VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISEDNVIQNFEKT
•			LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
l			nnklpdssp\fssfisvmptesnipqse\vshkbdqiqeilegl
İ			QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSR
1			-
}			MINIQPNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPR
1	•		MILEIKKNOLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
1			EEMVKLKIKRPYGRKSQSENVPASRSTQVKKQLAMTBENKKESQ
1 .			PALELRABTONTHSNVAVIPEKOLIEKKSPDKTESSLQVITVTS
			BOCNTNALTNTOTKGRKIRRHKKBKBEKKRKKPVSQSLEFPTRY
i			
j l			SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
į į			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1			HEMTPREIESMTASVDVGKFPCDQLECKSSFTTYLMYVVHLRAD
1			HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
1			l t
1			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
ł I			KMPKTKRKKKNNLENKNAKIVQIBENKPYSLKRGKHVYSIKARN
1	[DALSECTSRFVTOYPCMIKGCTSVVTSBSNIIRHYKCHKLSKAF
			TSQHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
i			
1			nsrttatvsqkevbkne*demdeltelfitklinedstsvbtqa
1 .			ntssnvsndfqednlcqserqkasnlkrvnkbknvsqnkkrkve
'	,	•	Karpasaarissvrkkebtavaiotiebhpaspdws9pkpmgfe
1	`		· ·
1			VSFLKFLERSAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
			TSGNHVCPCKESETPVQFANPSQLQCSDNVKIVLDKNLKDCTEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A-Alanine, C-Cysteine, D-Aspartic Acid, B-
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of amino acid	amino acid .	W=Tryptophan, Y=Tyrcsine, X=Unknown, *=Stop
	sequence	aedneuce	Codon, /=possible nucleotide deletion,
	Bequence		\-possible nucleotide insertion) VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGOY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 3303	""	/03	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
ł			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
1	į (QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
1.	l		PRAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	!		CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
i			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
1			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
J	[EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	i		DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQBTAVTQTYG
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
i			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
	<u> </u>		DNMKWCGTTQNYDADQKFGFCPMAAHERICTTNEGVMYRIGDQW
1	1		DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI GDSWEKYVHGVRYQCYCYGRGIGBWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
j			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1 -			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
İ			POAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1	ĺ		KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AKN
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1	,		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
ł			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN TEVTETTIVITWTPAPRIGPKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
}			LEANPOTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVP1SDT11PAV
1			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNB
I I			GRMLQSLS1FFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1	1		\LEGRORTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1 1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1 1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
			APAVTVRYYRITYGETGGNSPVQBFTVPGSKSTATISGLKPGVD
1		,	YTITVYAVTGRGDSPASSKPISINYRTBIDKPSQMQVTDVQDNS ISVKNLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
}			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
] .			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
			BLQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDGS
1			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
			DVRSYT1TGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQP?RARITGYIIKYEKPGSPPREVVPRP
			RPGVTEATITGLEPGTEYTIYVIALKNNQKSRPLIGRKKTDELP
			QLVTLPHPNLHGPRILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
) .			SGQQPSVGQQMIFREHGFRRTTPPTTATPIRHRPRPYPPNVGQE
		·	ALSQTTISWAPFQDTSRYIISCHPVGTDBEPLQFRVPGTSTSAT
			LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCOCLGFGSGHFRCD
 			SSRWCHDNGVNYKIGEKWDROGENGOMMSCTCLGNGKGEFKCDP
, 1	1		HRATCYDDGKTYHVGRQWQKEYLGATCSCTCFGGORGWRCDNCR
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
[ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
	ļ	-	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
			RCPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

Deginning coation coation coation coation corresponding to first anino acid sequence coation corresponding to first anino acid sequence coation coat	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not	ID	beginning	nucleotide	
to first anino acid residue of anino acid sequence sequence sequence sequence sequence sequence seque	No:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
to first amino acid am	ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid sequence seq	ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of antino acid sequence white antino acid sequence white according to the control of the control	1		amino acid	P=Proline, Q=Glutamine, R=Arginine,
andno acid sequence Colon, /spossible nucleotide dissertion) SCKENCTHRICKHYDINGOWERFYLENDAL MICCICLORGICESE PREETET-DEVITACHT WIND MICCICLORGICESE CTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT COTIANCHEGOSYKI GITHER PRETCOYMERCUL GROGGERT POTOTYC GROGGERT POTOTYCH GROGGERT GROGGERT POTOTYC GROGGERT POTOTYCH GROGGERT GROGGERT POTOTYC GROGGERCUL PPINAD PRESCITERCOM GROGGERT POTOTYC GROGGERCUL PPINAD PRESCITERCOM GROGGERT PRESCITERCOM DRUMCHTON GROGGERT GROGGERT AND GROGGERT POTOTYC GROWGEVEN GROGGERT GROGGERT GROGGERT AND GROGGERT GROGGER	1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
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CTIANCHEGGGSYKIGDTWRRHETGYMAWTCHCLGGGGG CICLAGKGPHANDTSTYRIGDTWRKKOMRGRULGCICTGRIGGE BRCKERFISVOTTSKERSPTVURGHKERFYQOMWMUTCHCLGGGGG BRCKERFISVOTTSKERSPTVURGHKERFYQOMWMUTCHCLGGGGGG BRCKERFISVOTTSKERSPTVERTHERFYSCTTERGOGGWANCGGFTAVTOTYG GRANGEFOLIPTHUNGTEGGGSKRALGIPPTLYMBINTTOCTSBURG RYSPCTDHITUNGTEGGGSKRALGIPPTLYMBINTTOCTSBURG DRIMKATTTOWNDADGEPOLIPTHITSGGFWANTEN DRIMKATTTOWNDADGEPOLIPTHITSGGFWANT DRIMKATTOWNDADGEPOLIPTHITSGGFWANT DRIMKATTOWNDADGEPOLIPTHITSGGFWANT DRIMKATTOWNDADGEPOLIPTHITSGGFWANT DRIMKATTORGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
CKPLASKCPUHAACTSTVAGFMERKPQGAMMUUTCTLEGEGGE TICTSRINCRODDTTSYSTRIGHTMERKENGENGLIGTCTCHNORGE BRACKERITSVOTTSSGSGPFTDVBAAVYDQDPPIDPPPYSHCUT DSGVVYSVGMQIA *KYCOKKMALCTCLGAGWGCGBTAVTOTYG GRINGEPCULPFTVINGETEYSCTTEGEGOGHLUGSTTSSYEDDO XYSPCTEDHTVAJOVGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA	1			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
### TOTSENNENDOPTRITSTERSENDENDELLACITCHSSIGNED BMCKERHTSVOTTSSGSGSPTOWANVGOPENPOP PYCHICUT BGGVVYSVGMCLA* KTOGKROML\CTCLGRUSCQFTAVTOTYC GISNOGEPCVL.PFTVGGSTPSTTERGROCHILUTGTTSSTPSDOO KYSPCTDITVILVOTEGGISRGLCHPPLINMENYTTCTSSGSTP BMCKGTTOWANDANGSPGFCPMANTESICTTSSGVGMYRIGOR DKGHOMGENRCCCVGGGIGERTCLAYSQLDDOCLUDDITTMS UPTHREHBERHLANCTPOGGGGRGKTCDTWOODDSTIGTTFYDI GDSWKKTVHCVRYQCYCYGRGILERHCCPPLOTDSSGVFRWT, UTHREHBERHLANCTPOGGGRGKKTCDTWOODDSTIGTTFYDI GDSWKKTVHCVRYQCYCYGRGILERHCCPPLOTTPSSGGVFRWT, TETPSGYRESTG JORNADOSHISTATSSFVWSWASADTI TETPSGRSESTG JORNADOSHISTATSSFVWSWASADTI TETPSGRSESTG JORNADOSHISTATSSFVWSWASADTI GHLASSTTIKOLKROVYKGQLISIQQYGRGVFTDFTTTSTST PYTSRT\VTGETTPSSTVATGGTTAFDAPPDFTVDQVDDTSIVVSKSG FQAPITGYRIVYSRSVSSTSTERMIPETRASSFVUSWASADTIV SGURVETELSSEGGGBRQTIJALGTATSSFVANTAGATUR TOTSAKERMOESTRVVIQOBTTGTRESDTVYSPROLGFVWSTVI KYTIRWTPPERAVTSKRYNDIJORGSGLIPTKATOR KYTIRWTPPERAVTSKRYNDIJORGSGVICHTGAPPDFTTTGTST TRYTETTIVITTTTATSKRYNDIPTROHGEGGGGLILLBANTP\ARK TGISRGVTYTYFVXFANSHGRSKRIDTAQTTTGLDAPTHLOPNY ETDSTVLUKRTPPERATOTRKNIDVSGGGRAPPETISDGSTV VSGLDFGVWVYTTQVLRRQGBRAP\TVMK\VTPISSPTMLOPNY ETDSTVLUKRTPPERATOTRKNIDVSGGGGRAPPETISDGSTV VSGLDFGVWVYTTQVLRRQGBRAP\TVMK\VTPISSPTMLOPNY TRYTETTIVITTTAPRICFTGGTGTTTTTTTTMQGGSSIPEVU HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTTAGGGSTLEVY VSGLAPGVWVYTYQTGTGSTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTAGGTSLLEVY WSGLAPGVWVYTYQTGTSTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTAGGTSLLEVY WSGLAPGVWVYTYQTGTSTGTTTTTTTTAGGGSTLEVY VSGLAPGVTYTYTTTTTTAGGGTGTTTTTTTTAGGTSLLTVSTDTTTTTTAGGTSLLTVSTDTTTTTTAGGGTSLTTTTTTTAGGTSLLTVSTDTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLTTTTTTTTTTTTTTTTTTTTTTTTTT	ľ	ſ		CTLANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
### TOTSENNENDOPTRITSTERSENDENDELLACITCHSSIGNED BMCKERHTSVOTTSSGSGSPTOWANVGOPENPOP PYCHICUT BGGVVYSVGMCLA* KTOGKROML\CTCLGRUSCQFTAVTOTYC GISNOGEPCVL.PFTVGGSTPSTTERGROCHILUTGTTSSTPSDOO KYSPCTDITVILVOTEGGISRGLCHPPLINMENYTTCTSSGSTP BMCKGTTOWANDANGSPGFCPMANTESICTTSSGVGMYRIGOR DKGHOMGENRCCCVGGGIGERTCLAYSQLDDOCLUDDITTMS UPTHREHBERHLANCTPOGGGGRGKTCDTWOODDSTIGTTFYDI GDSWKKTVHCVRYQCYCYGRGILERHCCPPLOTDSSGVFRWT, UTHREHBERHLANCTPOGGGRGKKTCDTWOODDSTIGTTFYDI GDSWKKTVHCVRYQCYCYGRGILERHCCPPLOTTPSSGGVFRWT, TETPSGYRESTG JORNADOSHISTATSSFVWSWASADTI TETPSGRSESTG JORNADOSHISTATSSFVWSWASADTI TETPSGRSESTG JORNADOSHISTATSSFVWSWASADTI GHLASSTTIKOLKROVYKGQLISIQQYGRGVFTDFTTTSTST PYTSRT\VTGETTPSSTVATGGTTAFDAPPDFTVDQVDDTSIVVSKSG FQAPITGYRIVYSRSVSSTSTERMIPETRASSFVUSWASADTIV SGURVETELSSEGGGBRQTIJALGTATSSFVANTAGATUR TOTSAKERMOESTRVVIQOBTTGTRESDTVYSPROLGFVWSTVI KYTIRWTPPERAVTSKRYNDIJORGSGLIPTKATOR KYTIRWTPPERAVTSKRYNDIJORGSGVICHTGAPPDFTTTGTST TRYTETTIVITTTTATSKRYNDIPTROHGEGGGGLILLBANTP\ARK TGISRGVTYTYFVXFANSHGRSKRIDTAQTTTGLDAPTHLOPNY ETDSTVLUKRTPPERATOTRKNIDVSGGGRAPPETISDGSTV VSGLDFGVWVYTTQVLRRQGBRAP\TVMK\VTPISSPTMLOPNY ETDSTVLUKRTPPERATOTRKNIDVSGGGGRAPPETISDGSTV VSGLDFGVWVYTTQVLRRQGBRAP\TVMK\VTPISSPTMLOPNY TRYTETTIVITTTAPRICFTGGTGTTTTTTTTMQGGSSIPEVU HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTTAGGGSTLEVV HADOSSCTV\DALBENGTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTTAGGGSTLEVY VSGLAPGVWVYTYQTGTGSTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTAGGTSLLEVY WSGLAPGVWVYTYQTGTSTGTTTTTTTTAGGGSTLEVY TOTRIRHPERP\SGURPERBRYVDFSLLATLTTTTTTAGGTSLLEVY WSGLAPGVWVYTYQTGTSTGTTTTTTTTAGGGSTLEVY VSGLAPGVTYTYTTTTTTAGGGTGTTTTTTTTAGGTSLLTVSTDTTTTTTAGGTSLLTVSTDTTTTTTAGGGTSLTTTTTTTAGGTSLLTVSTDTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLLTVSTDTTTTTTTTAGGTSLTTTTTTTTTTTTTTTTTTTTTTTTTT	1			
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GDSWERTYHGYRYQCYCGGSIGKTLERHRYRKSWARMKERATIE TETPSOPRIBIE JORNAPOSIISKYLLIRHRYRKSWARMKERATIE GHINSYTIKOLROGVUYBOOLISIQOYGHOEVTROPPTTTSTST PVTSNTIVUTGETTPSPEVATSBSVTEITASSPVUWANSASVYU SGRRVEYBLSEEGDBRQIVLVESTATSVINIP DELEGRKYLVA VQLISEDCEGSILLISTSQTTAPRAPPDETVOQVDDTSTVENSOR POAPITGYRTVYSPSVUGSSTEIMLPETANSVILDILOPGGYOYN ITITAVEENGESTPVUIQOETIGTPSANVASIGLOPGYOYN KVIIMMTPERSAVTGYRUDIVEVNLEGEHGGURLISKNTP VAEN GISPGVYYYFKVPAVSIGGRESKPLOTATOTYKLADAPTHLOPVN ETDSTVLLVHRYPPRADITGYRLTVOLTROCHYSVYNYO FENSTVLUMWTPPRADITGYRLTVOLTROCHYSVYNYO FENSTVLUMWTPPRADITGYRLTVOLTROCHYSVYNYO FENSTVLUMWTPPRADITGYRLTVOLTPHOGOGNIEGEVV VSCLPFGVEVYTTIQVLEDGGERDAP LVANKVVPTPLSPPTNIH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVV HADQSSCTP JONLEVGGERAVSVYTVXONESVPIGSTPNAH LEANDOTAVLTYSNERSTPDITGYRLTVITPTNOQCONSIGEVV HADQSSCTP JONLEVGGERAVSVYTVXONESVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVV HADQSSCTP JONLEVGGERAPRAVSVITSVSVENSVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVP HADQSSCTP JONLEVGGERAPRAVSVITSVONSVENSVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVP HADQSSCTP JONLEVGERAVSVATVANDSVENSVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVP HADQSSCTP JONLEVGERAVSVATVANDSVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITPTNOQCONSIGEVP HADQSSCTP JONLEVGERAVSVATATOOCH SEVILANDOTAVENSVPIGSTPNAH LEANDOTAVLTYSNERSTTPDITGYRLTVITTPTNOQCONSIGEVP HADGSCTPLANDOTAVATATICALLIANDOTAVENSVPIGSTPNAH LEANDOTAVLTYSNERSTPDITGYRLTVITTATICATPCTSTVAV SIVALNGEBSPLLICOGOSTVEDVERDLEVAATTTSLICLKTGOTOM TTTYAVATORGDSPASKPISTSTATLINGERGEPPRAVVICONS SIVALNGESSPATGAVATTYLOCHORSCOPLICATION PROLAFTU DUSSIKLAMSSPOGGOVSRYRVTYSSPROGTRIADERSTRATICKT GOOTOMATATITTSLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPPTOCHTTLANDOTASSPROGTPROCHTCANDOTASSPROGTPTOCHTOCHT CONSIGNATION TO DESCRIPTOTATATATATATATATATATATATATATATATATATAT	1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
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GHINSYTIKGLERGYVYBGOLISIQYGHORVIREDPITTSTST PVTSRT\VTGETTPFPFILVATSSEVTETLYBEVASPIVUSWASDYTU SGFRVEYELSEBGBEPQYLVLPSTATSV\NIT\DLLGGRKYIVN VQISBOCEGSILLSTSQTTAPRABPDETVDQVDDTSTVENSR PQAPITGYRTVYSPSWESSTEMIN,PETANSVILSDLQPGVQYN ITITAVEBNQESTPVVIQGETTGTPRSDTVPSSPDLQPVBVTDV KVTIMMTPPERAVTGYRUDVIVNLGGERGLISIRNTP\ARN TGLSPGVTYYFKVPAVSHGRSSKPLTAQOTTKL\DAPPTLQPVN KVTIMMTPPERAVTGYRUDVIVNLGGERGLISIRNTP\ARN TGLSPGVTYYFKVPAVSHGRSSKPLTAQOTTKL\DAPPTLQPVN ETDSTVLVRWTPPPRAQITGYRLTVRFSGGGBAPRVTEDGGSIV VSGLTPGGVEVYTJQULBGGRBAP\TVYTPTSPTNLGYGN TEVTETTIVITWTPAPRIGFKLGVRFSGGGBAPRVTEDGGSIV VSGLTPGGVEVYTJQULBGQRRBAP\TVYTPTSPTNGQCNSLBEVV VSGLTPGGVEVYTJQULBGGRRBAP\TVYTPTSPTNGQCNSLBEVV VSGLTPGGVEVYTJQULBGGRRBAP\TVYTPSPTNLH LEANDDTGVLTYSWRRSTTDDTGYRITTPTMGQCNSLBEVV VSGLTPGGVEVYTJQULBGGRRBAP\TVYTPSPTNGQCNSLBEVV HADQSSCTP\DANLBYGERTAVSVYTVSGVEVSTVSTVEHSETTLIPAV PPPTDLRFTN\TITGPTRWTW\APPPSIDLTNFLYRYSPVKNE GRALGSLSIFFLSDR\AVVLTNLHGGTXYVVSVSVYFQHESTP \LEGRGKKTGLDSP\GTAVSTYTVSTVCHGESTP \LEGRGKTGLDSP\GTAVSTYTVSTVCHGESTP \LEGRGKTGLDSP\GTAVSTYTSPRGGATTISGLKFGUV STVALNGRBSPLLIGGGSTUSPVRFDEXATTISGLKFGUV YTTTYAVTGGGSPASSKPLSINTRRTLGTEYVV STVALNGRBSPLLIGGGSTUSPVRFDSSPGGVTTVUQDNS ISVKMLPSSSPVTGYRVTTT\PKNGPG\PTKKTAGPDQTEMT EGLGPTVEXYVSVYAQNPSGESGELVUTAVTNINDRERLAFTUV DVDSIKLANBSPGQUVSRFVYTSSPRGGTLFLFPAPDGEBDTA ELGGLRGSSFYTUSVANHDDMSSGPLTGTGTSLAFPDLLAFTU OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFPAPDTLKFT OVTPTSLSAMUTPSPAVGLTSRFRGGTERLFTDPTTATTTRTPTPTTSPT DBGGGTETTGLTSRFRGGTTTTPTTATTPTPTPTPTDRTPTTTTTTTTTTTTTTTTTT	1			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
PVISHT\UTGETTPS PILVATSESVUETIASS PVUSWVSADIYU SGRRVEYSLE SEGORDOVILVESTATSV\NIP\DLAGGRYI VN SGRRVEYSLE SEGORDOVILVESTATSV\NIP\DLAGGRYI VN VQISEDCEGSLILSTGYTTAPDAPPPTVDQVDDTSI VVRNSR PQAPITGYRI VYSPSVEGSSTRIMI, PETARSVILSDLIG PGVQYIV ITITAVERIOCSSTPVI (OGGITTOPRSITVESPROLOFVEVTDV KVIIMMTPPSSAVTGYRDVI PVINLEGERIGGRIPLISHRYP\AEN TGISPCVITY FKVPAVSIGRESKPLTAGORDQVIAVOPSVEY PLENILQPAS FTYSIJVAI KRONGSPSATATILOPGS I PPYN ETDSTVLURWTPPRAQITGYRLTVGLTRGCOPRQVIAVOPSVEY PLENILQPAS FTYSIJVAI KRONGSPSATATILOPGS I IPYN TEVTETTI VITWTPAPRI GPKICUR PSQGGRAPREVIEDGS I V VSCLIPFGVEV VYTIQVLEDGGREDAP \ TVAK\VVTPISPTMIH LEANPOTMSVLITVSWERSTFIDTGYRITTYPINGQGGNSLEEVV HADQSSCTP\DNLSWFGLEXNSVYTVKDDKESVEY ISTI IPAN PPPTDLRFTN / IIGPDTMRVTW\APPPSIDITATILTYPINGQGNSLEEVV HADQSSCTP\DNLSWFGLEXNSVYTVKDDKESVEY ISTI IPAN GRALGSLSIFFILDDA \ AVVLINILLDTTAYVOSVSSVYTKORDETY \LEGGRAFINGLDSP\TSI (IIGPDTMRVTW\APPPSIDITATILTYPINGYSPVKHE GRALGSLSIFFILDDA \ AVVLINILLDTTAYVOSVSSVYTKORDETY \LEGGRAFINGLDSP\TSI (IIGPDTMRVTW\APPPSIDTAT) ISTI IPAN TGYRIR\HPPEHP\SGRPEDR\VPPSRNSI IIITTALTPCTEYVV SIVALINGRESSPILIGGSYTUSVURDLEVVARTTSILLI\SMD ARAVVVRXIK IITTGGTGGNSPUGPTVDRSATTSI GSLIKFGUD YTITYVAVTGRODSPASSED ISINYRTEIDKSOMQVYTDQDMS ISVAHLDSSSYTYSVTYTY PKNGGG PITVASHQTDAYNINDE EGIGPTVSYVSVAVANDPSGESGENGVATATINGERPAPDGEBDTA ELGIGPTSSSYTYSVVALHDDMRSQPLIGTGSTAI PAPTDLKPT DUDSIK IAMSSPQGVGSRYVTYSSPRGTHELPPAPDGEBDTA ELGIGPTSSKYVSVANATEXTRYTEKRTETTEGVDAVPANAGTFI LORTIKP QVTPTSLSAQWTPPNVQLTGYSKRVTYSRRGTGAPGVVTILENSYPPRR ARVTDATETTI I SMRTKTETTTGTGVDAVPANAGTFI LORTIKP PROVESATITIGLEPOTTYKI IYTALKNINGSGOVTTILENSYPPRR ARVTDATETTI I SMRTKTETTTGTGVDAVPANAGTFI LORTIKP PROVESATITIGLEPOTTYKI IYTALKNINGSELIGRRKTDELD QLAVILPHNLINGPEILDVSTVQKTPFVTHERTDELDPRAVOGGE ILGGREFSCDD ALSGYTINGAPPOTYSCHI IYTALAKNINGSELIGRRKTDELD DUGSTPFTYSHAVGDBMRSMSGGRELIGRRKTDELD ALGGYTINGAPPOTYSCHI IYTALAKNINGSCTILGRIGGREFICO HEATCYDOGKTYHVHAUGDRERMSSGGRELIGCTCLICRIGGREFICO HEATCYDOGKTYHVHAUGDRERMSSGGRELICCTCLORGGREFICO SGRGCYDNGKHYOINGGRERGAATTSLULCTFSVPPFVPFFTIMP PPSMRRQPFGGSRTGOSTGARREANLATCLEVRASLPHE].			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP.
SGRVEYELSEEGBBQTIJLDETATSVANIE\DLEGERYIVN VYQISEDCBQSLILSTSQTTAPDAPPDFYDQVDDTSIVVRWSR PQAPITGYRIVYSSSVGSSTRIALPETANSVTLSDLQPGVQYN ITIYAVEENQESTEVVIQQETIGTPREDTVPSPEDLQFVEVTDV KVTIMMTEPESAVTGYRVDVIVVENLEGENGLPISRNTY-\ABN TGLSPGVTYYRVDAVSHGRESKPLTAQQTTEL\DAPTNLQFVM ETDSTVLUWATPPPRAQITGYRLTQGPRQVAVUSPSVEKY PLENLQPASETYVSLVALKGNQESPRATGVFTLQPGSSIPPYN TEVTETTIVITWTPARRIGPKLGVRSQGGRAPERVTSDGSGSLV VSGLTPGVEVAVYTQVLRGOGGRAPALVTSDVGSSLEVV VSGLTPGVEVAVYTQLRGOGGRAPALVTSVTSPFTNLH LEANDDTGVLTYSKERSTTPDITGKRTTTPFNGQGGSASEEVVI HADGSSCTY\DNLEWGESPRATGVFTLQPGGSSEEVVI HADGSSCTY\DNLEWGESPRATGVFTLYPNGQGNSLEEVV SCLTPGVEVAVYTQLVLRGOGGRAPALVTSVTSVSSVKNG GRALGSLSIFPLSDN\AVVIINTLLGGTDKSFYFISTTIPAV PPPTDLRFTN\ILGPDTMEVTW\APPPSIDLINFILWYSSVKNG GRALGSLSIFPLSDN\AVVIINTLLGGTAVAVVSSSVVQHESTP \LEGRQKTGLDSP\TGJDFS\DITA\NSFT\VHW\LAPRA\TFI TGYRIR\HHBEHF\SGRPEDB\VPHSRSSTILITATPGTGYVV STVALNGERSBPLLLGGGSTBUDVBRAVATTFSLLA\SM APAVTVRYRITYGETGGNSPVQBFTVPGSRSTATIGGLRFGVD YTITTVAAVTGRGDSPASSFFISINNFTRUSSGMOVTTOVDONS LSVKULPSSSPVTGRGSSPFISHVATTSGLARFDQOTEMTI EGLQPTVEYVSVYAQNPGGSGPLVQTVATNIBSGRGLAPTDV DVDSIKIAMSSPQGVSKRVTYSSPRGGHELFPAPDCEEDTA HLQGLRFGSSFTTUSVALHDDMSSQPLIGTGSTAIPAPTDLKFT QVPPTSLSAGMVFPNNGJAGVGVTTARNOSPPRA ARVTDATSTTITISHRYTETTITGPQDAVPRNGOTPIQRTIKP DVRSYTITGLQFGTDYKIYLYTININARSSEVVIDASTALDAFS SVVUSGLMVATKYBVSVALADDTLASRPAGGVTTLENVSPPRA ARVTDATSTTITISHRYTETTITGPQDAVPRNGOTPIQRTIKP DVRSYTITGLAPGTDYKIYLYTININARSSEVVIDASTALDAFS NILEFLATTENSLLVSNQPPRARTIGVITKYBERGSPPREVVPRP RGVTEATITGSLEFGEFTTTPTTATPIRHTPNNGIGLPGF GGQSSVGGOMIFERIERFTTPPTTATPIRHTPNNDCDLPGT SGQDSVGGOMIFERIERFTTPPTTATSTILKPREFTYDPTANGGEPRCUDG RFGGGEFTTSSHAVDRSNEMBESGSFKLLQCLGFGGSFFRCD HRATCTYDGGTTVSHAVAUGBREMBESGSFKLLQCLGFGGSFFRCD BRACCTGGGFTTGSSTRUBERANAATCLFVRASLFRIRLMMI. RGGGFGGLLALAULCGTATNIYRQGTYTSPREDSKINDTGCTGARGRFRCD PPSMRQPFGGITRDFSRREBRESRALAGGCAVMCCTCGARGRFRCD CHANCTURGEGGFTQGARGTGTMCTCTGGGSRGCMCMCC CTANRCHECGGSFKICDTRIPHTROGTLGARGRGESK CTANRCHECGGSFKICDTRIPHTGGTLGARGRGESK CTANRCHECGGSFKICDTRIPHTGGTARLAUCCTGGGSRGCMCSCC CTANRCHECGGSFKICDTRIPHTGGTAMLAUCCTCGGSRGFICESK PRAB		_		GHLNSYTIKGLKPGVVYBGQLISIQQYGHQEVTRFDFTTTSTST
VYQISEDCEQSLILSTSQTAPDDAPPDTVDQVDDTSIVVRMSR PQAPITGYRIVYSPSVEGSTRINLPETARSVTLSDLQPGVQYN ITIYAVERNQSSTRVIVIQDETIGTPERADVTSPRDLQFVSVTDV KVTIMMTPPESAVTGVRUVI LYNLPGERGORLPISRYTE \ARM TGLSPGVTYYRVRAVBAYERGRSKPLTARQQTRL\DAPWINLQFVN ETDSTVLUWRTPPERAQTGVRUVITVGLTRGQQPRQVNGPSUSKRY PLENLQPAPETYTSLVAIKGNQESPRATGYTRL\DAPWINLQFVN ETDSTVLUWRTPPERAQTGVRUVITSLARGQPRQVNGPSUSKRY PLENLQPAPETYTTQVLRGQGRRAPRVTSDSGSTV VSGLTFGVEXYVTTQVLRGQGRRAPRVTSDSGSTV VSGLTFGVEXYVTTQVLRGQGRRAPRVTSDSGSTV VSGLTFGVEXYVTTQVLRGQGRRAPRVTSDSGSTV VSGLTFGVEXYVTYKADDKSSYP ISDTITPANQ PPPTDLRFTPN/ILGPDTMRVTN\APPSIDTNHQQGNSLEEVV HADQSSCTF\NDLSVPGLEXYNSYYTYKDDKSSYP ISDTITPAN PPPTDLRFTN/ILGPDTMRVTN\APPSIDTNHQCNSLEEVV HADQSSCTF\NDLSVPGLEXYNSYYTYKDDKSSYP ISDTITPAN PPPTDLRFTN/ILGPDTMRVTN\APPSIDTNHQCNSLEEVV HADQSSCTF\NDLSVPGLEXYNSYYTYKDDKSSYP ISDTITPAN PPPTDLRFTN/ILGPDTMRVTN\APPSIDTNHQCNSLEEVV HADQSSCTF\NDLSVPGLEXYNSYYTYKDKSSYVYEQHESTP \LEGRRYTSSPLAIGQGSTVSUPRDLAFNSITLTNLTPGFEYVV STVALNGRESSPLLICQQSTVSUPRPLSRVAATFTSLLI\SMD APAVTVRYYRYTRTTTYRRGSPYTATSILL\SMD APAVTVRYYRYTHTTYRRGSPYTHGRYTDLLYST DVSTKILMSSSSPVGSSCSPLUGTSTATIGLAFPTUV DVSTKILMSSSSPVGSSCSPLUGTSTATIGNAFTUKY DVSTKILMSSSSSPVTSVVSVALDHDMSSQP,IATNIDRRGALAFTUV DVSTKILMSSSPGGVSRYRVTYSSPRGGHELFPAPDGEBDTA RLQGIRPGSSYTVSVVANADHDMSSQP,IATNIDRRGALAFTUV QVIPTSLSAQMTPPNVOLTGVRVTPYRKRTGPMKBINLAPDSS SVVVSGLMVATKTRVSVTALLDDTMSSPAQGVVTTLENVSPPRR ARVTDATETTITISHTTETTICTGVDAYPANGTFICRTICH DVSSTTITGLQPGTDYKTLTTTRUBRRSPAPOPWVCR NLEFLATTENSLLVSMQPPRRATTGYTITYREGSPPREWVPRP RPGVTEATTTGLEPGTDYKTLTYTTRUBRRSPAPOPWVCR ALSQTTLSMAPFQDTSYTITYLARRSPRVTCHSVWERP PROVTGSTTNI IVERLDQQRHKYRGRSPATTGYTIRGTQLPGT DDSCPDPYTVSHYAVGDEWRMSCCTLGGKGFFKCDP HRACCTGGGGGTTPGASGKRGFAATTSLVLCTFSVPFPTDWP PSSWRQPPGGIKRDFSRRLERRANLVATCLFVGASIPHRLDMI RPGGGGLLLAVLCLGTAPFSTGASKRGFANGCCTLGGAGRGRIS PSSWRQPFGGIKRDFSRRLERRANLVATCLFVGASIPHRLDMI RPGGGGLLLAVLCLGTAPTTYRYRGGTYLERGSPMCDCC QSRPCCYDNGKHYOTNONGGTFTLGASGRGRIS CTLANRCHECGGSKYLGTWRPHETGGMLECCULGMCKGEFT CTLANRCHECGGSKYLGTGTWRPHETGGOMLECCULGMCKGEFT CTLANRCHECGGSYLGCTYRPHETGGOMLECCULGMCKGEFT	f			PVTSNT\VTGETTPFSPLVATSBSVTEITASSFVVSWVSASDTV
POAPTGYRIYYSPSWEGSTHIALPETANSUTLBDLQPGUQUN ITITANEENQESTPUVIQQETIGTPREDTUPSPROLQFVEVTDU KVTIMMTPESANTGYRVDVIEVELPGEHGGRLELSKRYP\AEN TGLSPGUTYYFKVRAVSHGRESKPLTAQQTTELJAPTALQFVEN ETDSTULWRTPPRAQITGYRLTUGLTREGQPRQYNUGSVESYS PLENILQPASETTUSLUAIKGNGESPRAGTAFTTLQPGSE IPPYN TEVTETTLYTUTMTPAR IGPKLGWRSGAPREVTESGGSIV VSGLTPGUEYVYTIQULRDGQERDAP\IVNK\VUTPLSPPTHLH LRAMPDIGULTUSWERSTTPDITGYRITTPTNOQQGNSLEEVU HADQSSCTF\DNIEWGESTNOWLTWUSSVEYCHGETP PPTDLRFTM\ILSPDTMRYTW\APPPSIDLINFLWYSPVKHE GRALGSLSIFFLSDN\AVULTILLDFTAWVSSVEYCHGETP \LAGROKTGLDSP\TGIDPS\DITA\BSFT\WHA\LARRA\TPI TGYRIR\HHPEHP\SGRPREDR\UPPSRDSTULTITITTTCTEYVU SIVALINGRESSPLIGQSTUSDVERDLEVAATTTSLLI\SMD ARAVTURYRRITTGETGGNSVUGFTVPGSKSTATIGGLRFGVU YTITTYANTGROSPASEPISIHNTETHORSOMOTHORDEN ISVKHLPSSSFVTGYRVTTT\PKNGPG\PTKKTAGPDGTEMTI EGIGPTUSYVUSVANDAPGSSGSPLOYMDINDPSGLAPTDV DVDSIKIAWSSPQGQVSRYEVTYSSPROGIHELPPAPDGEEDTA RLGGLRFGSRYTUSVVALHDMRSQDLIGTGSTAPTDLKFT QVTPTSLSAGAWTPPNOLIGTGWRAVITANIDRPSGLAPTDV DVDSIKIAWSSPQGQVSRYEVTYSSPROGIHELPPAPDGEEDTA RLGGLRFGSRYTUSVVALHDMRSQDLIGTGSTAPTDLKFT QVTPTSLSAGAWTPRNOLIGTGWRAVITARDRAGTPIGTKIRPBSF SWVUSGLMVATKYBUSVALAUDTLTSEPAQGUVTLENUSPPRA ARVTDATSTITISHRYTETTITGPUDANGOTPICKTIRP DVSTITITGLQPGTDYKIYLITANNARSSPVIDASTAIDAPS WILSFITTIGLAPGTETTITITISHTETTITGPURNOGTPICKTIRP ARVTDATSTITISHBEGRETTPPTTATIRRITTORITICHPGSPREVUPRP RGVTEATITGLAFGTETTITIVATIRRITRRPTYPPONUCGB ALSGYTIGMAPPGOTGETIIVATARNOKSEPLIGRKTTDELP GUTPTIGGATTHURGDGTHURGGREFRCDP DBSCPDPYTVSHYAVDENREMSESSFKLLCQCLGGGSSFFRCDP DBSCPDPYTSHYAVALDENREMSESSFKLLCCCLGGGSFFRCDP BRACTTGGGGFTPGASGKRGPAATTSLVLCIFSVPPPTFTLWP PSHRRQPFGGTHROFSTRERRERNIANTCLPVRASIPHRIMMI RGFGGGLLLAULCLGTATNIYRUGDTYRPRETTGGMEGGFFCODP HRACTTGGGGFTTPGASGKRGPAATTSLVLCIFSVPPPTFTLWP PSHRRQPFGGTHROFSTRERRERNIANTCLPVRASIPHRIMMI RGFGGGLLLAULCLGTATNIYRUGDTYRPRETTGGMEGGFFCODP PSHRRQPFGGTHROFSTRERRERNIANTCLPVRASIPHRIMMI RGFGGGLLLAULCLGTATNIYRUGDTYRPRETTGGMEGGFFCODE PSHRRCPFGGTHROFSTRETTPFTTGGRAGKRGOMOPODPOSPVAS GKRGCYDNGKHYQINQOMBCTTLGNALVCTYGGGRGFFCCDF PSHRRCPFGGTHROFSTRETGGTHECTGAGRGMES CTLANKCHECGGSYKIGTOFWRPHETGGGMECUCLGA	ĺ			SGFRVEYELSEEGDBPQYLVLPSTATSV\NIP\DLLPGRKYIVN
ITITANERNOESTEVUIQOETIGTPRSDTVBSPRDLOFVENTTV KVTIMMTPPESAVTGYRVDVIPVINDEGIGORLDFLSRNTF\AEN TGLSPCVTYYRKVRAVSHGRESHDITAQOTTKL\DAPTMLQFVM ETDSTVLURMTPPRAQITGYRLTVGLTRRGQPRQYAVGESVESKY PLENLQPASETYTSLVALIKONQESTAVFTTLQPGSESIPPVM TEVTETTIVITMTPAPRIGPKLGVRPSQGGEAPPEVTSDSGSIV VSGLTPCVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LRANDTGVLTVSWERSTTPDLTGYRITTPTMQQGCNSLBEVV VSGLTPCVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH LRANDTGVLTVSWERSTTPDLTGYRITTPTMQQGCSLBEVV HADQSSCTP\DNLEVPGLEXNVSVTVTVKDDKESPPISDTHILVSSPVKNE GRALGSLSIFFLSDN\AVVLTNLLPGTZYVVSVSVYEQHESTP \LEGRQKTGLDSP\TGIDPS\DITA\MSFT\VHW\LAPRA\TPI TGYRIR\HHPEHP\SGRPREDR\VPSSSTPLITTSILLI\SMD APAVTVRYRITTVGETGGSPPVGETVSGSSTATISGLKPGVD SIVALNGERSBPLLIGQGSTVSDVPRDLEVVAATPTSLLI\SMD APAVTVRYRITTVGETGGSPPVGETYPGSSTATISGLKPGVD YTITVAVTGRGDSPASSKPISINYRTEIDKPSGMQVTDVQDNS LSVKWLPSSSPVTGYRVTTT\PKNSPG\PYTKTKAGPQQTEMTI BELQPTVSSVVSGLMVATKYEVSVYALKDTHSPGMGVTDVQDNS LSVKWLPSSSPVTGYRVTTTYPKNSPGPLFTKTKAGPQQTEMTI BELQPTVSSVVSGLMVATKYEVSVYALKDTLSFPRAGGVUTDLERDFR QVVPSSLSAQMTPDNVQLTGYRVRVTPKBKTGPMKBINLAPPBS SVVVSGLMVATKYEVSVYALKDTLTSPRAGGVVTLLENVSPPRR RFGVTEATTTISHSKTKTETITGFQVDAVPANGGTPIGRTLDPS NILFILATTPHSLLVSMQPPRARITGYKTFKFSFSPRSVVRRP RFGVTEATTTGLRFGTTSYTTYLALKNNGKSBPLJGRKKTDLDPG SCQDPSVGQMIFFERIGRRRTTPPTTAPPRHEPRYPPNVCQF RFGVTEATTTGLRFGTTSYTTYLALKNNGKSBPLJGRKKTDLDPG ALSQTTLSWAPPQDTESYTTSCHPOTTBEPLJPRYPGTSTSAT LTGLTGRATYNTIVGLRALKOQGHRKYREVVTVCNSVMREDINOPT DDGCPPPYTVSHYAVGDEMERMSESGPKLLCQCLGFGSGHPRCD SSRCHDNGWYKLIGKKMDGOENGOMSCTLGMGCEFKCDP HABTCYDDGKTYHVGENQOKENGAGICSCTCFGGGRGMCDMC RFGGFGSLLLANLCLGTATAPSTGAGAGCAGAGCTCLGGGGRGCDHC RFGGFGSLLLANLCLGTATAPSTGAGAGCAGAGCTCLGGGGRGCDKC RFGGFGSGLLLANLCLGTATAPSTGAGARCDMCTCLGGGGRGCDK GGFGGLLLANLCLGTATAPSTGAARCRQOMMOTOGSPVASS QSKPGCYDNGKHYQINQQBRTLICNGTCGGSGFFNCCSK PPARROPPGGTGRRDFSRLIRREANLVATCLFVRASLPHRLMMI RGGFGGLLLANLCLGTATAPSTGAKRGROMMCTCLGGAGRGTK GFGGLLLANLCLGTATAPSTGAKRGROMMCTCLGGAGRGTK GGFGGLLLANLCLGTATAPSTGAKRGROMMCTCLGGAGRGTK CCTIANGCHECGGSTKGGTWRADHTGCTGGAGRGCBK CCTIANGCHECGGSTKGGTWRADHTGCTGGAGRGCBK CTIANGCHECGGSTKGGTWRADHTGCTGGAGRGCBK				
KVIIMMTPPESAVTGYRVDVIPVILGEGRGUPLISRNTF\AN TGLSPGVTYY RVPAVSIGRESKPLTAQOTTKL\DAPTILQFVM ETDSTVLIVRWTPPRAQITGYRLIVGULTRRGGPRGYAVGESUSKY PLENILQPASETTVSLVAIKGNQESPRATGYTTQGCSSIPPVN TETTETTTUTWTHEAPRIGHKIGHUSPSQGGRPREVTSDGSGLV VSGLTPGVBYVYTTQVLRDGQERDAP\INN\VVTPLSPPTILH LEANPDTGVLTVSWERSTTPDLTGYRITTTPTNGQGNSLBEVV HADQSSCTF\DNLSWPGLEXNGSVTVVKIDDRESVPLSDTIIPAV PPPTDLRFTN\ILGPDTMRTW\APPFIDLTMFLWRYSPVKNE GRILGSLSIFFISDN\AVVLTNLDAFZXVUSVSSVYSQGBSPEVTSQGNSLBEVV APAVTRYTALTYGERDRYDAVVLTNLDAFZXVUSVSSVYSQGBSTEV STUALINGERSSPLIGGQGSTUSDFLEVVANTPTSLILI\SMD APAVTVRYYR ITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITYAVAVGROBSPASSKPISINYTETBLKVSQMQVTDVQDNS SIVALINGERSSPLIGGGGSTUSPUSEVVANTPTSLILI\SMD APAVTVRYYR ITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD YTITYAVAVGROBSPASSKPISINYTETBLKVSQMQVTDVQDNS ISVKLIPSSSPVTSKVTTI\ENKSGPTRIKTASPDQTENTI EGIQPTVSYVVSVYAQNSSCSCEPLVQTAVTNIDRRGGLAFTUV DVDSIKINMSSPGGOVSRVRVYTYSGRIHELFPAPDCEEDTA BLQGLRPGSHYTVSVVALHDDMSQPLIGTQSTAIPAPTDLKPT QVTPTSLSAQWTPDNVOLTGYRRVRYTPKRKTGMKSINLAPDSS SVVUSGLMVATKYRVSVYALKDILTSRPAQGVVTTLENVSPPRR ARVTDATETTITISHPRTKTETTGGQDAVPARMGQTPIQRTIKP DVSSTITIGGQFGTDKYKINYTTHARSSPVUDASTAIDAPS NLRFLATTFNSLLVSWQPPRARITGYIIKYBKPGSPPRVVPRP RRGVTEATTTGLBFGTFTTYYIALKNNQKSSPLIGRKKTDELP QVITTISHNLAPPDTSTYIISUPSTVQKRYREVTVENSVNRGGLORGFRCSG SGQGSVGQQMIFREHSPRRTTPPTTATPIHRRPRPYPPDNVGGE ALSQTTISMAPPDTTSYIISCHPVGTGSGCTLGRKGFRCD DBGCPDPTTVSHVAVGDBWERMSESGFKLLQCLGFGSGHFRCD SGRGCDMGVNYKIGEKMDRQGENGGWSCTCLGNGKGEFKCDP HBATCYDDGKTYHVGRQMQKETIGAICSCTCFGGGGGMCDNCR RRGGFSSECTTTGGSYNQYSQRYHQKTNTNVNCPIECFMPLDVQ ADREDSR 5365 8066 703 BLCCTGGGEGTFGASGKRGPAATTSLVLCTFSVPFPVPFPTLMP PPSMRRQPPGGIRLDAFNTLGTAVPSTGASKRQAQMYNDGSPVASS QSEGCTONGKHYOINQGBRTYLGNALVCTCGGGGGGNCCKSK PEABETCFDKYTGNTYNCHOTYREPKDBLCVCLGRGKGERIS CTLANRCHECCQSYKLGDTWREPKTGGGRGRGRGSIS PEABETCFDKYTGNTYNCHOLTGGAGGRGRGS	İ			
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ADREDSRE 5365 8066 703 RICCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGTRDFSRRIRREANLVATCLPVRASLPHRIMMI. RGPGPELLLLAVLCLGTAVPSTGASKSKQAQMVQPQSPVAVS QSKPGCYDNGKHYQINQOWBRTYLGNALVCTCYGGSRGFNCESK PEABETCFDKYTGNTYRVGDTYBEPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT				
703 RLCCTGGGGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP PPSWRRQPPGGTRDFSRRLRREANLVATCLPVRASLPHRLMMI. RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK PBABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT		ļ		
PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLMMI. RGPGFGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQMBRTYLGNALVCTCYGGSRGFNCESK PEABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT		9000	702	
RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK PBABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT	2362	8066	703	
QSKPGCYDNGKHYQINQQWBRTYLGNALVCTCYGGSRGFNCESK PBABBTCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHBTGGYMLECVCLGNGKGEWT		ľ		
PBABBTCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS CTIANRCHEGGQSYKIGDTWRRPHBTGGYMLECVCLGNGKGEWT		ļ		
CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT		}		,
CKPLAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGGGR		1	ļ	
The state of the s	L			CKPLABACEDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I≈Isoleucine, K=Lysine,
1	(to first	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1		residue of	S=Serine, T=Threonine, V=Valine,
{	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	
	acquence		\=possible nucleotide insertion)
1	ł	ì	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
j		1	EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	i	1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1	j		GNSNGRPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
1		ľ	KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
}])	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1	ĺ	İ	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1	ł		DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQ1
1	}	l	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1	<u> </u>	1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
1	1	1	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ł	i	1	PVTSNT\VTGETTPFSPLVATSESVTRITASSFVVSWVSASDTV
1	}	1	SGPRVEYELSEBGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
	1	1	VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1	}		PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1	1	1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
İ	j	İ	TGLSPGVTYYFKVFAVSHGRBSKPLTAQQTTKL\DAPTNLQFVN
1	Ĭ	[ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
}	1	Ì	PLRNLQPASBYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
	j	j	TEVTETTIVITWTPAPRIGFKLGVRPSQGGBAPRBVTSDSGSIV
· I	1	1	VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
-	,	Į.	LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
ļ	į	į	HADQSSCTF\DNLRVPGLEYNVSVYTVKDDKESVPISDTIIPAV
1			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
1	[GRMLQSLSIFFLSDN\AVVLTNLLPGT3YVVSVSSVYEQHESTP
ł	1	Ì	\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
ı		1	TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
Ţ		(SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
		l	APAVTVRYYRITYGETGGNSDVQEFTVPGSKSTATISGLKPGVD
ł	1	!	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1	})	ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1	1		EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1		\	DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELPPAPDGEEDTA
1	1	1	ELQGLRPGSEYTVSVVALHDDME8QPLIGTQSTATPAPTDLKFT
1	ļ	J	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
]		SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1	1	[ARVIDATETITISWEIKTETITGFQVDAVPANGQIPIQETIKP
1		1	DVRSYTITGLOPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
	j	}	NIRPLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1	1	1	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
	1	1	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1	I	1	SCOOPSVGQOMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
1		1	ALSOTTISWAPPODTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
1		I	LTGLTRGATYNI IVEALKDQQRHKVRBEVVTVGNSVNEGLNQPT
.]	ŀ	1	DDSCFDPYTVSHYAVGDEWERMSESGFKLLCOCLGFGSGHFRCD
1	1	i	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
1 .	1	1	HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1		(RPGGRPSPEGTTGQSYNQXSQRYHQRTNTNVNCPIECFMPLDVQ
L	L	<u> </u>	ADREDSRE
5366	8066	703	RLCCTGGGBGTPGASGKRGPAATTSLVLCIPSVPPPVPPPTLWP
1	}	1	PPSWRRQPPGGIRRDFSRRLRRBANLVATCLPVRASLPHRLNML
1		1	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
	1	1	QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
i		1	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1		1	CTIANRCHEGGOSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1	Į.	1	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
j	j	1	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	1	1	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1	1	1	GNSNGBPCVLPFTYNGRTPYSCTTEGRQDGHLNCSTTSNYEQDQ

ID beginning nucleotide location corresponding to first amino acid residue of location to said location corresponding to first amino acid residue of location (A=Alanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, H=Histidine, I=Isoleucine, M=Methionine, N=Aspar Included location (A=Alanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, I=Isoleucine, M=Methionine, N=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, C=Cysteine, D=Aspar Glutamic Acid, F=Phenylalanine, D=Aspar Glutamic Acid, D=Aspar Glutamic Acid, D=Aspar Glutamic Acid,	, G=Glycine,
location corresponding to first location to first location acid location	
corresponding to first lamino acid lamino acid lamino acid lamino acid lamino acid lamino lam	reino.
to first amino acid P=Proline, Q=Glutamine, R=Argin	
amino acid residue of Sesetthe, Tellifeonine, Vevaline	
I location of location with McDownhous V-Thoughton V-Thoughton V-Thoughton	•
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Uni amino acid sequence Codon, /=possible nucleotide de	
sequence \=possible nucleotide insertion KYSFCTDHTVLVQTRGGNSNGALCHFPFLYN	
DNMKWCGTTQNYDADQKFGFCPMAAHEEICT	
DKQHDMGHMMRCTCVGMGRGBWTCIAYSQLF	•
DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVI	
GDSWEKYVHGVRYOCYCYGRGIGEWHCOPLO	
TETPSQPNSHPIQWNAPQPSHISKYILRWRI	PKNSVGRWKEATIP
GHLNSYTIKGLKPGVVYEGQLISIQQYGHQI	BVTRFDFTTTSTST
PVTSNT\VTGRTTPFSPLVATSESVTEITAS	SSFVVSWVSASDTV
SGFRVEYELSEEGDEPQYLVLPSTATSV\N1	IP/DLLPGRKYIVN
VYQISEDGEQSLILSTSQTTAPDAPPDPTVI	
. PQAPITGYRIVYSPSVEGSSTELNLPSTANS	· · · · · · · · · · · · · · · · · · ·
ITIYAVEENQESTPVVIQQETTGTPRSDTVI	
KVTIMWTPPRSAVTGYRVDVIPVNLPGBHGC	
TGLSPGVTYYFKVFAVSHGRESKPLTAQQTT	
ETDSTVLVRWTPPRAQITGYRLTVGLITRGÇ PLRNLQPASBYTVSLVAIKGNQBSPKATGVI	
TRVTETTIVITWTPAPRIGFKLGVRP6QGG	
VSGLTPGVEYVYTIQVLRDGQERDAP\IVNI	
LEANPDTGVLTVSWERSTTPDITGYRITTTI	
IIADQSSCTF\DNLEVPGLEYNVSVYTVKDDI	
PPPTDLRFIN/ILGPDTMRVTW\APPPSIDI	
GRMLQSLSIFFLSDN\AVVLTNLLPGTEYV	VSVSSVY EQHESTP
\LRGRQKTGLDSP\TGIDFS\DXTA\NSFT\	VHW\IAPRA/TPI
TGYRIR\HHPRHF\SGRPREDR\VPHSRNSI	
SIVALNGREESPLLIGQQSTVSDVPRDLEV	
APAVTVRYYRITYGETGGNSPVQEFTVPGS	
YTITVYAVTGRGDSPASSKPISINYRTEIDH	
ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTK BGLOPTVEYVVSVYAONPSGESQPLVQTAVI	
DVDSIKIAWESPOGOVSRYRVTYSSPEDGIE	
ELQGLRPGSBYTVSVVALHDDMESQPLIGTQ	
QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKT	
SVVVSGLMVATKYBVSVYALKDTLTSRPAQO	
ARVTDATETTITISWRTRTETTTGFQVDAVE	
DVRSYTITGLQPGTDYKIYLYTLNDNARSSK	PVVIDASTAIDAPS
NLRPLATTPNSLLVSWQPPRARITGYIIKYE	
RPGVTEATITGLEPGTBYTIYVIALKNNQKS	
QLVTLPHPNLHGPEILDVPSTVQKTPFVTHE	
SGQQPSVGQQMIFEKHGFRRTTPPTTATPIF	
ALSQTTISWAPPQDTSEYIISCHPVGTDEBE LTGLTRGATYNIIVRALKDQQRHKVREEVVI	
DDSCPDPYTVSHYAVGDEWERMSESGPKLLC	
SGRWCHDNGVNYKIGEKWDRQGENGQMMSCT	
HEATCYDDGKTYHVGEQWQKEYLGAICSCTC	
RPGGBPSPEGTTGQSYNQYSQRYHQRTNTNV	
ADREDSRE	_ !
5367 235 3591 KKILNMLCKKNIVIEYLADILYBYLYGFCPS	GIKKYLIIHVLRL
ILBLWMTRLLLEKSVSLQTQYLLLIVKILSW	
EVMMRKQDS/RIVGNGSEQQLQKELADVLML	
KRSQLDGBGDGPLSNQLSASSTINPVPLVGL	
GDSKASSPFTPVADEDSVVFSKLTYLGCASV	
SILRSQCQISLDVTLSVPNVSEGIVRLLDPQ	
LFCVRGHDGTPESDCFAFTESHYNAELFRIH	
LYSFATAFRRSAKQTPLSATAAPQTPDSDIF	
KGYPSAVPKDKDRQCPKLRQGIDKKIVIYVQ	
GLLLSPGKDVRNSDMHLLDLESMGKSSDGKS	
FQVVNBETPKDKVLFMTTAVDLVITBVQBPV	
NERLFWPFSKRSTTENFFLKLKQI KQRERKN	
ESERERRETTASPSVRLPQSGSQSSVIPSPE	
SGSGDVSKECAEKILETWGELLSKWHLNLNV PRALRGEVWQLLAGCHNNDHLVEKYRILITK	
FEWTINGS AND THE ARCHITICAL AND	The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(AmAlanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine,
}	location	corresponding	H-Histidine, I=Isoleucine, K=Lysine,
ŀ	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotice deletion,
1	sequence		\=possible nucleotide insertion)
			RTPPAHDYFKDTGGDGQDSLYKICKAYSVYDREIGYCQGQSFLA
1			AVLLIAMPEEQAFSVLVKIMFDYGLRELFKQNFEDLHCKFYQLE
ì	· ·		RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
1	i		IIDLLLCEGISVIFNVALGLLKTSKDDLLJ.TDFEGALKFFRVQL
		·	PKRYRSEBNAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
1		ļ	EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
1	J		NAKEKADALNKELLMTKQKLIDAEBEKRRLEEESAHLKKMCRRE
			LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
1			QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
			REMELELAQTKL\QLVEASCKIQD\LEHPP*GLPFNE\VQAA\K KTWFNRTLSSIKTATGVQGKETC
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFILLALVGAVLYLYPAS
	-		RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
1			FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
			WWQCE*KP\QRKKLYENGVTDSLKSNFALLLKLPERLLDKWLSY
1			PETQH\VPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHG
			TVWSBIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
			GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
I i	i		AIWPLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
1			ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
1 1			NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPBLRFAYMVT
5369	1	6622	TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREKAWITVSKRY PRSLCPSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
****	~	0022	CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
j			RCLKADVIG/VWRRDQRPERRE\L*IFWGGEDP\VILTLFTMTY
			QKKKMECGRMDFPMNAVLCFSKAVHNLLBRCLMNRNFVRIGKWF
			VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINQHQPVY
1 1			LLSREHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
1 1			LIGEWKQFYP1SCCLKEMSERKQEDMDWEDDSLAAVEVLVAGVR
1 1	i		MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
1 1			MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
1 1			GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGLCBEATA
1 1	•		AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ ILPKHKTNKKQKKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
l i			SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTRMANSPQ
1	1		PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
! [EDRIDSLEQSFPPQYQRAVEPTVYVGTAVNLEEDBANIAWKYYK
1		İ	PPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTBLMVQCKK
1 1	l		PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
[]	1		LFPDKKDRONSERBAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
!	1		IKODAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDRDELT
	į		PGSKRSANGSDDKASCKBSKTGNLDPLSCISTADLHKMYPTPPS
[]	1		LEOHINGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE
	ļ		VDBGPCSPRPSBIKDPSYVYKPRNCQILVGCSMPAPIKTLPSQY LPLIKLPEBCIYRQSWTVGKLRLLSSGPSMPPIKEGDGSNMDOE
	1		YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFFTPRTP
{	1	i	RTPRTPRGAGGPASAGGSVKYENSDLYSPASTPSTCRPLNSVEP
	Ì		ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
	j		GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDBLD
'	1		1 IGRNTDCGKRABKRPRALRATSAEHVNGGLKESEKLSDDLILL
}	į		LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVBERDCCNDCYLA
	1		LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
	j	İ	RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
	l		TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR
	ļ	}	DIAYVVLCPENEALINGAKSFFROLTAIYESCRLGQHRPVSRLL
	ŀ		TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
	ł		CRYDIGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
	j		NIPSAILASAASSIMIVIEGVAISTSVATANSILITASISSSS SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
i. I	1	ŀ	
, ,	i		OTSALOTAGISGRSSST, PTOPHPDIVGRSTMORDRIGGT PTYCYCU
			QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH AVTYPPAIVVYIIDPFTYENTDESTNSSSVWILGLLRCFLENVQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q≈Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
;	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
			TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPQHLKSLAFSAP
			TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPDRPECIRLYAPP
ł	l		FILAPVKDKQTELGETFGEAGQKYNVLFVGYCLSHDQRWILASC
1	1	•	TDLYGELLETCIINIDVPNRARRKKSSARKFGLQKLWEWCLGLV
1			QMSSLPWRVVIGRIGRIGHGELKDWSCLLSRRNLQSLSKRLKDM
j	1		CRMCGISAADSPSILSACLVAMEPQGSFVIMPDSVSTGSVFGRS
1			TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVASATYTTENLDL
1	i I		APNPNNDGADGMGIFDLLDTGDDLDPDIINILPASPTGSPVHSP
1			GSHYPHGGDAGKGQSTDRLLSTEPHEKVPNILQQPLALGYFVST
I)		AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVPSVQSDELLHS
1			KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPATQDRRSCLPTH
			FVVLNQLYNFIMMML
5370	1226	716	RWSRKLKLRRAAQATESRPPQSQEMHPPTGKEVHALKRLRDSAN
1	į į		ANDVETVQQLLEDGADPCAADDKGRTALHFASCNGNDQIVQLLL
1	(DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLRGGARVDALDR
			AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGEADHPYAEGVSG
1			APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTIWSLPLHEAKCR
	J i		AVRPLSSAAQGSAPSSSSCCTVSTSLALAESLSLFRACTSLPVG
F373			GCISWL
5371	1331	167	TAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLACFTYTTDKQS
1			SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMKPMLKKLRI/P
			LQELGADETAVASILERCPEAIVCSPTAVNTQRKLWQLVCKNEE
i '			ELIKLIEQFPESFFTIKDQENQKLNVQFFQELGLKNVVISRLLT
l			AAPNVFHNPVEKNKQMVRILQESYLDVGGSEANMKVWLLKLLSQ
1			NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLSKLKGFLFQLC
1			PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLYYSVPVLEERM QGLLREGISIAQIRBTPMVLKLTPQIVQYRIRKLNSSGYRIKDG
}			HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPLNVEB
5372	51	857	SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCFCPWLGKGGME
		σ.	PLRLLILLFYTELSGAHNTTVFQGVAGQSLQVSCPYDSMKHWGR
F i			RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNGSTAITDDTLG
· '			GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRKVLVEVLADPLD
f 1		•	HRDAGDLWFPG\DLRASRMPMWSTASPGASWKEKSPSHPLPSFS
l l			SWPASFSSRF+QPAPSGLQPCMDRSQGHIHPVNWTVAMTQGISS
1			KLCQG
5373	2814	346	VKKTKSIPNSAMQEMEVYVENIRRKFGVPNYSPPRTPYTPNSOY
1 1			QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGG
	· 		TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHPSASE
, (ı	ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSPQLSAPITTKTD
1 1	Í		KTSTTGSILNLNLDR9KAEMOLKBLSESVQQQSTPVPLISPKRQ
			IRSPFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSEDSEKS
]			DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
1 1			TNPVBIKEBLKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
	į		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
	1		GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPKTPVLTRSSAQ
	. [TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
	1		AVQRSCGTSSTVQQKRITQSPSTSTITLVTSTQSSPLVTSSGSM
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)			YNDLSKN\TTWKAQLARDSQGLRIEIEKLQWLHQQEL\SEMKHN
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[1		QMLLDPTNPSAGTAKIDKQEKVKLNPDMTASPKILMSKPVLSGG
	1	į	TGRRISLSDMPRSPMSTNSSVHTGSDVEQDABKKATSSHFSASK
	ľ	ľ	ESMDFLDKSTASPASTKTGQAGSLSGSPKPPSPQLSAPITTKTD
j j	j	·	KTSTTGSILNINLDRSKAEMDLKELSESVQQQSTPVPLISPKRQ
	j		IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVEHSDSERS DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKEPSAVKKKPKP
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No: location location corresponding to first maino acid to first maino acid main	_			(A=Alanine, C=Cvsteine, D=Aspartic Acid, E=
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amino acid		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of anino acid sequence (2000, 1-possible nucleotide deletion, 1-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide insertion) (2000, 1-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible nucleotide deletion, 2-possible deletio			amino acid	
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PDLVGAPGSHFCFLNIALLRYNSHTM. 5382 1536 203 GARGSQQDAPALQEABVEGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHPYLHTSPSRPHTGPPLPTPGPDRDRE LITADSDVDEFILDKFLSAGVKQSDLPRKETEQPPAPGSMBESVRG YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPPD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*POVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH]		
5382 1536 203 GARGSQQDAPALQRABVRGPERAQPARGRMTKARLFRLWLVLGS VFMILLIIVYWDSAGAAHPYLHTSPSRPHTGPPLPTPGPDRDRE LTADSDVDBFLDKFLSAGVKQSDLPRKETEQPPAPGSMRESVRG YDMSPRDARRSPDQGRQQABRRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANFIQYLLDPHTSKLAPFNEH				1
VEMILLIIVYMDSAGAAHFYLHTSPSRPHTGPPLPTPGPDRDRE LTADSDVDBPLDKFLSAGVKQGDLPRKETEQPPAPGSMRESVRG YDMSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACTINKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRYGKLSRHLMKVKL KKYTKPLFVKDPFVRLISAFRSKFBLENERF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH	E202	1536	202	
LTADSDVDEPLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRG YDMSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD DIPNSELSHLIVDDRHGAIYCYVPKVACINWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSHHLMKVKL KKYTKPLFVRDPFVRLISAFRSKFBLENERF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH	2202	1236	203	
YDWSPRDARRSPDOGRQOAERRSVLRGFCANSSLAFPTKERPPD DIPNSELSHLIVDDRHGAIYCYVPKVACINWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKFLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTEKLAPFNEH				
DIPNSELSHLIVDDRHGAIYCYVPKVACINWKRVMIVLSGSLLH RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKPLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH]	
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RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL KKYTKPLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH			[DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
KKYTKPLFVRDPFVRLISAFRSKFBLENEEF/*PQVRRAHAAAV RQPHQPARLGARGLPRWPQ\VSPANPIQYLLDPHTSKLAPFNEH				
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MEGA I KIPCHE CÓT DI DE ACCUPATIVA COMPANSA DE COMPANS				
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SEQ Predicted beginning hospinning beginning hospinning hospinning hospinning nucleotide location corresponding to first amino acid residue of amino acid sequence bequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid sequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid residue of amino acid sequence beginning to first amino acid sequence beginning signal proposed for the following for the first amino acid sequence beginning signal proposed for the first acid flustamic Acid, F=Phenylalarine, G=Glyc H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Asparagine, P=Proline, Q=Glutamine, N=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, **Codon, /=possible nucleotide deletion, N=possib	d, B= ine, =Stop FGYPKP ELKKLS VQDFSN CPRAVI RIREEL MBARRC JIEEAQ MESRFN
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence 5383 45 5250 WERLIGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEI PHICKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPIG PSVPFLDFLVVPPSRSRPVSRLGQMFINGQTVNLQAVMENTS	=Stop FGYPKP ELKKLS VQDFSN CPRAVI SIREEL MNAKRC SIEBAQ MESRFN
location corresponding to first amino acid residue of amino acid sequence 5383 45 5250 L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *: Codon, /=possible nucleotide deletion, _=possible nucleotide insertion) PELPGTGPPSSWEEDWFAKTPLAWRQQLYKLYEADFVLI ENLLRD VERLLGCRNSKRTWRMLISKNMPWRRIQGISFGMYSAEI VKSITMPRYLDSLGNPSANGLYDLALGPADSKSVCSTCC CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTC HLLLCQLRVLRVGALQAVYELBRILSRFLEENADPSASE EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHB PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPILG IGKRGYLTPTSARRHLSALWKNEGFFLNYLFSCHDDOGA PSVPFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVM	=Stop FGYPKP ELKKLS VQDFSN CPRAVI SIREEL MILEEL MILEEL MILEEL MESRFN
to first amino acid residue of amino acid residue of amino acid sequence 5250 Testidue of Enlight	PGYPKP ELKKLS VQDFSN CPRAVI SIREEL MNAKRC 3IEEAQ MEGRFN
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion, bequence PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLI KNLLRD 5383 45 5250 VERLIGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEI VKSITNPRYLDSIGNPSANGLYDLALGPADSKEVCSTCU CSGHLGHIELPLTVYNPLLFGKLYLLLRGSCINCHMLTGCU CLGRUEVGALQAVYELBRILSRFLEBNADPSASE EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHM PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPIG IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSCHDDDOG PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVM	PGYPKP ELKKLS VQDFSN CPRAVI SIREEL MNAKRC 3IEEAQ MEGRFN
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, K=Unknown, *: Codon, /=possible nucleotide deletion, \	PGYPKP ELKKLS VQDFSN CPRAVI SIREEL MNAKRC 3IEEAQ MEGRFN
amino acid sequence Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLI ENLERD 5383 45 5250 VERLLGCRNSKETWRMLISKNMPWRRLQGISFGMYSAEI VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCU CSGHLGHIELPLTVYNPILFDKLYLLLRGSCLNCHMLTG HLLLCQLRVLEVGALQAVYELBRILSRFLEENADPSASI EQYTTEIVQNNLLGSQGAHVKRVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPILG IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSCHDDDGR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVM	PGYPKP ELKKLS VQDFSN CPRAVI SIREEL MNAKRC 3IEEAQ MEGRFN
sequence sequence	ELKKLS VQDFSN CPRAVI SIREEL MNAKRC GIEEAQ MESRFN
PELPGTGPPSSWEEDWFAKTPLAWRQQLYKLYRADFVLI ENLLRD 5383 45 5250 VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEI VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCY CSGHLGHIELPLTVYNPPLLFDKLYLLLRGSCLNCHMLTY HLLLQQLRVLEVALQAVYELBRILSRFLEKNADPSASI EQYTTELVQNNLLGSQGAHVKNVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPLA IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSCMDDDGR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	ELKKLS VQDFSN CPRAVI SIREEL MNAKRC GIEEAQ MESRFN
ENLLRD 5383 45 5250 VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEI VKSITMPRYLDSLGNPSANGLYDLALGPADSKEVCSTCV CSGHLGHIELPLTVYNPPLLFDKLYLLLRGSCLNCHMLTV HLLLCQLRVLEBALQAVYELKRILSRFLEKNADPSASI EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPLA IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	ELKKLS VQDFSN CPRAVI SIREEL MNAKRC GIEEAQ MESRFN
5383 45 5250 VERLIGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEI VKSITNPRYLDSIGNPSANGLYDLALGPADSKEVCSTCY CSGHLGHIELPLTVYNPILFDKLYLLLRGSCINCHMLTO HLLLCQLRVLEVGALQAVYELKRILSRFILEBNADPSASE EQYTTEIVQNNLIGSQGAHVURTCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPLK IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAV	VQDFSN CPRAVI SIREEL MNAKRC GIEEAQ MESRFN
VKSITMPRYLDSIGNPSANGLYDLALGPADSKEVCSTC' CSGHLGHIELPLTVYNPILLFDKLYLLLRGSCLNCHMLTC CSGHLGHIELPLTVYNPILLFDKLYLLLRGSCLNCHMLTC HILLCQLRVLEVGALQAVYELERILSRFLEKNADPSASI EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHP PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPLC IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSCHODDOR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	VQDFSN CPRAVI SIREEL MNAKRC GIEEAQ MESRFN
CSGHLGHIELPLTVYNPILLFDKLYLLLRGSCLNCHMLT(HILLCOLRVLBVGALQAVYELBRILSRPLEBNADPSASI BQYTTELVQNNLLGSQGAHVKNVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITPPAMVHRTAGQKDSEPLC IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSCHODDOR PSVPPLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	CPRAVI BIREEL MNAKRC JIEEAQ MESRYN
HLLLCQLRVLEVGALQAVYELKRILSRFLEKNADPSASI EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLO IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGN PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	rireel Mnakrc Jieeaq Mesryn
BQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHN PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLO IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGN PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	nnakrc Sibeaq Mbsryn
PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSBPIG IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGR PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVM	Gibeaq Megren
IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGN PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	Mesrfn
PSVFFLDFLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVN	
TRUTT I I TRUTT I TRUTT I	
IRKIJALMAQEQKLPREVATPTTDEEKDSIJAIDRSPLS	
SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQI GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFAT	
QPVTPWNVQELRQAVINGPNVHPGASMVINRDGSRTALS	
QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNE	
RPSIQAHRAR L LPERKVLR LHYAN CKAYNAD PDGDEMNZ	-
RLGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGAS	
CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTG	
TILINIIPEDHIPINLSGKAKITGKAWVKETPRSVPGFN	
ESQVI LREGELLCGVLDKAHYGSSAYGLVHCCYE I YGGE	
LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIJ	EESTR
CSPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNM	
KEBUNHYSNBINKACMPFGLHRQFPENTLQLMVQSGAKG	
MQISCILGQIELEGRSTPLMASGKSLPCFEPYEFTPRAG	
RFLTGIKPPKFVFHCMAGREGLVDTAVKTSRSGYLQRC1	
GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQ SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHF	
RCAPLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RM	
BLDEESRRKYQKKAAACPDPSLSVWRPDTYFASVSETFE	
YSQBWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEP	
LLAAQSIGEPSTOMTLNTFHFAGRGEMNVTLGIPRLREI	
ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQ	KIDVQ
ESFCMEEKQNKFQVYQLRFQFLPHAYYQQBKCLRPEDII	RPMBT
RFFKLLMESIKKKNNKASAFRNVNTRRATORDLDNAGBL	GRSRG
EQEGDERESGHIVDAEASEGDADASDAKRKBKQBESEVDY	
. ERREGRENDDBDMQEERNPHREGARKTQEQDEEVGL/GH	
PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFID	
TERSLWCQVTVKLPLMKINPDMSSLVVSLAHGAVIYATK	
LINETTWIKNEKELVLNTEGINLPELFKYARVLDLRRLY	- 1
Alantygieaalrvirkrikdvpavygiavdprhlslya	
EGVYKPLNRFGIRSNSSPLQQMTFBTSFQFLKQATMLGS SPSACLVVGKVVRGGTGLFELKQPLR	HURTK
5384 196 886 QSCGQRLPTVL+L+GPPGSCPCILSLF\PGRPHALPRIR	DVYNY
TILKGDKGDPGPMGLPGYMGREGPQGBPGPQGSKGDKGB	
APCQXRFFAFSVGRKTALE3GKDFQTLLFERVFVNLDGC	
GOFAAPLRGIYFFSLNVHSWNYKETYVHIMHNOKEAVIL	
ERSIMQSQSVMLDLAYGDRVWVRLFKRQRKNAIYSNDFD	
SCHLIKAEDD	
5385 326 799 LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVESHKK	NKIHM
SPTFRRPKTL+LRRQPKYPWKSTPRRNKLDHHVIIKPPL	
VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKV	_
SDGERKAYVRLAPDYDALVVATKIGIT	1
5386 326 799 LMVPRTKKEAPAPPKARAKAL\KAKKAVLKDVHSHKK	
SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPL	
VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKV	NTLIQ
SDGERKAYVRLAPDYDALVVATKIGIT	1
5387 2 2117 FVVAASGGCNFVLGERRAGSLLSASYGTFAMPGMVLFGR	
SDDLVFPGPFELVVRVLWWIGILTLYLMHRGKLDCAGGA:	
LIVIMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKL	
ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSW	
TVVSIIIVFDPLCGKMAPYSSAGPSHLDSHDSSQLLINGLI	ATAAT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
	 	 	SVWBTRIKLLCCCIGKDDHTRVAFSSTABLFSTYFSDTDLVPSD
1			IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
1	į.	i	HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
I			VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
1		1	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
		· ·	KGISQAARYVYQRLINDGILSQAFSIAPBYRLVIVGHSLGGGAA
1		1	ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
ł	ì		KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
i	1	i	CNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAXSFSSDSPL
1			DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
1	Ĭ	1	PSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV
1	Į.		DVA
5388	1569	753	
-300		/33	TADGGAGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
1		{	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDG3VPBAQSALDST
i	l	ł	
ļ	1	ł	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMP
1	Ĭ.	•	TVVYTVIQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
1	l .		ILEHLQTKN
5389	1569	753	TADGGAGGGRQAGVRHYLYPFTGGYRRRAACQAERPAARS
5555	1305	/	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
ł		j	TNGMCSVCYKKHLQRQNSSNGRISPPVQCTDGSVPZAQSALDST
			SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
l .			DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
ì		ł	TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
1			ILEHLQTKN
5390	217	1332	EDPRKLMEDKNWSECEGPEMSLVCLTDFQAHAREQLSKSTRDF1
	l	1332	EGGADDSITRDDNIAAPKRIRLRPRYLRDVSEVDTRTTIGGEEI
İ			SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
}	1		LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
}	Į .		LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
[TSLCWNDLSWFQSITRLPIILKGILTKEDAKLAVKHNVOGIIVS
			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
-		•	ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
1 .			LTGCRSVAEINRNLVQFSRL
5391	1	1292	VKKAAGRERGPPTAGGQRCBEAPGTVMERRLGVRANVKENRGS?
			QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEBGEEVFYQLBGDM
			VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
<u> </u>	}		RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
ļ .			SBOYRTGXPIPDOLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
l · · ·		• .	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
			VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
			DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
[YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
]		PVLPGGLPPAPLLPIPLSLQTQCSTSTPRRPSIKAS
5392	1	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
		•	CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
	ļ		PIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
			RTOVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
			GMSI8IHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
[[YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
}			LHSPPKVALPPERLAGPEESAWGDBEDSLEHNYYNSIPGKEPPL
ļ	J		GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
			PGDGYVQADARGPPDHREHLYVNTQGLDAPEPEDSPKKDLFDMR
		į	PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTERQ
		.]	LRQEPWYHGRMSRRAABRMLRADGDFLVRDSVTNPGQYVLTGMH
		İ	
			AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE SELHLRGVVSREP
5393	2	982	
	- 1	704	GGDSAGMTMBTQMSQNVCPRNLWILLQPLTVLLLLASADSQAAAP
<u> </u>			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWPHNG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
i	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence	sequence	\=possible nucleotide insertion)
<u> </u>	sequence		\nLipthtqps\yrfkannn\dsgrytcqtgqtsl\sdpyhltv
ľ	ł		TOPOLITIONS (TREADING DOCUMENT PORTS) TOPOLITY
}	}	ļ	LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
			SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
(QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1			STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTINP
6304			RAPTODOKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
ĺ			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
J .			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
] '			LSEWLVLQTPHLEFQBGBTIMLRCHS\WRDKP\LVKVTFFQNGK
l			SOKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
Į			QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
]			STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
F305	34.5		RAPTDDDKNIYLTLPPNDHVNSNN
5395	3135	531	RASDAKNOEGILNTRRKSTDSVPISKSTLSRSLSLQASDPDGAS
ļ			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
1			KPTETPPVKBTQQEPDERSLVPSGENLASETKTESAKTEGPSPA
	·		LLBETPLBPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
}			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVR_RFDYSEDKS
			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPRKLDNTPASP
			PRSPARPNDIPIAKGTYTYDIDKWDDPNFNPFSSTSKMQRSPKL
i i			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
j			ANGVDGDGLNKPAKKKTPLXTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDREKLAVTNQKWTCMTVDLRADKQD
1	İ		YPQPSDLSTFVNETKFSSPTEELDYRNSYEIRYMERIGSSLPQD
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELRAMGLGTP
			SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN PPLFAQKLQRRAAHPTDVSISKTALYSRIGTABVEKPAGLLFOO
1			PDLDSALQIARAEIITKEREVSEWKDKYERSRREVMEMRKIVAE
\			
			YEKTIAQMIEDEQREKSVS\HQIVQQLVLEKEQA\LADINSVEK \SLADLFRRYEKMKEVLEGFRKNEKVLKRCAQEYLSRVKKEEQR
			YQALKYHA\BBKLDRANAB\LAQVRGKAQOBQAAHQASLABRSS
ł i			CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5396	3135	531	RASDAKNOBGLINTRRKSTDSVPISKSTLSRSLSLOASDFDGAS
3370	3133	331	SSGNPBAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
i i			KPTETPPVKETOOEPDEESLVPSGENLASETKTESAKTEGPSPA
l .			LLEBTPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG RKTLPLTTAPRAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
			SWDNQQKNPPPTKKIGKKPVAKMPLRRPKMKKTPKKLDNTPAS?
	,		PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMOESPKL
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
			ANGVDGDGLNKPAKKKETPLKTDTFRVKKSPKRSPLSDPPSOD2
ļ.			
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLRADKQD
	ſ		YPOPSOLSTFVNETKFSSPTEKLDYRNSYEIFYMEKIGSSLPOD
			DDAPKKQALYIMPDTSQBSPVKSSPVRMSBSPTPCSGSSFKETB
	1		ALVNTAAKNOHPVPRGLAFNOESHLOVPBKSSQKELEAMGLGTP
			SEAIRITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLARKN
			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
			PDLDSALQIARABIITKERBVSEWKDKYBESRRBVMEMRKIVAB
	į	l	YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
	Ì	1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
		i	YQALKVHA\BEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
	3,5,5		CRV\DALERTLEQKNKEIEBLTKICDELIAKMGKS
5397	3135	531	RASDAKNOBGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	l	l	SSGNPBAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
	.]	. }	KPTETPPVKBTQQEPDBBSLVPSGBNLASETKTESAKTEGPSPA
		l	LLBETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
	ł	l	RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
' <u> </u>	}		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
		<u> </u>	PRSPARPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	_	\=possible nucleotide insertion)
1			POOSYNFDPDTCDRSVDPFKTSSKTPSSPSKSPASFEIPASAME
1		1	ANGVDGDGLNKPAKKKKTPLKTDTPRVKKSPKRSPLSDPPSODP
1		İ	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKOD
ł			YPQPSDLSTFVNETKPSSPTEBLDYRNSYBIKYMEKIGSSLPOD
1			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
			ALVNTAAKNOHPVPRGLAPNQESHLQVPEKSSQKELEAMGLGTP
j			SEATETTAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
	ĺ		PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFOO
1	ł		PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAR
1			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
1	Į		\SLADLFRRYEKNKEVLEGFRINEEVLKRCAQBYLSRVKKEEQR
1	ł		YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
<u></u>	L		CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5398	56	5426	SGEVCRMESNENGEGVPRPSYVFSADPIARPSEINFDGIKLDLS
1	1		HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
	}		ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKPSFPPGFLGPAT
			TQKEPFQGCIMHP\VKDLLKGQSRLIPTYGLTNSGKTYTFQGTB
1	1		ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYLRLSSBQEK
ł			EEIASKSALLRQIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
			DYEQANLNMANSIKFSVWVSFFBIYNBYIYDLFVPVSSKFQKRK
Í			MLRLSQDVKGYSFIKDLQWIQVSDSKRAYRLLKLGIKHQSVAFT
1			KLNNASSRSHSIPTVKILQIEDSEMSRVIRVSELSLCDLAGSER
1			TMKTQNEGBRIRETGNINTSLLTLGKCINVLKNSBKSKFQQHVP
			FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
1			AIAQKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
1		,	ATISWENSLEDIMEDEDLVEBLENABETED/VGETKLLDEDLDK
1	·		TLEENKAPISHERKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
		i	EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
			KCDTRBEAAKDICATKVBTEBATACLBLKFNQIKAELAKTKGEL IKTKEBLKKRENESDSLIQELETSNKKIITONORIKELINIIDO
			KEDTINEFONLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
1			PKDSKSKICSERKRVNENELQQDBPPAKKGSIHVSSAITEDOKK
)			SBEVRPNIARIEDIRVLQENNEGLRAFILTIENELKNEKREKAE
i i			LNKQIVHFQQZLSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
			SKNQEQBEKIMKLSNBIETATRSITNNVSQIKLMHTKIDELRTL
) .			DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV
	•		KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHOIKELEO
(}		QIEKLQABVKGYKDENNRLKEKEHKNQDDLLKEKETLIQOLKEB
) i			LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
1			TOKVERSHSAKLEODILEKESIILKLERNLKEPOEHLODSVKNT
(KDLNVKELKLKEBITQLTNNLQDMKHLLQLKEBEBETNRQBTBK
			LKEBLSASSARTON\LNADLORKEEDYADLKEKLTDAKKQIKQV
			QKEVSVMRDEDKLLRIKINBLEKKKNOCSQELDMKQR\TIQQLK
()	İ		EQLINQKVEEAIQQYBRACKDLNVKBKIIBDMRMTLKEQEQTQV
			EQDQVL\BAKLEBVERLATELDRWRVKCNDLETKNNQRSNKEHE
			NNTDVLGKLTNLQDBLQKSEQKYNADRKKWLEEKMMLITQAKEA
[ENTRNKEMKKYAEDRERFFKQQNEMETLTAQLTEKDSDLQKWRE
			erdqlvaaleiqlkalissnvqkdneieqlkriisetskietqi
			MDIKPKRISSADPDKLQTEPLSTSPEISRNKIEDGSVVLDSCEV
			STENDOSTRPPKPELBIQFTPLQPNKMAVKHPGCTTPVTVKIPK
	į		ARKRKSNEMEEDLVKCENKKNATPRTNLKPPISDDRNSSVKKEQ
1 1			KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
[[{		PSILQSKAKKIIETMSSSKLSNVRASKENVSQPKRAKRKLYTSB
l		·	ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
1	ł		ASPTPGEVQRHLQTHG1DGNGELDFSTFLTIMHMQ1KQEDPKKE
]			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
<u> </u>			\adibpngkvkydefihkitsyldgty
5400	931	248	SHCSSGMBIPPTNYPASRAALVAQNYINYQQGTPHRVFBVQKVK
į 1	Į.		QASMEDIPGRGHKYRLKFAVEBIIQKQVKVNCTAEVLYPSTGQE
<u> </u>	!		TAPEVNFTFEGETGKNPDREDNTFYQRLKSMKEPLEAQN1\PDN

Seginating medicatide corresponding corresponding to first anino acid amino acid amino acid amino acid sequence	SEO	Predicted	Predicted end	I mino poid
NO: loucion corresponding to first amino acid residue of samino acid residue of samino acid residue of samino acid sequence designed for since and said sequence sequ			1	Amino acid segment containing signal peptide
Corresponding to first and acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid sequence sequence Peroline, Gellutamine, Rehylinine, Sequence Peroline, Gellutamine, Kalylinine, Sequence Peroline, Gellutamine, Malikinine, Sequence Peroline, Gellutamine, Malikinine, Sequence Peroline, Gellutamine, Malikinine, Sequence Peroline, Gellutamine, Malikinine, Sequence Peroline, Gellutamine, Malikinine, Sequence Peroline,	1			
to first amino acid residue of amino acid sequence sequ	NO:			Giulamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid amino acid amino acid amino acid amino acid amino acid sequence s	į.	1 '		
amino acid sequence anino acid sequence codon, /=possible nucleotide deletion FRAVSPERTIMILARYAGOTITEOSITEMPEMENTO/TOKOV CODON (=possible nucleotide deletion) FRAVSPERTIMILARYAGOTITEOSITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTO/TOKOV CRENDPILE/DITTLIAIN/TASSBITEMPEMENTIMESTYPMS KNAPRODMIN-TYMERICA/SCSSBASC/DMCTRADE/DEVILE/THEMS SKALEGIGADPOIDMESSUCIAILIA/KLOMMYCA/CATEADOCOD HIKKKASQO/MASPS/SHEMPS/SCSSBAS/DMISHIPS/TEPTPEPPEMENTO/ SEKULPCIA/DMCT/CATEADOCOD HIKKASQO/MASPS/SHEMS/SCSSBAS/DMISHIPS/TEPTPEPPEMENTO/ DRAVS/SARHOA/CHEMPS/SCSBAS/DMISHIPS/TEPTPEPPEMENTO/ DRAVS/SARHOA/CHEMPS/SCSBAS/DMISHIR/TESTPEPPEMEND/A PEPSPELIKAR/PRATA/DARABOK/SESSBAS/DMISHIPS/TEPTPEPPEMEND/A PEPSPELIKAR/PRATA/DARABOK/SESSBAS/DMISHIPS/TEPTPEPPEMEND/A PEPSPELIKAR/PRATA/DARABOK/SESSBAS/DMISHIPS/TEPTPEPPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADILI/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTPEMEND/A PROBADA/SARJAGIA/CHERPS/TEPTP				
xesidus of amino acid sequence (Codon, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide insertion) 5401 3 1360 TREATILLANIASQRIIPMOMQVIMHEQIGITKUKINE REPERVOLE 5401 3 1360 TREATILLANIASQRIIPMOMQVIMHEQIGITKUKINE REPERVOLE SKRICALGOPIUMERSUSCOSMOCREDGUIVETUMENSTYLENE REPERVOLE SKRICALGOPDIUMESUSCOSMOCREDGUIVETUMENSTYLENE REPERVOLE SKRICALGOPDIUMESUSCOSMOCREDGUIVETUMENSTYLENE REPERVOLED HIHKKSQQVPASSICHMICALGUIVETUMENSTYLENE REPERVOLED HIHKKSQQVPASSICHMICALGUIVETUMENSTYLENE VISCONTORIALGUIVETUMENTA VISCOSSGODERRABERVEVEVIVIRD SEVEN VISCONTORIALGUIVETUMENTA VISCOSSGODERRABERVEVEVIVIRD REPERVOLENTA VISCOSTORIALGUIVETUMENTA	ĺ			
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FRINSPERMITUHILAWARGGI LINGSSTEDIWIKWWKIGTVKOV QRINDPI KILDYTILIAINTASGEI ISWOOQVIAHIPQYGTKVKIRIS \$1360 \$13	1	sequence		\=possible nucleotide insertion)
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TVERSCHOODBTIETIENJEAREALLAMDBROGMALDERINNNITES PEDDWVAPVTHVSVTLDGIPEVMETQQVQBKYADSPGASSPEQ PERKERETEPPROBPATTENISVKKNKDCKGNTITLMEFILL ALLQDKATCPKYIKMTQRKGIFKLVDSKYPEKMEKHKNKPQD MINTEPMERALHYYYGRILAKVGGQRIVYQFKEMPKILIVINDE DPSSSIESSDESLESSATSINNOTSRERVSSSFGVKGGATTVLK PGSIKAARKHDVEVADPSBULTRVOTGSPYPTOLPRTVIVVQ PVQAVPGGBARTSTMQDETLNSVQSIR\TIQAPTGVPVVVSP RNQQ\LHTVILQTVPLTTVIASTDERAGTSSQKFILQAIPSSQF MTVLKENVMLQSQKAGSPFSIVLGAPQVQVTSNVQTICNGT VSV\ASSPEPS\ATAPVVTLIFLGSSQLVAHPPGTVTTSVIKTQ ETTELTQVBUKKESSEDHLKENTEKTEQQPQPYVMVVSSSNGFTS QVAMKQNELLEPNSP 5403 3445 1563 GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV PGADILISYAGLACVEEPRIDHITSSSLDVARERIIDDDDDITL TVRASCHDCDETITSTIRAARALLANNOSPGEMLDERINNITFSS PEDDWVADAVTHVSVILDGIPEVMETQQUFYADSPGASSPD PKRKKGRKTKPPRDSPATTPNISVKKNKDGKGNTTYLMEFIL ALLQDKATCPKYIKWTQREKGIFKLVDSKYPSKHRGKNKPQD MYREPMERALRYTYGGGILAKVGGQUKYADSPGASSPD PKRKKGRKTKPPRPDSPATTPNISVKKNKDGKGNTTYLMEFIL ALLQDKATCPKYIKWTQREKGIFKLVDSKYPSKHRGKNKPQD MYREPMERALRYTYGGGILAKVGGQUKYADSPGASSPD PKRKKGRKTKPPRPDSPATTPNISVKKNKDGKGNTTYLMEFIL ALLQDKATCPKYIKWTQREKGIFKLVDSKYPTQLRFTUFVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHVVQ PVQAVPBGEBAPTSTMQDETLINSSVQSIRVTTQAFTVHSSGP TUPUTLIFAKRETLQSTLLLLLLVPLIKPAPPTQQDSRTITDYGT UNFRSIFSQDYBCKSSEDHLKENTEKTEQQPQPVVMVVSSSNGPTS QVMKQNIKLKRINSPS 5404 187 1111 LEVUTLIFAKRETLQSTLLLLLLVPLIKPAPPTQDESRTITDYGT DNFRSIFSGPQHARSERSTRUPPARGEMERTHSII PINVANNYSHRITSHITBHGBAPVPSRLDFTSILLSITGTSGAFSGS KNSHAGSPSTVRRTERSTRUPPARGEMERTHSII PINVANNYSHRITSHTBHGBAPVPSRLDFTRAFTGAASSGS NSSASBGGLIGHSPTTREPSVVRRPAPRTARQEMERTHSII PINVANNYSHRITSHTBHGBAPVPSNARGFLIRSTSTGASASSGS NSSASBGGLIGHSPTTREPSVVRRPAPRTARQEMERTHSII PINVANNYSHRITSHTBHGBAPVPSNARGFLIRSTSTGASASSGS NSSASBGGLIGHSPTTROFLPS	1			
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PERKKGRITKPPRPDSPATTPNISVKKNINDKKSMTITIANBFIL ALLQDKATCPKYIKWTQREKSIFKLVDSKGVSRLWRRHKNKP\D MNTEPMGRALAYYQRGILAKVEGGRIVVQFKEMPKOLIYINDB DPSSSIESSDBSLSSSATSMRNOTSSRSVOSSSFOVKGGATTVLK FGSKKAARKENDEVAUQPGSPLINTUPTGSPYPTQLFTVHKVQ PVQAVPBGRAARTSTMQDETLINSVQSIR\TIQAPTQYPVVVSP RNQ\LHTVILQTVPLTTVIASTDPSAGTGSQKFILQAIPSQP MTVLKENVMLQSQKAGSFPSIVLGGSRV\QQVLTSNVQTICNGT VSV\ASSESFS\ATAPVVTLFLGGSQLVAMPFGTVTISVIKTQ ETKILTQEVEKKESSDBHLKENTEKTGQCPPYVMVVSSSGFTS QVAMKONELLEPNSP OVAMKONELLEPNSP OVAMKONELLEPNSP PGADILNSYAGIAC-VERPIMMITESSLDVABEBIIDDDDDITL TVBASCHDQDBTISTIBABALLAMDSPGPHDLBKRINNNIFSS PEDMWVAPVTHSVYTLDGIPEWBTQQVQKKYADSBGASSPDQ PKRKKGRITKPPRPDSPATTPNISVKKNKDGKGNTIYLMEPIL ALLQDKATCPKYIKWTQREKGIFKLVDSKFVSRLMRKHKNKP\D MNTEPMGRALRYTYQRGILAKVGGQRLVYQFKEMPKOLIYINDD PSSSIESSDBSLSSSATSBRNQTSSRSVVGGGATTVLK PGASKAAKKNDVPVXPAQPSSVLRTVQPTQSYPTQUFRTVHKVQ PVQAVPEGRAARTSTMQDETLANSVQSIR\TIQAPTQVVVVSP RNQQ\LHTVILQTPUTTVIASTDPSAGTGSQKFILQAIPSSQP HTVILKENVMLQSQKAGSPPSIVLIGPARV\QQVLTSNVQTICNGT VSV\ASSPSSS\ATAPVVTLFILGSQLVAHPPGTVITSVIKTQ EKTILTQEVEKKESBEDHLKENTEKTEQQQQPYVMVVSSNGFTS QVAMKQNRILLEPNSP 5404 187 1111 LEVTLIFARMSTLQSTLLLILLLUPLIKPAPPTQQDGRIIYDYGT DMFRESIFSQDYBKYLDGKNILGETGMLEBILBGTFSKL LYARPIKKIKLT\ANDFOLIKVERSQLVCBEVDTAVPLERRSAY LYARPIKKIKLT\ANDFOLIKVERSGTUNAUPPSLLQTFRALEDFTSKL LYARPIKKIKLT\ANDFOLIKVERSGTUNAUPPSLLQTERSQFTA SLVEBLSLABRQLLKLPVILGHPNSPICLKRLDIGSFT SLVEBLSLABRQLLKLPVILGHPNSPICLKRLDIGSFT CKNNITSTYRIPRIEBIRLREDFTGMLEBILGGTFSKL SLVEBLSLABRQLLKLPVILGHPNSPICLKRLDIGSFT SLVEBLSLABRQLLKLPVILGHPNSPICLKRLDIGSFT TILLIQUIKAIRGSBRTTEGSPATAPRRUPBERTHBII PINNNNYEHRIPSHIGHAVLPSNARGPILDRERTREFTHBII PINNNNYEHRIPSHIGHAVLPSNARGPILDRERTREFTHBI PINNNNYEHRIPSHIGHAVLPSNARGPILDRERTREFTHBIC PINNNNYEHRIPSHIGHAVLPSNARGPILDRERTREFTHBIC PINNNNYEHRIPSHIGHAVLPSNARGPILDRERTREFTHBIC PINNNNYEHRIPSHIGHAVLPSNARGPILDRERGCCKCNS SMWKGTCMCL\VKG FYHICSNDDBGDSYSDNPCSCSOSHCCSR YLCMGAMSLPLPCLLCLYPPPAKGCLKLCRCYDMIHRPGCRCKNS NTYCKKLBSCPSRCQCKRS	1			PEDDMVVAPVTHVSVTLDGIPEVMETOOVOEKYADSPGASSPRO
ALLQDKATCPKYIKHTQREGSIFKLWDSRPWSRLMRKHRNKP\D MINTEPMGRALRYYYQRGILAKVEGGRIVVQPKEMPKDLIYINDE DPSSSTESSDPSLSSSATSMRNDTSRSRVSSSPCWKGGATTVLK PCMSKAAREKDDVEWAQDSBULKTVQPTQSPYPTQLPRTVHVVQ PVQAVEGGARITSTMQDETIASSYGIR\TIQAPTQPVVVSP RNQQ\LHTVTLQTVPLTTVIAGTDPSAGTGSQKFILQAIPSSQP MIVLKENNVALQSQKAGSPFSIVLGPARV\QQVUTSNVQTICMST VSV\ASSPSFS\ATAPVVTLFLISSQLVARIPEGTVITSVIKTQ ETKTLTQEVEKKESEDHLKENTEKTEQQFQPYVMVVSSSNGFTS QVAMKQNBLLEPNSF 5403 3445 1563 GECFIMAAVVQQNDLVFFFASNVMEDERQLGDPAIFPAVIVEHV PGADILNSYAGLACVERPNDMITESSLDVARERIIDDDDDTITL TVASS-GHODDTTISTRARALILANDSPGPNLDEKRINNIFSS PEDDMVVAPVTHVSVTLDGIPKWMTQQQKKYADSRGASSPSQ PKRKKGRYKPPRPDSPATTPNISVKKNKDGKGNTIYLWEFLL ALLQDKATCPKYIKWTQREGIFKLVDSKPVSLMKRCHKNKP\Q MYMPPMGRALRYYQGGILAKVUSQRLVQVYKMPKDLIYIMDB DPSSSIESSDESLSSSSTSSNNTSVSROSTRVSGGATTVLK PCMSKAAROKDPVSVAQPSSVLRTVQPTQSPYPPQLFRTVHVVQ PVQAVPEGBAARTSTMQDBTLMSSQGILVTQPKRMPKDLIYIMDB DPSSSIESSDESLSSSSTSSNNTSVSSVSVSGGATTVLK PCMSKAAROKDPVSVAQPSSVLRTVQPTQSPYPPQLFRTVHVVQ PVQAVPEGBAARTSTMQDBTLMSSQGILVTQAPTQSPYPPQLFRTVHVVQ PVQAVPEGBAARTSTMQDBTLMSSQGILVTQAPTQSVTSVTGTT VSV\ASSPSS\ATSPAPVUTLFLLSSQLVAMPPGTVLTSVILTSVILTQ ETKTLTQEVERKESEDHLKENTEKTEQQPQPYVMVVSSNNGFTS QWMKQNBLLEPNSP 1111 LPVTLTFARMWTLQSTLLJLLLVPLIKPAPPTQDDSRITYDVGT DNFERSIPSQDYBOKYLDGRIKERETVIIPNAKYNKIKSSGIKANAFK KLNMLTFYLJCHNALSVPLANPESLYHLLGPNILASTTDDTF SLVERISLSLARNQLLKLPVLPPRLITLFNAKYNKIKSSGIKANAFK KLNMLTFYLJCHNALSVPLANPESHVHLDGNNLASTTDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFILLERDTFSKL SLVERISLSLARNQLLKLPVLPPRLITLFNAKYNKIKSSGIKANAFK KLNMLTFYLJCHNALSVPLANPESHVHLDGNNLASTTDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPRSFILDTERGFDF 1220 QNSRSLIMDPQNQHGGGSSSLVVIQQPSLDSRPFLDYERSIGF NSSASSRGGLLGRSPPTRVPSHABRERNIETPREDFVUKRERTHBII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSRGGLLGRSPPTRVPSHABRERNIETPREDFVLDCLCCSS SWWEYGTCMCLVVKLESDDDGGGSSSLVCCGSSCHCCGS SWWEYGTCMCLVVKLESDDDGGGSSSLVLCCRCCTOWHIRPGCCCKNS NVYYCKLESCCSRGQKRS	1			
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DNFERSIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDBAI TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKBSAY LVARFNIKKLT\AKDFADIPNLERLDFTGBIJEDLEDGTFSKL SLVEBLSLAENQLLKLPVIPPKLTLFNAKYNKIKSEGIKANAFK KLINLTFIYLDHALESVPLINLPBSLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHBII PINVINNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	5404	187	7117	L
TPLPPKKENDEMPTCLLCVCLSGSVYCEBVDIDAVPPLPKBSAY LYARFNKIKKLT\AKDFADIPNLRKLDFTGNLIEDIEDGTFSKL SLVERLSLABNQLIKLPVI.PPKLTLFNAKYNKIKSEGIKANAFK KINNLTFLYLDHNALESVPLNLPBSLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYP 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQBKHERTHBII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAIRTOPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS			-44	
LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL SLVEBLSLABNQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAPK KLINLTFLYLDHNALESVPLNLPBSLRVIHLQPNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSPICLKRLPIGSYP 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDVEREIQPTA ILSLQIKAIRGSNEYTBGPSVVKRPAPRTAPRQEKHERTHBII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAIRTOPKOLIVDDLKGS LKEDLTOHKPICEQCGKCKCGGCTAPRTLPSCLACNGCLCSAE SMVEYGTCMCLVVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS				
SLVEBLSLAENQILKLPVLPPKLTLFNAKYNKIKSRGIKANAFK KLNNLTFLYLDHNALESVPLNLPBSLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSPICLKRLPIGSYP 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDVEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHRII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTOHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SWEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLPLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	1 1			· ·
KLNNLTFLYLD#NALESVPLNLPBSLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGBSVVKRPAPBRTAPRQBKHERTHBII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTSSASSGS NSSASSEGGILGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACRRQCLCSAE SWEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	1 1	ſ		•
CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYP 5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYRREIQPTA ILGLDQIKAIRGSNEYTEGPSVVKRPAPPRTAPRQBKHERTHBII PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAITGPKQLIVDDLKGS LKEDLTOHKFICEQCGKCKGECTAPRTLPSCLACNRQCLCSAE SMYEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	1 1			-
5405 2199 1220 QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHBII PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKPICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SWVEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS] }	j		_
ILSLDQIKAIRGSNEYTBSPSVVKRPAPRTAPRQEKHERTHBII PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEGGLLGRSPPTRPVPGHRSERAIRTOPKOLIVDDLKGS LKEDLTOHKPICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	<u>l</u>			
PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRCQGKPS	5405	2199	1220	
PINVNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRCQGKPS	} I			ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
NSSASSEGGLLGRSPPTRPVPGHRSERAIRTOPKOLIVDDLKGS LKEDLTOHKPICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	} I	j		
LKEDLTOHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	} [
SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	í í			=
YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS NTVYCKLRSCPSRGQGKPS	[J		
ntvycklrscpsrcqgkps	1 1		,	
	ļ j		·	
2/32 RWKTYNVBGPLTFMDVALEMCLEEWQCLDTAQQNLYKNVMLENY	1 540c	276	7720	
	1	413	4132	KMKIINARGEFIFMDAVIRECTERMÖCTDLYÖÖUTIKUAMPENA

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid sequence	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, P=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) RNLVPLG/IIAVSKPDLITCLEQEKEPWEPMRHEMVAKPPVMC SHPTQDFWPEQHIKDPFQXATLRRYKNCEHKNVHLKKDHKSVDR CKVHRGGYNGFNQCLPATQSKIFLFDKCVKAFHKFSNSNRHKIS HTEKKLFNCKECGKSFCMLSHLAQHKIIHTRVNFCKCEKCGKAF NCPSIITKHKRINTGEKPYTCEBCGKVFNWSSRLTTHKKNYTRY KLYKCEBCGKAFNKSSILTTHKIIRTGEKFYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCEGCKAFKWSSKLTEHKLTHTGEKPYKCR KCGKAFNQPSNLTTHKRIHTA\EKPYKCTECGEAFSRS\SNL TKHKEIHTEKKPYKCBCGKAFKWSSKLTEHKLTHTGEKPYKCR KCGKAFNCPSIITKHNRINTGEKPYTCEBCGKVFNWSSRLTTHK KNYTRYKLYKCEECGKAFNKSSILTTHKKHIEKKFYKCEECGK AFKWSSKLTEHKITHTGEKPYTCERCGKVFNWSSRLTTHK KNYTRYKLYKCEECGKAFNKSSILTTHKKHIEKKFYKCEECGK AFKWSSKLTEHKITHTGEKPYKCBECGKAFNHFSILTKHKRIHT
			GRRPYKCEBCGKAFTQSSNLTTHKKIHTGBKFYKCEECGKAFTQ SSNLTTHKKIHTGGKPYKCBECGKAFNQPSTLTKHKIHTERKP YKCEBCGKAFKWSSTLTKHKIIHTGEKPYKCBCG\KAFKLSST LSTHKIIHTGBKPYKCBKCGKAFNRPSNLIBHKKIHTGBQPYKC ERCGKAFNYSSHLNTHKRIHTKBQPYKCKBCGKAFYQYSNLTTH
5407	3	659	NKIHTGEKLYKPRDVTVILTTPQTFSNIK RPRRRQSSCCTGWLAGWILIRAAPRFCRRTETDMRQGKGLAVLIL AIILLQGTLAQSIKGMHLVKVYDYQEDGSVLLTCDAEAKNITWF KDGKMIGPLTEDKKKWNLGSNAKDPRGMYQCKGSQNKSKPLQVY YRMCQNCIRLNAATISGFLPARIVSIFDLAVGVYFIAGTGMEFR QS\RASDKQTLLP\NDPAPTQPLKDPRKMTQYSHLQGN\QLRRN
5408	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQR'LP
5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFORPICSASPPWASRP STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRPLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQARHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNIGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKVAPRFNGFQQQDSQEILLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWBVAAEANDNHLRRNRS IVVDLPHGQLRSQVKCKTCGHISVRPDPFNFISLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAPRIPVPVSPISASSP TQTTDFSSSPSIMEMFILITINGDLPRPIFIEMGMPNTVVPCGTEX NFTMGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYPLSSQKNR PSLEGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHRSVEQSKRAQ VEPINLDSCLRAFTSBEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCOHKPLTPQGDELSEPRILARRVKKVDAQSSAGEEDVILSKS PSSLSANIISSPRGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGGSKNKLSSSERNLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHRACGNGCGNGYSNGQLG NHSBEDSTDDQRBDTRIKPIYNLYAISCHSGLLGGGHYVTYAKN PNCKYYCYNDSSCKRLHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFSDY\EKYCVLQ
5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSBPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFPRDFXDSAAKREQGSL STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTULDIGGGWFPHYDPERSCWVRALSQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTHPIGMKGHMAKCYGD LVQBLMSGTQKNVAPLKLRWTIAKYAPRPRGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDMHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL BITVIKLDGTTPVRYGLRLNMDBKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKMFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amine acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	_	\=possible nucleotide insertion)
1	l —	<u> </u>	TOTOFSSSPSTNEMPTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
]	NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
i !			PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPOEASNH
1 1		1	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
1 1		l	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
1 1	Ì	1	VBPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
1 !			LPPILITHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
1 1			ALCOHKPLTPOGDELSEPRILARBVKKVDAQSSAGEEDVLLSKS
1 1		ł	PSSLSANIISSPKGSPSSRKSGTSCPSSKNSSPNSSPRTLGRS
1 1			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
1 1			VLGGSQPELVTPQDHEVALANGPLYEHEACGNGCGNGYSNGQLG
1 1	ĺ	Ï	NHSBEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
1			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
1. 1		1	TDGKKMADTSSMDEDFESDY\BKYCVLQ
5410	2	710	LRPPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
	_	/	VHQNPSSHYRATIGVDFALKVLHWDPBTVVRLQLWDIAGQERFG
			MMTRVYYREAMGAPIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
1 1			KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFBTSAK
1 1			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
]]			SG\CAKILVGTFAGVW
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
		207	GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLONHQQPN
1 1			GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
1			QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNKLILKTLKEITEG
1 1			KTVQIPVYDFVSHSRKEETVTVYPADVVLPEGILAFYSQER/IR
i I			DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
1			KPA\PBBFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
i i	,		LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	QGISNFFHKBANFWFEVSGYLISPLRSPFVDFALEWSLMASPWN
1 1			KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
1]		•	NEQSQITRRKKRKKDFQHLISSPLKKSRICDETANATSTLKKRK
; i			KRRYSALEVDERAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
1 }		-	IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
1 1		,	KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
1 1			HKNKSKKKKKSSNRBYET\LAMPEGSQAGREAGTDMQESQPTV
1 1			GLDDETPQLLGPTHKKKSKKKKKKKKNHQBFBSLAMPEGSQVGS
1 1			EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
1 1			EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
1 1			SKKRKLTSVKRARVSGDDFSVPSKNSBSTLFDSVEGDGAMMEEG
1		•	VKSRPROKKTOACLASKHVOEAPRLEPANEEHNVETAEDSEIRY
			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
1 1			LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
1 1			KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
ļ 1			KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
) · [SVALKFSQISSQRNRGAWSKSETRKLIKAVEEVILKKMSPQBLK
1 1			BVD9KLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
1 I	i	1	KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYBINVBDTNEI
			DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPBIIDYL
1	1		
	1		
F 4 3 3			YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD SEGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	YETTLPLLKEKLBKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHREKKRPPREHAWFTPVIPVLWEAKAGWII RPPAGVAPRRAMANVSKKVSWSGRDRDDEBAAPLLRRTARPGGG
2413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKRKRRPREHAWPTPVIPVLWEAKAGWII RPPAGVAPRRAMANVSKKVSWSGRDRDDEBAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALPRVGHMSSVKLDDELLEP\DMDPP
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKRKRRPREHAWFTPVIPVLWEAKAGWII RPPAGVAPRRAMANVSKKVSWSGRDRDDEBAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALPRVGHMSSVKLDDELLEP\DMDPP HPFPKBIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKRKRRPRHAMFTPVIPVLWEAKAGWII RPPAGVAPRAMANVSKKVSWSGRDRDEEAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKCNID
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKEKRPPRHAWFTPVIPVLWEAKAGWII RPPAGVAPRRMANVSKKVSWSGRDRDDEBAAPLLERTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDELLEP\DMDPP HPFPKBIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKKNID KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSCIPQ
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKEKRPPREHAWFTPVIPVLWEAKAGWII RPPAGVAPRRAMANYSKKVSWSGRDRDDEBAAPLLERTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPPPKBIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKCNID KFTEKGGLSFSLLWATLNAAFVLVGSVILSVVGGLAVGKEGPMIH
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKEKRPPRPHAWFTPVIPVLWEAKAGWII RFPAGVAPRRAMANYSKKVSWSGRDRDDEBAAPLLRTARPGGG TPLLNGAGPGAARGSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPFPKBIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR TVBIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKCNID KFTERGGLSFSLLWATLNAAFVLVGGVIVAFIEPVAAGSGIPQ IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH SGSVIAAGISQGRSTSLKRDPKIPEYLRRDTEKRDFVSAGAAAG
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRKRKRPPRHAWFTPVIPVLWEAKAGWII RFPAGVAPRRAMANYSKKVSWSGRDRDDERAAPLLRTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPFPKEIPHNEKLLSLKYESLDYDDSENQLFLEEERR INHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKCNID KFTEKGGLSFSLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG VSAAFGAPVGGVLPSLEEGASFWNQPLTWRIFPASMISTFTLNF
5413	3753	1304	YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPPRDIFYYEDD SEGGHRRKKRPPRHAWFTDVIPVLWEAKAGWII RPPAGVAPRAMANVSKKVSWSGRDRDEEBAAPLLRRTARPGGG TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEBERINHTAFR TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKCNID KFTEKGGLSFSLLLWATLNAAFVLVGSVILSVVGGLAVGKEGFMIH SGSVIAAGISQGRSTSLKRDPKIFEYLRRDTEKRDFVSAGAAAG VSAAFGAFVGGVLPSLEEGASFWNQPLTWRIFPASMISTPTLNF VLSIYHGNWWDLSSPGLINFGRFDSEKMAYTIHEIFVFIAMSVV
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corresponding to first amino acid residue of residue of residue of amino acid sequence sequen	ID	beginning	nucleotide	
Cocrtesponding	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first maino acid residue of amino acid sequence sequ	i	location	corresponding	H=Histidine. I=Isoleucine. K=Lvsine.
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NPTSWNADLRALARNSFY-SISTLEPT-LAVEPTOSLALWAPAPLL RSRVVLGETPP CLPGDSCSSDSLI PGLITCLTVG/LGVGLVEI SREHESPRADELVCATGLIGSAPPLFISLACARGSIVATYIF IFIGETILLSWNADTVADILLYVI PTRESTARAG/LYLSHLLGD ASSPILIGLI EDELRRINPSPSILSPRAQPSIM-CAPYGALG AASLGTARIL 5415 693 2966 IPPETELSCORN/LTTLT/NOGOATIPEEVQKLRPRNEGRENEL LISPLRCLPEERQKEHIHIGEMKQTSQMAAENIGSELPPSATRF RLDMLKNICAKRSLTESLES ILSRGNEARGLGRHSISTSUDLOSLIS STLSHTSKRESPCVERKADIP ISESSFILLOSSEDLISSDSSKILPE EPAPLSPQOAPRRRANTLSHTELGEPPLECQEPQPARGSPOYGQKLM RYHSVSTETPPLEKNDERSEKANHLCDSGGTVERRIBWGQIFL RVATDQKACDSSRYEDVSELSELDPRSPLEEVCE-LOPRGPPPPE EKKRTSRELRELWQKALLQQI LLLLRMSEKORQLQASENDLLMKR LKLDYBELTPCLEEVTTWEEKHLSTEGRSKILFDMSRMISSNCQ GVP\RRHRGBTWEFLAEQPHLKRUPPSKQQCKOPVPYKELLKQLT SQQHAILLIDGRTPPTHPTPSAQLGGGQISJNTILKAYSLLDQS WGCQGLSFVAGILLIMMSERAFRHLKSTEGRSKLRPMRRHISNCQ GVP\RRHRGBTWEFLAEQPHLKRUPPSKQQCKOPVPYKELLKQLT LLCIUMYGLSRLIHDVIRGLENDLYNHLERSHEDSLYAAPHFITMF ASQPHGFVARVEDHUFLQGTEVLFFKVALSLLGSHKRLTLQCBW UPGCGLSFLYAGITLLIMMSERAFRHLKVILMGLRKQYRPDM ASQPHGFVARVEDHUFLQGTEVLFFKVALSLLGSHKRLTLQCBW VGCQLSFLYAGITLLIMMSERAFRHLKVILMGLRKQYRPDM LETVUDFIKSTLPNICLVQMRTIRQVPEMINKQLAVEVEYH VQBGLIDSSRLDDNIGRNDKLENTNSSLRKÄNLDLLEQQVANG RIGSLBATTEKLLSSSKLRQAMITLELERSALLQCYVEBLRRRS ASPENERSECTQPPPTGG SAPARAFTERSSKSSLRQAMITLELERSALLQCYVEBLRRRS AKPSBREPSECTQPPTGG SAPARAFTSOMGSSSKSKNOKAMITLELERSALLQCYVEBLRRRS AKPSBREPSECTQPPTGG SAPARAFTSSMGSSTRHSPISSGGISTPYTNVSPMILGHIRBQM ALALKALKELBEGQVRTI-DUJAVKISVLGROUVSGLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGRLYITDTERBMT KLKQRLQAAGSKKVNKAMAQFLVERKVQFUVSGLKNORAA SQINVCGVRKRSYSAGNASQLEQLSRARRSGGRLYITDTERBMT KLKQRLQAAGSKKVNKAMAQFLVERKVQFUVSGLKNORAA NDLVDTCVGTSVETNSVGISCQPECKNKVVQPELPHNWIVVER VBHIBGRGAGRSVERKCOKNSVSUBVSVCBTGSNTESSVDLITLLKT NLHAKEVES IGCGGCSVDVTVGSPKCASRGFBNTEAVSQVSRAW MAPPRADQDTSTILEQVQPGTNTETATI.ISCCTNTCLSTLDKQ TSTQTVETRTVAVAKGRRYBOUNSSTKTNSTKGGCTLSTLISSGFDR PSAVXKRSGGQQININDNYLVGLKMRTIACGPPQLTVCLTASS RSVGODDPVCESLERPPQQQAILGMMTGLDBYTHERGCHLLASSGFDR PSAVXKRSGGODDFRINGSTKTNISTTNISSTMKSASST	l	į.	I	
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NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO.	location		Glutamic Acid, F=Phenylalanine, G-Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
		 	QEVGTSEGKPISSLDAFPTQEGTLSPVNLTDDQIAAGLYACTNN
1	Ì		ESTLKSIMKKKDGNKDSNGAKKNLOFVGINGGYETTSSDDSSSD
1	ĺ		ESSSESDDECDVIEYPLEBEEEEEDRDTRGMAEGHHAVNIEGL
1	l .	Ì	KSARVEDEMQVQECEPEKVEIRERYELSEKMLSACNLLKWTIND
			PKALTSKDMRFCLNTLQHEWFRVSSQKSAIPAMVGDYIAAFEAI
i	i	1	<u> </u>
1		j	SPDVLRYVINLADGNGNTALHYSVSHSNFRIVKLLIDADVCNVD
ŀ	ļ		HONKAGYTPIMLAALAAVEAEKOMRIVEELFGCGDVNAKASQAG
i	1		QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
ļ	,		HVEIVKLLLAQPGCNGHLEDNDGSTALSTALRAGHRDIAVILYA
L			HVNFAKAQSPGTPRLGRKT8PGPTHRGSFD
5417	27	4074	KSQLFCFWGGKAGDILSGDQDKBQKDPYFVETPYGYQLDLDFLK
1	1		YVDDIQKGNTIKRLNIQKRRKPSVPCPBPRTTSGQQGIWTSTES
[LSSSNSDDNKQCPNFLIARSQVTSTPISKPPPPLETSLPFLTIP
1	ì		ENRQLPPPSPQLPKHNLHVTKTLMETRRRLEQERATMQMTPGEF
1	I		RRPRLASFGGMGTTSSLPSPVGSGNHNPAKHQLQNGYQGNGDYG
1	ĺ		SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIREQM
1	J		AIALKRLKELEEQVRTIPVLQVKISVLQEEKRQLVSQLKNQRAA
1			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYBREEMB
ì	1		TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCRASSELRENGEC
			RSVAVGARENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTK
	į		ANLGVMTRADKEIBLQQQTIESLKEKIYRLEVQLRETTHDREMT
i			KLKQRLQAAGSRKKVDKATMAQPLVFSKVVBAVVQTRDQMVGSH
}			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
1			VEMHDRCAGRSVEMCDKSVSVEVSVCETGSNTERSVNDLTLLKT
1.	}		NLNLKEVRSIGCGDCSVDVTVCSPKECASRGVNTEAVSQVEAAV
1			MAVPRTADQDTSTDLEQVHQFTNTETATLIESCTNTCLSTLDKO
1			TSTQTVBTRTVAVGEGRVKDINSSTKTRSIGVGTLLSGHSGFDR
1			
			PSAVKTKESGVGQININDNYLVGLKMRTIACGPPQI.TVGLTASR
1	!		RSVGVGDDPVGESLENPQPQAPLGMMTGLDHYIRRIQKLLAEQQ
1			TLLAENYSELARAFGRPHSQMGSLNSQLISTLSSINSVMKSAST
1			EELRNPDFQKTSLGKITGSYLGYTCKCGGLQSGSPLSSQTSQPE
ł			QEVGTSEGKPISSLDAPPTQEGTLSPVNLTDDQIAAGLYACTNN
1			ESTLKSIMKKKDGNKDSNGAKKNLQFVGINGGYETTSSDDSSSD
1			ESSSESDDECDVIEYPLEEEBBEEDEDTRGMAEGHHAVNIEGL
1			KSARVEDBMQVQECBPEKVEIRERYELSEKMLSACIJLLKNTIND
1			PKALTSKDMRFCLNTLQHENFRVSSQKSAIPAMVGDYIAAFEAI
i i		•	SPDVLRYVINLADGNGNTALHYSVSHSNFRIVKLLLDADVCNVD
1			HONKAGYTPINLAALAAVRABKOMRIVEELFGCGOVNAKASQAG
1			QTALMLAVSHGRIDMVKGLLACGADVNIQDDEGSTALMCASEHG
1			HVBIVKLLLAQPGCNGHLEDNDGSTALSIALRAGHRDIAVLLYA
1			HVNFAKAQSPGTPRLGRKTSPGPTHRGSFD
5418	24	1133	SVPRAGGDMRTGAAELYDQALLGILQHVGNVQDFLRVLFGFLYR
1 1			KTDFYRLLRHPSDRMGFPPGAAQALVLQVFKTFDHMARQDDKKR
1			ROELEBKIRKKEEERAKTVSAAAARKEPVPVPVQEIEIDSTTEL
1 1			DCHQEVEKVQPPGPVKEMAHGSQRAEAPGAVAGAAEVPR\EPPI
(1		LPRIQEQFQKNPDSYNGAVRENYTWSQDYTDLEVRVPVPKHVVK
j .			GKQVSVALSSSSIRVAMLBENGERVLMEGKLTHKINTESSLWSL
j l			EPGKCVLVNLSKVGEYWWNAILEGERPIDIDKINKERSMATVDE
			1
1			EEQAVLDRLTPDYHQKLQGKPQSHELKVHEMLKKGNDABGSPFR
E410	1200		GORFDPAMFNISPGAVQF
5419	1395	259	GTHPLDPDLVSRTSVQGPLMTMACPGMSDTEESPFLGPRAAREG
			SESEACEAFGRRESEBEGRREDTSGFGRSREHKVNWKHPERADA
((j		KDPASLPQC/LGP/DCVRPAQPSSKYCSDDCGMKLAANRIYEIL
) 1			PQRIQQWQQSPCIAEBHGKKLLBRIRREQQSARTRLQEMERRFH
j l		•	BLEAIILRAKQQAVREDBESNEGDSDDTDLQIFCVSCGHPINPR
{		i	VALRHMERCYAKYESQTSPGSMYPTRIEGATRLFCDVYNPQSKT
j l			YCKRLQVLCPEHSRDPKVPADEVCGCPLVRDVFELTGDFCRLPK
; l	•		RQCNRHYCWEKLRRAEVDLERVRVWYKLDELFEQERNVRTAMTN
]	1	ı	RAGILALMLHOTIOHDPLTTDLRSSADR
5420	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
1 1			GGFLPARPPRAQRHLGFSHARQSMEAPDYEVLSVREQLFHERIR
			The state of the s

SBO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i -	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1		ļ	BCIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1			LIBECTFTLAIALGAVELLPPSIISNZVLLSEPRNYYIQWENGS LIHGEWNLVFLFSNESEIFLMPFAYFFTESEGFAGSRKGVLGRV
1			YETVYMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1	İ		YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEB
			QLYCSAFKEAALTRRICMPTSCWLPLDMRLLHRQVLALQTQRVL
1			LEKRRKASAWORNLGYPLAMLCLLVLTGLSVLIVAYHILELLID
1)			BAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
1			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
			RABLIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
J		}	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
			BCIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
	'		LIRICTFTLAIALGAVLLLPFSIISNEVILLSLPRNYYIQWLNGS LIHGLWNLVFLFSNLSLIFLMPFAYFFTESBGPAGSRKGVLGRV
1			YETVYMLMILITLLVLGMVWVASAIVDKNKANRESLYDFWEYYLD
			YLYSCISFIGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEB
1			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
1 1			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILBLLID
1			KAAMPRGMQGTSLGQVSFSKLGSPGAVIQVVLIPYLMVSSVVGF
1			YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
ľ			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
5422		1853	RAKLIRAFGERE
5422	3	1263	SCGBSLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
1 1			KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
1 .]			TVFVSERELDWAKVMVEKSRMGVVPPGTQVBQLi.YAKKLYDSAF
			HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
			NOSFNALVNYTNRNAASPTSVROMALSYFTATTTAVATAVGMNM
1 1			LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQBLIKGICVKDRN
i i			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
			PMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
			BPKLQDTIKAKYGBLEPYVYFNKGL
5423	3186	905	GVSMALGBEKARAKASEDTKAQSYGRGSCRERELDI PGPMSGEQ
		1	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
	i		ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQOPHSSG
	. !	•	LSCLSOWKSVLSPGSAAOPSSCSISASSTGSSLOCHORRABPRG
			GSLAKVSSSLEPVVPQRPSSVVGLGPRPQWSPQPVFSGGDASGL
]]	 		GRRRLSFQABYWACVLPDSLPPSPDRHSPLWNPNKBYEDLLDYT
			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
	ſ		TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
[SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
1			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
			PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
]]		GGEOGKESLVOC\VKTFC\COLBELICVLYNV\ADVTDHGTPAR
			SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
1 1			NTPVLEDVIGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
		ì	DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEABASEDTKAQSYGRGSCRERELDIPGPMSGEQ
		}	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
]	1		ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
	Ī	i	EFPOTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
1	!	İ	LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQBRARPRG
1	1		GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
	į		GRRLS FQARYWACVLPDSLPPS PDRHS PLWNPNKEYEDLLDYT
			GRRRISFQAKYWACVLPDSLPPSPDRHSPLWNPNKKYKDLLDYT YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP TNVSPNCPPAKATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

SEQ	Predicted	Predicted end	I amino paid assessed assessed assessed
ID	beginning	nucleotide	Amino acid segment containing signal peptide
No:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
,,,,,	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
[corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
ł	to first	amino acid	LaLeucine, MaMethionine, NaAsparagine,
]	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
ļ	residue of		S=Serine, T=Threonine, V=Valine,
1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	l .	sequence	Codon, /=possible nucleotide deletion,
}	sequence	L	\=possible nucleotide insertion)
l			SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
ĺ	1	ļ	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEKVESDDEY
1	İ		LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
	ļ	[PASPPSSSSQSQLPPGAALQGSGDPBGQNPCFLRSPVRAHDSAG
1	<u> </u>	1	BGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
ł			GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
}]	ļ	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGBILLQCLLB
l	ì		NTPVLEDVLGRIAKQSGELRSHADRLYDSILASLDMLAGCTLIP
			DKKPMAAMBHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
}	1		NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWRFPSML
1	1		ALSGYIQACRALMITAILLGFLGLLLGIAGLRCINIGGLELSRK
1			AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
ł		·	KYELGPALYLGNSASLISILGGLCLCSACCCGSDEDPAASARRP
			YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
Ĺ	Í		PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
			NCSWEVAYLPSRAGSLIF
5426	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
			PAAHAKPDPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA
	ļ		GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
1			TAKTLYMSHRELPAWVSFPDVKKAEWLNKIVAQVWPPLGQYMEK
j	1		LLAETVAPAVRGSNPHLQTPTFTRVELGEKPLRIIGVKVHPGQR
l			KBQILLDLNISYVGDVQIDVEVKKYPCKAGVKGMQLHGVLRVIL
			RPLIGDLPFVGAVSMFFIRRPTLDINNTGMTNLLDIPGLSSLSD
			TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
1			POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
			LOASVIDDWPPLQGGOGQVHLRLEWISLLSDAEKLEQVLQWNWG
	,		VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
		•	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGFNSRLYM
			KLVMRILYLDSSRICPPTVPGCPGAWDVDSENPQRGSSVDAPPR
			PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
			DKDLDKDDFIGRCKVRLTTVLNSGFLDEWLTLRDVPSGRLHLRL ERLTPRPTAARLEBVLQVNSLIQTQKSARLAAALLSIYMBRAED
			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDRSASPLI
			RKPHTESLELQVRGEGTGVLGSLSLPL8ELLVADQLCLDRWPTL
			SSGCCOVLLRAQUGILVSOHSGVEAHSHSYSHSSSSLSEBPELS
		,	GGPPHITSSAPEV\RORLTHVDSPLEAPAGPIGOVKLTLWYYSE
			ERKLVSIVHGCRSLRONGRDPPDPYVSLLLLPDKNRGTKRRTSO
			KKRTLSPEFNERFEWELPLDEAORRKLDVSVKSNSSFMSREREL
			LGKVOLDLARTDLSOGVARWYDLMDNKDKGSS
5427	42	3435	ATSSQSLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
	-1.6		PAAHAKPDPGSGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
			GAVGLSVGFVLFGLALYLGWRRVRDBKBRSLRAAROLLDDBEOL
			TAKTLYMSHRELPAWVSFPDVEKAEWINKIVAOVWPFIGOYMEK
			LIAETVAPAVRGSNPHLOTFTFTRVELGEKPLRIIGVKVHPGOR
			KEOILLDINISYYGDVOIDVEVKKYFCKAGVKGMOLHGVLRVIL
			EPLIGDLPFVGAVSMPFIRRPTLDINWTGMTNLLDIPGLSSLSD
	i		TMIMDSIAAFLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEBLN
	,	i	POMORTARAMANEA DE CONTROL DE CONT
	l		-
			LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
	ł		VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
		1	MVQLSIQDVTQESKAVYSTNCPVWEKAFRFFLQDPQSQELDVQV
		i	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
	ļ	1	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
		ļ	PCHTTPDSQPGTRHVLRIHVLEAQDLIAKDRPLGGLVKGKSDPY
			VKLKLAGRSFRSHVVREDLNPRWNEVPEVIVTSVPGQELBVEVP
			DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL

			
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methicnine, N=Asparagine,
ł.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	1	sequence	1.
	sequence		\=possible nucleotide insertion)
1	i	1	BRLTPRPTAAELEBVLQVNSLIQTQKSAELAAALLSIYMBRABD
1 .	Į.	ì	LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
}	1	1	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
í	i	1	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	Į.	ł	GGPPHITSSAPEV\RORLTHVDSPLRAPAGPLGQVKLTLWYYSE
1		Ì	BRKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
ŀ		ł.	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
Į.	į.	1	
<u> </u>	<u> </u>		LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
5428	3	1839	SSRSERLSACATAPPWLVSSRPARPAQLQRPGKMVEDGAEGLED
i		ì	LVHYSVSELPSRGYGVMEBIRRQGKLCDVTLKIGDHKFSAHRIV
)			LAASIPYPHAMFINDMMECKQDRIVMQGMDPSALEALINFAYNG
1	i	Į.	NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
Ī	1 .		ROFARTMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
ł		1	VSRDELNVKSBEQVFEAALAWVRYDREQRGTPL\RNLQSNIRLL
1	[1	FCRPOFLSDRVOODDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
1	1	1	AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
	Į	Į	CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
l			WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVBTYSPE
ĺ	1	1	
}	į.	,	TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
	i	Į	YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
!	ł	ł	AENYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
1 .			TGQSNL\SSVGDVLTPRTDCWTFM\APMACHEGGVGVGCIPLLT
ĺ	•		I ·
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
!			AQRERFHREQPTYPYLQHEIDLPPTISLSDGEEPPPYQGPCTLQ
•		1	LRDPEOOLELNRESVRAPPNRTIPDSDLMDSARLGGPCPPSSNS
1)	1	GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
		1	LEGTRLHHTHIAPLESAAIWSKBKDKQKGHPL
5430	441	1507	QKRRKRRKKIMKTIQPKMINSISWAIFTGLAALCLFQGVPVRS
3430	***	1 1307	GDATPPKAMDNVTVRQGBSATLRCTIDNRVTRVAWLNRSTILYA
Ī	1	1	-
	ì	1	GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
1			HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
[(l .	TVTWRHISPKAVGPVSEDBYLEIQGITREQSGDYECSASNDV\A
l	1	l	APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
ŀ	i	ì	EPQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSRHDYGNYT
1	1	1	CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
1			HLLLKF
5431	1 2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
I			LPGITINP\TTAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
]	1	Į.	KKRLRAFLTOKAKVGELKDDDFBRISELGAGNGGVVTKVOHRPS
1		1	GLIMARKLIHLBIKPAIRNQIIRBLQVLHBCNSPYIVGFYGAFY
l	1		SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
l		1	•
1	1	S	YLREKHQIMHRDVKPSNILVNSRGBIKLCDFGVSGQLIDSMANS
l	1	l	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
	1	}	DAKELBAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
i		1	AMAIFRILDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
!			DLKMLTNHTFIKRSEVBBVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	1		LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
!	}		KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
[
1		j	GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
1	1	1	SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
ł		l .	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
l	I	1	FVGTRSYMAPERIAGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
1		I	DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
l	l	ł	AMAIFELLDYIVNEPPPKLPNGVFTPDFQBFVNKCLIKNPABRA
İ	1	1	DLKMLTNHTPIKRSEVBEVDFAGWLCKTLRLNQPGTPTRTAV
5433	360	1885	SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
223	, 500	1882	
1		1	LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
L	<u> </u>	L	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
l No:	location	corresponding	H=Histidine, I=Isoleucine, R=Lysine,
!	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	i .	Codon, /=possible nucleotide deletion,
Į.	P '	sequence	\=possible mucleotide insertion)
<u> </u>	sequence		IAFTSAGGAVLLFLAMPMLTIGGILFLITNLQIGNLFGQHRSTI
ļ	Į.		
1			ITLYNGAPDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
]			STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
Į	ļ	Į.	GSYSORSSFORRKRPOGOGRSRNSAPSGATL/CSRRFAWHLVWL
i	1	}	SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
i	i	l	CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
Į.	l	1	LCLGFALCASVPILPLQYLTFILQVISRSPLYGSNAAFLTLAFP
i			SEHPGKLPGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
L			MLAILLTFFHPFLVYRECRIWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLWWLF/GSGK
1			HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1	ł	1	LRQGRFGMFIGCINYPECEHTBLIDKPDETAITCPQCRTGHLVQ
	1		RRSRYGKTPHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
	<u> </u>		AQGVKHFCASKQCGKPVSAK
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
	!		HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEQSSSK
1	1	1	GMFRKKGGWKAGPKGTSQEIPKYITASTFAQARAAEISAMLKAV
ļ	Į.		TOKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQBIAQKBABKA
ķ.	ţ	Į.	VHQKKEHSKNKCHKARRCHMNRTLBFNRRQKKNIWLETHIWHAK
i	1		RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
J	1	Į	LKGKBEBILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
1	1		KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
ŀ	İ		IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
ì		į	KDDGENAKPIKKIIGDGTRDPCLPYSWISPTIGIIISDLTMEMN
1			RFRLIGPLSHS1LTEAIKAASVHTVGEDTEETPHRWWIETCKKP
ł	į.		DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
		· .	KKSKALPNPEKCODNEKVROLLLEGVPVECTHSFIWNODICKSV
{	1		TENKISDQDLNRMRSELLV9GSQLILGPHESKIPILLIQQPGKV
}		1	TGEDRIGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKBSAVH
Į.			SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
	.	1	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
1 .		•	RRSKVPCAPMPKKTHQPSDEVGTSIEHPREAEKVMDAGCQESAG PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
į.		ļ	
1			REGERAPERGOOGLITERACISIIGHPPRALVWVSLSLLSKGSPE
1		į	PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
1		1	KKREKROKP\GRASEDGPAGEBPVAGQBALITIGLWSGPLPRVTL HCSRTILIGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
1		1	RGLVILLRPPASLOYRFARIAIRV
	 	ļ	ASDS I PWSEARTTRKLAORGCOWSLPERMPLVVFCGLPYSGKSR
5436	1781	635	
[(RAKELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
1		1	ALRASVERRLSRHDVVILDSLNYIKGPRYBLY\CLARAARTPLC LVYCVRPGGPIAGPOVAGANENPGRNVSV8WRPRAEEDGRAQAA
1	1	i	
1	}		GSSVLRELHTADSVVNGSAQADVPKELEREESGAARSPALVTPD
	1]	SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
	1	l	EEPLPLAGIRSALFENRAPPPHOSTOSOPLASGSFLHOLDOVTS
1		ł	QVLAGIMEAQKSAVPGDILTLPGTTEHLRFTRPLTMAKLSRLRR
			QFISYTKMHPNNBNLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEPGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPR
1		Į.	PRRVDSSSENSGSDWDSAPETMBDVGHPKTKDSGALRVSRAASE
1	1	1	PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1]		WDHVD9GGTRRPGV\$PEGGL\GVPGPGAPLEKPGRREKLLGWLR
1	ļ		GBPGAPSRYLGGPEECLQISTNLTLHLLELLASALLALCSRPLR
1		Į.	AALDTLGLRGPLGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1			CLFGLLQALVLAVSLREPNGDEAATOWBSEGLEREGEEQRGDPG
<u></u>	<u>l</u>	<u>L</u>	KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
}			LAPPSLRRPMMCQSBARQGPBLRAAKWLHPPQLALRRRLGQLSC
			MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
[VPTRLLSRAWGRLNQVBLPHWLRRPVYSLYIWTFGVNMKBAAVE
1	1		DLHHYRNLSBFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
1		1	NCEVEQVKGVTYSLESPLGPRMCTRDLPFPPAASCDSFKNQLVT
E .	I	I	MCPADMAMAT ISTREAMORALKDPALANWSCOSA WINGDAT

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A≈Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location corresponding	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	to first	to first	L-Leucine, M-Methionine, N-Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	bequence	\=possible nucleotide insertion)
·			REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHFPGSLMSVNP
1	}		GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
i			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/OS
1	1		FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGRALGSL
5439	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
			LAPPSLRRPMMCQSBARQGPBLRAAKWLHFPQLALRRRLGQLSC
l	i	ĺ	MSRPALKLRSWPLTVLYYL:PFGALRPLSRVGWRPVSRVALYKS
	ŀ	}	vptrllsraugrlngvblphwlrrpvyslyiwtfgvnmkraave
			DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
			NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
ł	l		REGNELYHCVIYLAPGDYHCFHSPTDWTVSHRRHPPGSLMSVNP
1	<u> </u>	ļ	GMARWIKELFCHNERVVLTGDWKHGFFSLTAVGAT\NWGSIRIY
			FDRDLHTNSPRHSKGSYNDFSFVTHTNREGVPMALRGEHLG/QS
5440	693	253	FNLGSTIVLIFEAPKDFNFQLKTGQKIRFGEALGSL BPIPVTPDHRLVTMTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA
)	ددء	MIGAPHNPAPPMSTVIHIRSETSVPDHVVWSLPNTLFMNTCCLG
	}		PIAPAYSVKSRDRKMVGDVTGAQAYASTAKCLNIWALILGIPMT
ł	(ILLIIIPVLVVQAQR
5441	2	2054	CRDGGKNGFMVSPMKPLEIKTQCSGPRMDPKICPADPAFPSFIN
	Ì		NSDLWVANIETGEERRLTFCHQGLSNVLDDPKSAGVATFVIQEE
			FDRYTGYWWCPTASWEGSEGLKTLRILYEEVDESBVEVIHVPSP
ļ.	J		ALEKRKTDSYRYPRTGSKNPKIALKLAEFQTDSQGKIVSTQEKE
			LVQPPSSLFPKVEYIARAGWTRDGKYAWAMFLDRPQQWLQLVLL
ĺ		ı	PPALPIPSTENEEQ\RLASARAVPRNVQPYVVYBBVTNVWINVH
}		1	DIFYPFPQSEGEDELCFLRANECKTGFCHLYKVTAVLKSQGYDW
'		,	SEPFSPGEGEQSL'INAIWVNEETKLVYFQGTKDTPLEHHLYVVS
	(4.5	YEAAGEIVRLTTPGFSHSCSMSQNFDMFVSHYSSVSTPPCVHVY KLSGPDDDPLHKQPRFWASMMEAAKIFHFHTRSDVRLYGMIYKP
1			HALQPGKKHPTVLFVYGGPQVQLVNNSFKGIKYLRLNTLASLGY
			AVVVIDGRGSCQRGLRFEGALKNQMGOVEIEDOVEGLOFVAEKY
1		•	GFIDLSRVAIHGWSYGGFLSLMGLIHKPOVFKVAIAGAPVTVMM
}			AYDTGYTERYMDVPENNQHGYEAGSVALHVEKLPNEPNRLLILH
			GFLDENVHFFHTNFLVSQLIRAGKPYQLQVALPPVSPQIYPNER
			HSIRCPESGEHYEVTLLHFLQEYL
5442	1	3474	CGQRSRRRSPDMPBAKPAAKKAPKGKDAPKGAPKBAPPKBAPAB
	·	İ	APKEAPPEDQSPTAEEPTGVPLKKPDSVSVETGKDAVVVAKVNG
	1		KELPDKPTIKWFKGKWLELGSKSGARFSFKESHNSASNVYTVEL
			HIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRODASGOSL
			ESFKRTSEKKSDIAGELDFSGLLKKREVVEERKKKKKDDDDLG IPPEIWELLKGAKKSEYEKTAFQYGITDLRGMLKRLKKAKVEVK
			KSAAFTKKLDPAYOVDRGNKIKLMVEISDPDLTLKWFKNGOBIK
			PSSKYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFV
			KEPPVLIVTPLEDQQVFVGDRVEMAVEVSBEGAQVMWMKDGVBL
			TREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQCE
	[AELIVEEKQLEVLQDIADLTVKASEQAVPKCEVSDEKVTGKWYK
			NGVEVRPSKRITISHVGRFHKLVIDDVRPEDEGDYTFVPDGYAL
			GSLSAKINFLEIKVEYVPKQ\BPPKIPLGFASGGKTSENAD/IV
	[VVAGNKLRLDV\SITGEAPSPFAT\NLKG\DEVFTTTEGRTRIE
	l		KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFLQVVDVP
			DPPEAVRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQ
			RWMKLNPEVPTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN
			TKPPMPIAPTSEPLHLIVBDVTDTTTTLKWRPPNRIGAGGIDGY
			LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN
			IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN
			LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
			RSDSGEYELSVQIENMKDTATIRIRVVERAGPPINVMVKEVWGT
			NALVENQAPKDDGNSEIMGYFVQKADKKIMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK
1			PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV
			VWMKNKMBIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV
			NEIGEALABCELEVEVPO

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
MO:	location		H=Histidine, I=Isoleucine, K=Lysine,
i .	1	corresponding	
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S≃Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	aequence	Codon, /=possible nucleotide deletion,
ŀ	sequence		\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSPRRSRSAAEPA
ľ		ľ	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
ĺ		ſ	LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
1	l		NKIEEPLEEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
j	1]	RPEANEALERGILKTLOKLDRYLNSPLPDBIDENSMEDIKFSTR
1	ł	1	KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
1			
<u>}</u>	J	j	LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHQVKSRLLKEVS
L			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
ļ		t '	RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
[ŀ	IKVKAADMARAKALI.GGPGEELKADTRYLDPFDAQPHPAPPDDG
}	i	1	YMEPYDAQWVMSELPGRGVQLYDTPYREQDPETADGPPSGQKPR
}	J	1	QSRMPQBDERPADEYDQPWBWKKDHISRAFAVQFDSPEWERTPG
Ī	1		SAKELRRPPPRSPOPAERVDPALPLEKOPWFHGPLNRADAESLL
I	1]	SLCKEGSYLVRLSBTNPQDCSLSLRSSQGFLHLKFARTRENQVV
1	I	l	LGQHSGPPPSVPELVLHYSSRPLPVQGAKHLALLYPVVTQTP*Q
1	j .	ł	*PDWGDRRPNGQVATGLPELWGARAPSAAAHPGLHRERHPEGLP
1	[Í	RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH
Į.	1	l	QGGGCGYGQSQGPSGRPRGGAGSRH
5445			ILSRGFIGSVEICIOLPLPASEPVLLLTWARRRNRETRSRREPT
5445	2364	486	
1			TLRAQSVCPWW1*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
	\	1	BEESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
1	ł		QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSBP
l	ł		ASESVVGALPARHQPSPMEKRNQWLVSQLSAASPDTGHDSDKSD
l	· ·		QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
ĺ			DVLGIRQLBRPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
ł	}		QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1			ALPGOPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSPPG
1.	}		LPRHODOPHHOPPNRAGAPGESLECPABLRPOVPOPPSPAAVPR
1	}		PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
J			NGFQTAID1FEDRIRGID11KWMERYLRDKTVM11VAISPKYKQ
}	· ·		DVEGAESOLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRPIPVLF
	ľ	•	PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEXVAPPRGP
1	ļ		, · · · · · · · · · · · · · · · · · · ·
			LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
	Ì		TLDVKCDYTLEKPASSQKANQIIRDGEMPKTLACTERPSKNSHP
			VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
	1		MLFDRIRLVVTKGPSGTPGSNENSTQNVYKIPPTTTKALCPLYT
ł			TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
i	1		GGFLSKSLVFSVLFAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
I			KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSBAETBHAGSFNATGQQKDTSGVAR
			PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
1			GSCPSQRLQWPGKRPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
1	l '		RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
ļ]		TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
1			IOPYLNSHYKETTVPRKVLPHLRGHRGPVNTIQWCPVLSKSHML
Ì			LSTSMDKTFKVWNAVDSGHCLOTYSLHTBAVRAARWAPCGRRIL
l			<u> </u>
l			SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
ľ			GFSSBMKANDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
 			ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
l			FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
1			GDLLVTGSADGRVLMY8FRTASRACTLQGHTQACVGTTYHPVLP
ŀ			SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
			KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1		2000	HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
[RWNLQVTSKVIPPWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
1			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRRKLRKAAHLEV
1			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
L			GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET

	T S 1/2		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, GeGlycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ľ	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
j .	sequence	Bequence	\=possible nucleotide insertion)
	sequence		1 7
1		f	IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
į.	!		RRHVDRTSEGVLRNRKSHHYKKHYPNEJAPKSGTSCSSRCSSR
i .	1	i	QDSESARPESETEDVLWEDLLHCARCHSSCTSETDVENHQINPC
l	ì	į.	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
}	İ	j	VLBISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
l .	Į.		TDLBQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
ł	1	l	FFFILCVARRTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDAPK
		1	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
	1		
Į.	1	ì	SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKTSAI
	1		VWEGNDCKKADMSVLBISGMIMNRVNSHIPGIGYQIFGNAVSLI
1	i	l	LGLTPPVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
<u>L</u> .	L	Ĺ	IISFVVRVSLVWIFFFLLCVAERTYKQVGIM
5449	194	1833	MASKVTDAIVWYQKKIGAYDQQIWBKSVBQREIKGLRNKPKKTA
	[ĺ	HVKPDLIDVDLVRGSAFAKAXPESPWTSLTTKGIVRVVFFPFFF
	ł	1	RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
]	ļ	1	GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKLRKAAHLEV
1	}		HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLMHAAFFLS
	l .		GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIONHEPQCST
1	İ		
	[ł.	IRPEBTAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
l		ł	RRHVDRTSBGVLRNRKSHHYKKHYPNEDAPKSGTSCSSRCSSSR
1			QDSBSARPESETEDVLWEDLLHCAECHSSCTSETDVENHQINPC
1		!	VKKEYRDDPFHQSHLPWLHSSHPGLEKISAIVWEGNDCKKADMS
	}	l	VLEISGMIMNRVNSHIPGIGYQIFGNAVSLILGLTPFVFRLSQA
l			TOLEQLTAHSASELYVIAFGSNEDVIVLSMVIISFVVRVSLVWI
i	ł		FFFLLCVAERTYKQVGIM*TSEGVLRNRKSHHYKKHYPNEDA>K
J		,	SGTSCSSRCSSSRQDSESARPESETEDVLWEDLLHCAECHSSCT
1			SETDVENHQINPCVKKEYRDDPFHQSHLPWLHSSHPGLEKISAI
1 .	1	f	VWEGNDCKKADMSVLEISGMIMNRVNSHIPGIGYQIFGNAVSLI
	I	Į.	
1			LGLTPFVFRLSQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV
	L		IISFVVRVSLVWIFFPLLCVAERTYKQVGIM
5450	B136	1242	GQQFASFFG*NHPEVTVAMALTDIDLQLQFSMSQPEALLLLAAG
		1	PADHLLLQLYSGHLQVRLVLGQEELRLQTPAETLLSDSIPHTVV
1	1		LTVVBGWATLSVDGFLNASSAVPGAPLEVPYGLFVGGTGTLGLP
1 .		}	YLRGTSRPLRGCLHAATLNGRSLLRPLTPDVHEGCAEEFSASDD
			VALGFSGPHSLAAFPANGTQDEGTLEFTLTTQSRQAPLAFQAGG
í	[•	RRGDFIXVDIFEGHLRAVVEKGQGTVLLHNSVPVADGQPHEVSV
}			HINAHRLRISVDQYPTHTSNRGVLSYLEPRGSLLLGGLDAEASR
1	 		HLOEHRLGLTPEATNASLLGCMEDLSVNGORRGLREALLTRNMA
i			AGCRLBEREYEDDAYGHYEAFSTLAPRAWPAMELPRPCVPBPGL
5	İ		PPVFANPTOLLTISPLVVARGGTAWLEWRHVOPTLDLMEARLRX
	ļ		SQVLPSVTRGAHYGELELDILGAQARKMFTLLDVVNRKARFIHD
1	·		· ·
i	}		GSEDTSDQLVLEVSVTARVPMPSCLRRGQTYLLPIQVNPVNDPP
			HIIFPHGSLMVILEHTQKPLGPEVFQAYDPDSACEGLTFQVLGT
1	(SSGLPVERRDQPGEPATEFSCRELEAGSLVYVHCGGPAQDLTFR
}			VSDGLQASPPATLKVVAIRPAIQIHRSTGLRLAQGSAMPILPAN
[]			LSVETNAVGQDVSVLFRVTGALQFGELQKHSTGGVEGAEWWATQ
1	1		AFHQRDVEQGRVRYLSTDPQHHAYDTVENLALEVQVGQBILSNL
]]		SPPVTIQRATVWMLRLEPLHTQNTQQETLTTAHLEATLEBAGPS
l 1			PPTFHYEVVQAPRKGNLOLQGTRLSDGQGFTQDDIQAGRVTYGA
} ;	ł		TARASKAVEDTFRFRVTAPPYFSPLYTFPIHIGGDPDAPVLTNV
]			LLVVPEGGEGVLSADHLFVKSLNSASYLYEVMERPRLGRLAWRG
i	· ·		TODKTTMVTSFTNEDLLRGRLVYOHDDSETTEDDIPFVATROGE
			SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL
	!		TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
	1	}	TONDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP
			YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT
	1		AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF
	1		SVEAGEVHTDATLOVTIALEGPLAPLKLVRHKKIYVFQGEAAEI
4			RRDQLRAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
			, AUGUS
i	[*-
			LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLB GVLVELBVLPAAIPLRAQNFSVPEGGSLTLAPPLLRVSGPYFPT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}	}	1	LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVEEQLIRYV
1	1	f	HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
1		Ì	TNTGLQMWBGATAPIPABALRSTDGDSGSBDLVYTIEQPSNGRV
1)	j	VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
1	i		TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
ł	·	· ·	SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA GNILYEHRMPPEPFNEAHDTLELOLSSPPARDVAATLAVAVSFE
Į.		•	AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPO
1			RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGOLV
1	į i		YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
j	j	Ì	BRPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGRIEYEVQ
			RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
1	(i	QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
1			SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
	Į ·		DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
			WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
1			VVRVPRARTEPGGSQLVEQFTQQDLEDGRIGLEVGRPEGRAPGP
	<u>'</u>		AGDSLTLELMAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
1			ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
1			IIPMCLVLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
1			GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP ALKNGQYWV
5451	1 i	2274	RDSSEQGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
	-		KNSEPGSPHSLEALRDAAPSQGLNFLLLPTKMLF1FNFLPSPLP
1			TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
1 .			GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
1 .			PYRWLSYKQVSDRABYLGSCLLHKGYKSSPDQFVGIFAQNRPBW
i .			IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
- 1		•	KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIRILSL
1 .			YDABNIGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHQN
1			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
			CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
1			AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
1			GGRVRVIVTGAAPMSTSVMTPFRAAMGCQVYEAYGQTECTGGCT FTLPGDNTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
1			THYPKGYLKUPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
[KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
	·		VVPDTDVLPSFAAKLGVKGSFEELCONOVVRRAILEDLOKIGKE
			SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYPRTO
			IDSTARHIOD
5452	1833	1138	SRVPSLCLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
]			LGSLLSLSCLALSVLLLAQLSDAAKNPEDVRCKCICPPYKENSG
1			HIYNKNISQKDCDCLHVVBPMPVRGPDVBAYCLRCECKYRRRSS
		i	VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
			DDDIGDHQPFANAHDVLARSRSRANVLNKVBYAQQRWKLQVQEQ
F450			RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREBTVTATATSQVAQQPPAAAAPGRQAV
			AGPAPSTVPSSTSKDRPVSQPSLVGSKBEPPPARSGSGGGSAKE
			PQEERSQQQDDIEELETRAVGMSNDGRFLKFDIEIGRGSFKTVY
			KGLDTETTVEVANCELQDRKLTKSERQRFKEEARMLKGLQHPNI
]			VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
,			RSWCRQILKGLQFLRTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1 1			LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
j			LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII EGCIRQNKDERYSIKDLLWHAFFQESTGVRVELAEEDDGEKIAI
ļ [į	KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVRSG
} [)		YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5454	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
			AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1 1			PORERSQQQDDIERLETKAVGMSNDGRFLKFDIEIGRGSFKTVY
<u>L</u>			KGLDTETTVEVANCELQDRKLTKSERQRPKEEAEMLKGLQHPNI

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ſ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	i -	\=possible nucleotide insertion)
			VRFYDSWESTVKGKKCIVLVTBLMTSGTLKTYLKRFKVMKIKVL
í	(RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
ì	1		LGLATLKRASFAKSVIGTPEFMAPEMYERKYDESVDVYAFGMCM
1	{	{	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKBII
1	1	l	BGCIRONKDERYSIKDLLNHAFFQEETGVRVELAERDDGEKTAI
1		ĺ	KLWLRIEDIKKLKGKYKDNEAIEFSFDLRRNYPEDVAQEMVESG
ł	ì		YVCEGDHRTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRILO
1	1	{	WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
j	j		GALEBLIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAABIL
1		ŧ	-QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1	}	l	KALLPSMIKRRQGHIVAISSIQGKMSIPPRSAYAASKHATQAFF
I			DCLRARMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
ì	Ì	1	TAQGRSPVEVAQDVLAAVGKKKDVILADLLPSLAVYLRTLAPG
	i .		LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
}	}		TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
1			QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
1			QXVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
ľ			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
1			DAQQQVKALGTERTTLEGHLAKVQAQABQGQQELKNLRACVLEL
)			EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
			ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
} .			QELKGNIRVFCRVRPVLPGBPTPPPGLLLFPSGPGGPSDPPTRL
			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
			MLVQSALDGYPVCIFAYGQTGSGKTFTMBGGPGGDPQLEGLIPR
		-	ALRHLFSVAQELSGQGWTYSFVASYVEIYNBTVRDLLATGTRKG
			QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARQNR
1 :			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
			SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
j .			ASKVBPSVLFGTAQSHRKWKTDPDLCVCVCVCVCVCVCVCVCVP MSMYRVRGGRVAGGCPIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
	-	1310	LLRSABRLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
j i			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
<u> </u>			APHDFQFVQKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
ł			RKEALLLLSWKOMLDHFQATPHHGVYSRERELLRERKRLGVPGI
f l			TSYDPHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1 1			PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
			RLTPCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWNCPTASW
, 1	Ì		EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
1 1		į	GSKNPKIALKLARFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
			ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTKNBEQA
L	,		ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEBYARLVMEAQPEWLRAEV
	ł		KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFERLEVDYEA
l i			IRSEMEQLKEAFGQAHTNHKKVAADGRSREESLIQESASKEQYY
[[ļ	VRKVLBLQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
]			QRGRLRDDIKEYKFREARLLQDYSELERENISLQKQVSVLRQNQ
ļ [[VEFECLKHEIKRLBEETEYLNSQLEDAIRLKEISERQLEBALET
} }	ļ	1	LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
	1	į	EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
		į	DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
			SLSEQQEKVTRLTENLSALRRLQASKBRQTALDNEKDRDSHEDG
[[1	DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
	1	ļ	HAREKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
	1		DVAGETOGSLSVAQDELVTPSEBLANLYHHVCMCNNETPNRVML
	į	ł	DYYREGOGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPBAGRA
	i		DGGTGDSSPSPGSSLPSPLSDPRREPMNIYNLIAIIRDQIKHLQ
L			AAVDRTTRLSRORIASQBLGPAVDKDKEALMBBILKLKSLLSTK
			

SEQ	Predicted	Predicted end	I Amilino and I ambalanta de la companya de la comp
ID	beginning	1	Amino acid segment containing signal peptide
NO:		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, K=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
!	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first .	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
	1		REQITTLRTV_KANKOTAEVALANLKSKYENEKAMVTETMMKLR
1			
1	ľ	ľ	NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAABDE
1		! .	KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
	L		PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
1 -		i	KGPKRLEKFSDERAAYFRCYHKVTBLNNVKNVARLPKSTKKHAI
1			GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGRP
i	{	1	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
1			DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLF1P
(1	1	QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
1	J		SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
			PAYRSEH
5460	45	2097	
3300	13	4071	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
I	i	j	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
1		l	GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1	}	l	ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
1	i	ł	CEKCHHFFVVLSEADSKKSIIKEPESAARAVKLAFQQKPPPPPK
ł	ì)	KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAB
			VBKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
ì	1.	<u> </u>	QQVNQQIPQKKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
1			AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
1	Ì		VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
1			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
1	1		NEKYLGFGTPSNLGKGRRAAAADLANRSGESNTHODIEEKDRL
l			LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
i .	l		NAVIPQYQALFSMDKCELNVTEDALKALARLALERKTGARGLRS
}			IMBKILLEPMPEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
	· ·		SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	
3401	1401	700	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
j			SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
1	į		SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
1 .	}		NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGBLVESLKRFC
1			ASTRLPPTPLLLFPEERATNGREGLLRFSSWPFSIQDVVQPLTL
1 .			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
1	•		EANBEFALRVQQLVAKBLGQTGTRLTPADKABHMKRQRHPRLRP
1	i .		QSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
			TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
1			TPOPTALTFAKSSNARQESLQERKQALYBYARRRFTERRAQEAD
5462	663	3353	KIKBROMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA
_			RLSNGSPSAPSLTNSRGSVHTVSFLLQIGLTRESVTIRAQELSL
			SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILOLIT
1	į		SADEIHEGDLVEVVLSALATVEDFOIRPHTLYVHSYKAPTFCDV
]		
[1	CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
		i	VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
[WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLPRQGMQC
j l			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
]			NDINSDSSRGLDDTBEPSPPEDKMFFLDPSDLDVERDBRAVKTI
} !			SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGMMVHYTSRDNLRK
]	ļ		RHYWRLDSKCLTLFQNBSGSKYYKEIPLSEILRISSPRDFTNIS
]			QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
]	!		WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
<u> </u>]		NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
į			
j j			RFPTKQBSQLRNBVAILQNLHHPGIVNLBCMFETPERVFVVMEK
1 1			LHGDMLEMILSSBKSRLPBRITKFMVTQILVALRNLHFKNIVHC
, ,	J		DLKPENVLLASAEPFPQVKLCDFGFARIIGEKSFRRSVVGTPAY
ş l			LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTYPFNEDEDINDQI
.)			QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
, ,			THE OPERATED BY DATE OF THE PARTY OF THE PAR
()	· 1		WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
	·]		KHFIMAPNPDDMEEDP KHFIMAPNPDDMEEDP
5463	237	1012	KHPIMAPNPDDMERDP
5463	237	1012	

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
[Į.		LSPCBCTGTLGTIHRSCLEHWLSSSNTSYCELCHFRPAVERKPR
i	ł	ł	PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGNLCLRGAV
1	j	ļ	DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNEWR
			RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYREYQTTL
ł	i		GASILSKIIILGDTTLKIQIWDTGGQBRVRSMVSTFYKGSDGCI
1	}		LAFDVTDLESPEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA DRKYQSILENHLTESIKLSPDQSRSRCC
5465	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKOOGPAAVRA
3403	3270	3340	VNVFHHLPYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
1		ł	PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
i			KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1	i		RLGTYBSDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
1	1	ł	VWEMSTSKEKAKTVTLKQALLGHTDTVTCATASLAYHI IVSGSR
ļ	ļ)	DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
l			THOWSINGNPIOSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
	1	1	HSDGVVRFWRMEFLQVPETFAPEPAEVLEMQEDCPEAQIGQEAQ
1			DEDSSDSRADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
j	}	_	TDSGSDDSRRNSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
	Į.		HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHFA
1 .	1		EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDR
ļ	Į.		GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
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1			RFALPTAHHTLGLPVGKH1YLSTRIDGSLVIRPYTPVTSDBDQG
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1			RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQBEWECLQPDQRTL
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1			RRYPOLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
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1			IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
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SEO	Predicted	Predicted end	Amino agid compat
1D	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
į.	to first	amino acid	P=Proline, Q-Glutamine, R=Arginine,
1	amino acid	residue of	S-Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
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1	•		NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPDRG
, .)		HEBLEKLESTLDGLERSRERQERRIQVTLEKWERFETNKETVVR
		 	YLPQTGSSHERFLSPSSLESLSSELEQTKEFSKRTESIAVQAEN
ı	[LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLERBYVIDK
F474			S
5474	2	780	TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQSTI
1			LKRWKKNWFDLWSDGHLIYYDDQTRQWIEDKVHMPMDCINIRTG
	ĺ		QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLANKFT
1			LODSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPRVGRTLS
1			LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLYGQQ
5475	2	506	PANQVIIRBRYRDNDSDLALGMLAGAATGMALGSLFWVP ARGWLESLSLTCQTTPPPSSPCLLHSPBTFIHTMPPNLTGYYRF
	•	200	VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTL
1			STERNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQK
1			GEVPNRGWRHWLEGEMLYLKLTARDAVCEQVFRKVR
5476	192	1457	SDSMSLLDCFCTSRTQVBSLRPBKQSBTSIHQYLVDBPTLSWSR
			PSTRASEVLCSTNVSHYELQVEIGRGPDNLTSVHLARHTPTGTL
1 1			VTIKITNLENCHEERLKALQKAVILSHFFRHPNITTYWTVFTVG
			SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVRGLN
1 1		i	YLHQNGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQRHR
1	•		AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITACEL
1 '			ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSBSRMKNSQ
			SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLVQLC
			LOODPEKRPSASSLLSHVFFKOMKEBSODSILSLLPPAYNKPSI
5477		· · · · · · · · · · · · · · · · · · ·	SLPPVLPWTEPBCDFPDEKDSYWEF
54//	3	1044	RGNSRLRYSHEDELQLPRLPELFRTGRQLLDEVEVATEPAGSRI
	·		VQEKVFKGLDLLEKAAEMLSQLDLFSRNBDLEBIASTDLKYLLV
l i			PAPQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVAEF3 LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKKELE
1 .			HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIBSIDO
1			BIKILRERDSSREASTSNSSRQERPPVKPPILTRNMAQAKVFGA
1			GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPEEFRKAAQQQE
ł i			EQERKEEEDDEQTLHRARENDDWKDTHPRGYGNRONMG
5478	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
) 1	}		VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
[]	ļ	:	LWDKSSRECVHSYCKHGGFVTYVDPHPSGTCIAAAGMDNTVKVW
ļ i			DVRTHRLLQHYQLHSAAVNGLSPHPSGNYLITASSDSTLKILDL
1			MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWKSNP
]]			DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLERDKLKQC
<u></u> 1			LENQQLIMQRATP
5479	2	835	KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASDDKT
		İ	VKVNATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDKTVK
Į [LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTVKVW
] [DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKILDL
{	,	1	MEGRLLYTLHGHQGPATTVAPSRTGEYFASGGSDEQVMVWKSNF
ļ [1		DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLERDKLKQC
- <u></u> -			LENQQLIMQRATP
5480	444	1952	LSLTSRMEEABLVKGRLQAITDKRKYQEBISQKRLK1EBDKLKH
1		•	QHLKKKALREKWLLDGISSGKEQBEMKKQNQQDQHQIQVLEQSI
1	ł	ľ	LRLEKEIQDLEKAELQISTKEKAILKKLKSIERTTEDIIRSVKV
		Ī	EREBRAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDEQNR
	ł		KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYDDGQ
			KSVYAVSSNHSAAYNGTDGLAPVEVERLLRQASERNSKSPTEYH
	ļ		BPVYANPFYRPTTPQRETVTPGPNFQERIKIKTNGLGIGVNESI
L	l		HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTPQKR

Degining nucleotide location corresponding to first amino acid residue of amino acid sequence		nucleotide	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid. R=
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequ	NO:		location	
Corresponding to first amino acid residue of amino acid sequence L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Veline, G=Glutamine, amino acid sequence N=Tryptophan, Y=Tyrosine, X=Unknown, *=St Codon, /=possible nucleotide deletion,	ļ	logarion		Glutamic Acid, FaPhenvlalanine, G-Glycine
COPTESPONDING to first amino acid residue of residue of amino acid sequence	-	TOCALTON	corresponding	H=Histidine, I=Isoleucine, K=Tamine
amino acid residue of amino acid residue of secure. T-Threonine, V=Valine, amino acid sequence S-Serine, T-Threonine, V=Valine, sequence S-Serine, T-Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=St Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) IMTFWEESNVWQDKDAPSPERPRISPRTIFCKSEHQNSSFT DEEDVYNTVHSLPPDINDTEPVTMIFMCYQQAEDSEBCKK GYDGIIHAELVVIDDEEEDEEGAEKPSYHPIAPHSQYYQP TPLPRKRSEASPHEKHKS S481 3 1422 NSPGSVCLCQCVCPSLLHCLPPLLLLLLPLLHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTTKRCBEKEKFPEPTVFRD QGLMRAGDDLEANAKFLDSTGSRLDVRRYADTLFDILVAGS PGGTRIDDGDKTKNTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLFLKAFSETEQTKLAMISGILLGNGTIILTSLFTDSLVKEGIAASFAVKLFKAMMAEKDANSVTSSLE LDKRILESPVNRQSUDHFAXYFTDAGLKELSDFLRVQQSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMMAVEMNKKERLVAEQALKHLKQVAPLLAVFSSQGQSEL QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEESJIKWYKE AKKSVFLDQMKKFVEMLQNAEESSESBEEN THVWMTCMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS BGLQEKUSGPYSCSVNYQQMCQLKSRGHSINTLEILVVLVPPA CRLQSVPHVGANVTLSCQSPRSKPAVQYQMDRQLPSFQTFF LDVTRGSLSLTHLISSSMAGVVVCKAHNEVGTAQCNVTLEVS GAAVVAGAVGTLVGIGLLAGLVLLYHRRGKALEEPANDIK LAPRTLEMPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TFSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRNG. VNVPAQSQAGSLU VNVPA	Ì	corresponding		L=Leucine, M=Methionine, N=Asparagine
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Veline, mino acid sequence Sequence Sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) IMTPWEESNVMQDKDAPSFKPRLSPRETIFGKSEHQNSSPT DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSERDKK GYDGI HABLVVIDDEEEDEGEABKPSYHPIAPHSQVYQE TPLPRKRSEASPHEKHKS S481 3 1422 NSPGSVCLCQCVCPSLLHCLPPLLLLLLFILLHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKPBPTVFRD QGLNKAGDDLEAVAKFLDSTGSRLDYRRVADTLEDILVAGS PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIN LLTSLFTDSLVKEGIAASFAVKLFKAMMABKDANSVTSSLR LDKALLELPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKELGERLSQECPIKEVVLYVKEPMKRNDLPETAVIGL CIMMAVEWNKKERLVAEQALKHLKQYAPLLAVFSSQGAGSL KELQKELGERLSQECPIKEVVLYVKEPMKRNDDLFETAVIGG CKVQEYCYDNIHPMKAFQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKPVEWLQNAREESESEGEEN THVVMTCMCYAPHQVLSYINGVTTSKPGYSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQKSGRSIKTLELNVLVVPS CRLQGVPHVGANVTLSCQSPRSKPAVQYQMDRQLDSFQTFF LDVIRGSLSITNLSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLWGIGLLAGLVLLY:HRRGKALEEPANDIK LAPRTLPWFKSSDTLSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGVVVAQAGSLV		to first	amino acid	P=Proline, O=Glutamine, R=Arginine.
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide disertion) LMTPMEESUVAYUNGDKDAPSPKPRLSPRETIFGKSEHQNSSPT DEEDVRYNIVHSLPPDINDTERVTHIEMGYQQAEDSERDKK GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQP TPLPRKRSEASPHEKHKS S481 3 1422 NSPGSVCLCQCVCPSLLHCLPPLLLLLLLPLLHESPQPPA VATSSDRNFMNKHQKPVLTQQRFKTRKRDEKEKFEPTVPRD QGLMRAGDDLEAVAKFILDSTGSKLDYRRYADTLFDILVAGS PGGTRIDDGDKTKMTMHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTL ILTSLFTDSLVKEGIAASFAVKLIFKARMAEKDANSVTSSLR LDKKLLLELPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKELQBERLSQBCPIKEVVLYVKEEMKKNDLPETAVIGL CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVPSSQGGSEL QKVQEYCYDNIHFMKAFQKIVVLPYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNAREESSEGEEN THVVMTCMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGFYSCSVMVQDKQGKSRGHSIKTLELNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQMDRQLPSFQTFF LDVIRGSLSITNLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGILAGLVLLYHRRGKALEEPANDIK LAPRTLPWPKSSTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALFSPRLFTTDGAHPQPISPIPGGVSSSGLSRMGVVVVPAQSQAGSLV	1	amino acid	residue of	S=Serine, T=Threonine, V=Veline
Sequence Sequence Codon, /=possible nucleotide deletion, =possible nucleotide insertion)		residue of	amino acid	W=Tryptophan, Y=Tyrosine Y-Unknown t-Ston
Sequence Sequence Sequence IMTPMRESNVMQDKDAPSPKPRLSPRFTIFGKSEHQNSSFT DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEBUKK GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQF TPLPPKRESASPHEKHKS TPLPPKRESASPHEKHKS SPGSVCLCQCVCPSLLHCLPPLLLLLLPLLHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVPRD GGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKMTNHCVFSANEDHETIRNVAQVFNKLIR YLEKAFEDEMKKLLPLKAFSETEQTKLAMLSGTLLGNGTL LDKRLLELPPUNRQSVDHFAKYFTDAGLKELSDFLRVQQSL LDKRLLELPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMMAVBWNKKBELVAEQALKHLKQYAPLLAVFSSQGQSBL QKVQEYCYDNIHFMKAFQKTVVLFYKADVLSEKAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESESEGEN AKGKSVFLDQMKKFVEWLQNABEESESEGEN THVVMTGMCYAFHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLEINVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLLGGLLAGULLYHRGKALBEPRADIK LAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG. VNVPAQSQAGSLV		amino acid	I .	Codon. /=possible nucleotide deletion
LMTPWEESNVMQDKDAPSPKPRLSPRTIFGKSEHQNSSPT DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSBEDKK GYDGIIHAELVVIDDEBEEDEGEABKPSYHPIAPHSQVYQP TPLPRKRSEASPHEKKS 5481 3 1422 NSPGSVCLCQCVCPSLHCDPPLLIDLLPLDHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDBKEKFBPTVPRD QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKNTNHCVPSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLPLKAFSETEQTKLAMLSGTLLGNSTL ILTSLFTDSLVKEGIAASPAVKLFKAMMABKDANSVTSSLK LDKRILELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQGSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMNAVBWNKKBELVAEQALKHLKQYAPLLAVFSSQGQSEL QKVQEYCYDNIHFMKAFQKTVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESBESEEN THVVMTGMCYAFFHQVLSYINGVTTSKPGVSLVVSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPPTLPWKSSDTISKMGTLSSVTSARALRPPHGPPRPGA VNVPAQSQAGSLV		sequence	1	\=possible nucleotide insertion)
DEEDVRYNIVHSLPPDINDTEPVTMIFMCYQQAEDSERDKK GYDGI HARLWUIDDEEEDEGEAEKPSYHPIAPHSQVYQP TPLPRKRSEASPHEKKS 3 1422 NSPGSVCLOCVCPSLHCLPPLLILLLPLLHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFBPTVFRD QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLIPLKAFSETEQTKLAMLSGTLLGNSTL ILTSLFTDSLVKEG IAASPAVKLFKAMMAEKDANSVTSSLR LDKRLLEPPVNRQSVDHFAKYFTDAGLKELSDFLRVQGSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLFBTAVIGL CIMNAVBWNKKBELVAEQALKHLKQYAPLLAVFSQGQSEL QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESESEGEN THVVMTGMCYAFFHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQXQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGIGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKMGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG.			<u> </u>	IMTPWEESNVMODKDAPSPKPRT.SDRRTTRCKGEHONGCDTCOR
GYDGI IHAELWUIDDEEEEDEGEABKPSYHPIAPHSQUYQE TPLPRKRSEASPHEKHKS 5481 3 1422 NSPGSVCLCQCVCPSLHCLPPLLLLLLPLLHESPQPPA VATSSDRNFNNKHQKPVLTGQRFKTRKRDEKEKFBPTVFRD QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILWAGS PGGTRIDDGDKTKNTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTL ILTSLFTDSLVKEG IAASFAVKLFKAWMAEKDANSVTSSLR LDKRLLGEPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKRLQBRLSQBCPI KEVVLYVKEEMKRNDLPETAVIGL CIMNAVBWNKKBRLVAEQALKHLKQYAPLLAVFSSQGQSRL QKVQEYCYDN IHFMKAFQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVBWLQNARESSESBGBEN THVVMTGMCYAFHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQXQMDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSTISKMGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG.	-	1	l .	DEEDVRYNIVHSLPPDINDTEPVTMTPMCVOOAFDGREDRYFT T
TPLPRKRSEASPHEKHKS 3 1422 NSPGSVCLCQCCPSLLHCLPPLLILLLPLLHBESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFBPTVFRD QGLNRAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLPLKAFSETEQTKLAMLSGILLGNGTL ILTSLFTDSLVKEG IAASFAVKLFKAMMABKDANSVTSSLR LDKRLLBLFPVNRQSVDHFAKYFTDAGLKELSDFLRVQOSL KELQKRLGBRLSQBCPIKEVVLYVKEBMKRNDLPETAVIGL CIMNAVBWNKKBELVAEQALKHLKQYAPLLAVVSSQGGSEL QKVQEYCYDNIHFMKAPQKIVVLFYKADVLSEBAILKWYKE AKGKSVFLDQMKKFVEWLQNABESSESBGBEN THVVTMCCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLGGVPHVGANVTLSCQSPRSKPAVQYQMDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALBEPANDIK IAPRTLPWPKSSTISKMGTLSSVTSARALRPPHGPPRPGA VNVPAQSQAGSLV			1	GYDGIIHAELVVIDDERREDEGEARKPSYHDTADHSOVVODAVO
1422 NSPGSVCLCQCVCPSLLHCLPPLLILLLPLLHESPQPPA VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVPRD QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKMTNHCVFSANEDHETIRNVAQVFNKLIR YLEKAFEDEMKKLLPLKAFSETEQTKLAMLSGTILGNGTL ILTSLFTDSLVKEG IAASFAVKLFKAWMAEKDANSVTSSLR LDKRLLBLPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMMAVEWNKKERLVAEQALKHLKQYAPLLAVFSSQGQSBL QKVQEYCYDNIHFMKAFQKTVVLFYKADVLSEKAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESEGEEN THVVMTGMCVAFHQVLSYINGVTTSKPGVSLVVSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLEINVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBERANDIK IAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG-	- 1	f		
VATSSRNFMNKHQKPVLTGQRFKTRKRDEKEKFBPTVFRD QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKNTHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLLPLKAFSETEQTKLAMLSGILLGNGTL ILTSLFTDSLVKEG IAASFAVKLFKAWMAEKDANSVTSSLR LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQOSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMMAVEWNKKERLVAEQALKHLKQYAPLLAVFSSQGQSEL QKVQEYCYDNIHFMKAFQKLVVLFYKADVLSSEAILKWYKE AKGKSVFLDQMKKFVEWLQNAKEESESEGEN THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG	5481	3	1422	
GELNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGS PGGTRIDDGDKTKNTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLPLKAFSETEQTKLAMLSGTLICMSTIL ILTSLFTDSLVKEG IAASFAVKLFKAWMAEKDANSVTSSLR LDKRILBLFPVWRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKELQERLSQBCPIKEVVLYVKEEMKRNDLPETAVIGL CIMMAVBWNKKBELVAEQALKHLKQYAPLLAVFSSQGQSEL QKVQEYCYDNIHFMKAFQKTVVLFYKADVLSBRAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESESEGEN THVVMTGMCYAFHQVLSYINGVTTSKPGVSIVVSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG- VNVPAQSQAGSLV				VATSSDRNFMNKHOKPVI/TGORFKTRKRDRKRKFRPTURDDTT
PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIR YLEKAFEDEMKKLLIPLKAFSETEQYKLAMISGILIGMGTI ILTSLFTDGLVKEG IAASPAVKLFKAMMAEKDANSVTSSLER LDKARLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKBLQERLSQBCPIKBVVLYVKEEMKRNDLPETAVIGL CIMNAVBWNKKBRLVAEQALKHLKQYAPLLAVFSSQGQSEL QKVQBYCYDNIHFMKAFQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESESEGEEN THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKMGTLSSVTSARALRPPHGPPRFGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG VNVPAQSQAGSLV			İ	OGLNEAGDDLEAVAKFI.DSTGSRI.DVRRVADTI.PDTI.JACCMT.N
YLEKAPEDEMKKLLLPLKAPSETEQTKLAMLSGILLGNGTL ILTSLFTDSLVKEG IAASFAVKLFKAWMAEKDANSVTSSLR LDKRLLBLPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKRLQBRLSQBCPIKEVVLYVKEBMKRNDLPETAVIGL CIMNAVBWNKKERLVAEQALKHLKQYAPLLAVFSSQGSEL QKVQEYCYDNIHFMKAPQKIVVLPYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVBWLQNABESSESBGBEN 5482 1492 528 THVVTMCCYAPFULSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQEVPHVGANVTLSCQSPRSKPAVQXQMDRQLPSPGTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKMGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG VNVPAQSQAGSLV				PGGTRIDDGDKTKMTNHCVFSANRDHRTTRNVACVFNKT.TDDVK
ILTSLFTDSLVKEGIAASPAVKLFKAWMAEKDANSVTSSLR LDKAILELFPVWRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKBLQERLSQBCPIKEVVLYVKEBMKRNDLFBTAVIGL CIMNAVBWNKKBRLVAEQALKHLKQYAPLLAVFSSQGQSBL OKVQEYCYDNIHFMKAPQKITVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNABEBSESBGBEN 5482 1492 528 THVVMTCMCYAPHQVLSYINGVTTSKPGVSLVVSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBPANDIK IAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG.	1			YLEKAFEDEMKKLI LPLKAFSETROTKI AMI SCITLI CNICTI DAT
LDKRILBEPPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSL KELQKBLQBRLSQBCPIKEVVLYVKBEMKRNDLPBTAVIGL CIMMAVBWNKKBELVAEQALKHLKQYAPLLAVVFSSQGGSEL QKVQBYCYDNIHFMKAPQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKPVEWLQNABEESRSEGEEN 5482 1492 528 THVVMTCMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSPQTFF. LDVLRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG. VNVPAQSQAGSLV	- 1		1	
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CIMMAVBWNKKBELVAEQALKHLKQYAPLLAVFSSQGQSEL QKVQEYCYDN HEMKAFQKIVVLFYKADVLSBEAILKWYKE AKGKSVFLDQMKKFVEWLQNABEESESESEEN THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS BGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG. VNVPAQSQAGSLV	1			
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THVVMTCMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLS EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLBLNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQMDRQLPSFQTFF LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPPTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTGAHPQPISPIPGGVSSSGLSRMG VNVPAQSQAGSLV	- 1			
EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPA CRLQGVPHVGANVTLSCQSPRSKPAVQYQMDRQLPSPQTFF LDVIRGSLSLTMLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGLULLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG VNVPAQSQAGSLV	5482	1492	528	
CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF. LDVIRGSLSLTMLSSSMAGVYVCKAHNEVGTAQCNVTLKVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG. VNVPAQSQAGSLV	j			
LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVS GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRNG VNVPAQSQAGSLV				
GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALBEPANDIK IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGA TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMG VNVPAQSQAGSLV	- 1			
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VMVPAQSQAGSLV	- 1			TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
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5483 1 788 FFFFKGCRAGRGNESDYRKLEEMHORFLVSERSKDDLOLRL	483	ī	788	PFFFKGCRAGRONESDYRKLEEMHORFLVSERSKDDLQLRLTRA
	ļ		•	ENRIKOLETOSSEEISRYQEMIQKLQNVLESERENCGLVSEORL
KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIK	i		,	KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHBFSIKERG
FEVQLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLT	. 1			FEVOLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
RIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILE	j		•	RIRINNLKSELSROKLHTOELLSOLEMANEKVARNEKLILEHOR
				KANRLORRLSQAEERAASASQOLSVITVORRKAASLMNLENI
	484	3	1997	IMADMEDLFGSDADSRAERKDSDSGSDSDSDQENAASGSNASGS
	ł			ESDQDERGD3GQP3NKELFGDDSEDEGASHHSG3DNHSERSDNR
	i			SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
	· · · · · · · · · · · · · · · · · · ·	,		ABGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
	- 1			LONSDDDEKMONTDDEERPQLSDDERQQLSEEEKANSDDERPVA
SUNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDREHRHS	1			SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
REEQDHKSBSARGSDSEDEVLRMKRKNAIASDSEADSDTEVI	- 1			BEBODHKSBSARGSDSBDEVLRMKRKNAIASDSBADSDTEVPKD
	}]	,	NSGTMDLFGGADDISSGSDGBDKPPTPGQPVDBNGLPQDQQRRR
	1			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYK
	- 1	. i		DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNBIKESNAR
	- [-		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
	- 1			VFKTKLTFRPHSTDSATHRKNTLSLADRCSKTOKIRILPMAGRD
	- 1	1		PECORTEMIKKEBERIRASIRRESOORRMREKOHORGLSASYLE PDRYDREEEGKESISLAAIKNRYKGGIREERARIYSSDSDEGSE
	- 1			
EDKAQKILTSDEVRPNLFNSRGLSCTQEPTALNERIA ACTN	1	1		EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEKLTDQ
	485	161	1074	
A STATE OF THE STA		***	20/4	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
		1		CCAAPNNVAITFPIOKVLFROOLYGIKTRDAILQLRRDGFRNLY
	- 1	ŀ		RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA
CDVVDCI UDTI DDNIV ONU BEST POLITICAL CO	ł	1	i	VIAGTTEATFTELERVOTLLODHKHHDKFTNTYQAFKALKCHGI
		ļ	i	GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
	Į			DFICGGLIGAMIGFLFFPINVVKTRIQSQIGGEPQSFPKVFQKI
WLERDRKLINLFRGAHLNYHRSLISWGIINATYBFLLKVI 5486 1404 142 IPGSTISWSPAARGLSVCRCCRLHDASAMOLEGDLDEDEDE	486	1404		
110D11DHDFANANDDSVCRCCRDHPASAMDDFGDDFEPRRS		7403	147	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
		}		PAAGKEAOKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
	1	ĺ	i	GSLATS I SOMVKTECKGAKRKTSRERKNGSEKLVEKKVCKASSV
IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRV				TROUNG I VARKIGEKERMODAHVILINDITEECRPPSSLITRVSY
		ł	i	
			į	FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
				FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVBKTVKRCL LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
DGRVLGVLBVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFI				FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL LDTFKHTDEBFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG DBRAILCRYNEBSQKHAALSLSKEHNPTQYEBRMRIQKAGGNVR

	T Day 37 - 1	1 5 17 1 1	Daving and American and American
SEQ	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	beginning nucleotide		
NO:		location corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location		H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
i	1	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1 .	į.	ł	ACDGLPKVFTPEEAVNFILSCLEDRKIQTREGKSAADARYEAAC
			NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
}			LEANDPFANKDDPPYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
L	<u> </u>		CKCKSSQKQHSPVPBKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
}	j	l	GHKPFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSPGNDYIEN
	İ		LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
i	İ	ł	NTEDLRAAANVISRAKVMVCQLBITPATSLBALTMARRSGVKTL
ļ	j	Į.	FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
i	l	}	AALVILKRGCQVVIITLGAEGCVVLSQTBPEPKHIPTEKVKAVD
L	1	i	TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDFKIFLGQWREEPKMPLLLLGETEPLK
1	1	1	LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1	i	1	LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
j			LAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNERQYCGDFDSF
ì			FSAKEENI IYSFLGLAPPPDSKGSEKAREGGETEAQKEGSEDVG
ł	ł	İ	nlpeaqekneregetatreteelamegaegeabbeeetaegeep
ı			GEDEDS
5490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGRTEPLK
1			LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
ļ.	•	Ì	LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
1			IAGDEDNRRWMRKNVPGBKKPQNGIPLPPQIFNEEQYCGDFDSF
1			FSAKRENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
1		}	nlpraqeknrregetateeteeiamegaegrabeebetaegbep
l			GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
1			QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
			LAKLFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
1			SFFDFEGKQKWRAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
i			PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
ſ · · · · ·			ITKAIKSKNVDVNVKDBEGRALLHWACDRGHKELVTVLLQHRAD
i	ł		INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
i e	ļ		BEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNTPYRATEE
ł	1	l	QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
		J	RNLNGREFSGRALRVDNAASEKNKBELKS1.GPAAPIIDSPYGDP
[IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML
1	l	I	LONPOLAYALLOAQVVMRIMDPEIALKILHRKIHVTPLIPGKSO
1		I	SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
	ſ	1	PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
	l	į.	VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
1	l	1	GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
	[[GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
	i	1	VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
1	1	1	MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMQGTGIQ
1	1		GTGMQGAGIQGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
1	1	1	PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQLAMLPPEQRQSI
	1		LILKEQIQKSTGAS
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
]	}	TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
	1	1	VOKSDVDLMRTKLRRLBEENSRKDRQIEQLLDPSRGTDFVRTLA
l		İ	BKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
l	1		BMRIAMBTYYEBVHRLOTILIASSETTGKKPLGKKKTGAKRQKKM
1	ĺ		GSALLSLSRSVQELTERNQSLKEDLDRVLSTSPTISKTQGYVEW
1	1	i	SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
			HROPRGDRNKDHERLRGAVRDLKBERTALQEQLLQRDLEVKQLL
	ĺ	1	QAKADLEKBLECAREGEEERREREBYLREBIQTLTSKLQELQEM
1	[Į.	KKEEKEDCPEVPHKAOELPAPTPSSRHCEQDWPPDSSEEGLPRP
		l	RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR
		,	I KAPLAKKUANANVIKIAUWKVYKHKKKKANDEAHVVLKAKKK [

CRO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		location	
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknowc, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	"	\=possible nucleotide insertion)
 		 	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
1]	1	PVOKEAIVIIOSALRAHLARARHSATGKRTTTAASTRRRSASAT
1	į	ł	HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
!	Į.		
L	L		SLPTKNPPV
5494	71	536	RSKAKIGTPTREVPSTDMXVRRESSSSUTHRPAPSPATPRLLGT
1	Ì	}	RRVLLGVSBGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
1	l .		PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
ł	l .		GDEEAQVENLITANATEPQKARN
5495	273	2168	DSILLIQVOTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
į.	ł	1	RLRPASLVVLPRSLAPAPERFCQVNTGPLPLLGQSEPRKWMLPP
ì	1		QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
i	i		GCSFSLERALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
1	ļ		LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
1	ĺ		SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
ŀ	1	l	
ì	1]	CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
1	1		KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
}	l	ł	GFPTHPNHEPPEETDGPPGAVALVAFLQALEKEVATIVDQRAWN
ł	ľ	1	LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAPLCKNGDPQT
i	í	ļ	PRYDHLVATERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
}	Ì		1PG19STGVGDGGNELGMGKVKEAVRRHIRHGDV1ACDVEADFA
l	ł		VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
ł	į.	{	WTQALPSVIKBEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
1]	}	AEMIQKINDVTTAQV
5496	3	2408	ODTKMHETYKGNITPOLNKNTLKTSAATDVWAVYFSQFWIDY3G
	1		MKSGKGRPISPVDSPPLSIWICQPTRYAESQKBPQTCNQVSLNT
į.			SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
Į.	i		PSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHRSLILLSE
į.		. ,	NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDQANTLK
1		ł	SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
1	i		
1]	MSDKRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
Į.			LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
Ì	1	ł	DSNILSFDSDGNQNILSSTLTSKGNBTIBSIPKAEDLLPBAASL
l			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
ſ	S	(NKRSSSQMSLDTISLDSMILEEQLLBSDGSDSHMFLEKGNKKNS
1]	TINYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
ĺ		ļ ·	VVVFKITGVNGBIDIRGEDTBICLQVNQVTPDQLGNISLRHYLC
I	ł	i	NRPVGSDQKAVIHSKSSPEISLRFRSGPGAVIHSLLAEKNGFLQ
ì			CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
1	{	ļ	KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
1		}	GNDLKENVKSDSVLLTSGKYDLKKORSVTOATQTSPGVPWPSQS
			ANFPERSTOPTREQLMEENESLEQBLAKAKMALAEAHLEKDALL
}]	HHIKKMTVB
F402	 	——————————————————————————————————————	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
5497	1821	3308	
1	!	j	CFIYKYSGFPSLBCQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
1			GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
1	}]	YYTIGPGMFPSSQ1PSWKDWAKPGPYDQPLVNTLQRRKEKREPD
Į	l		PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMBACEELA
1	1	1	LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
i .	Í		DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
j i	1	}	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
}	1	}	TPVIPVKTPTVPDLPGVLPAPPDGPBERGEHSPESPSVGEGPQG
1	l		VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER
Į.	ţ.		EPPSATVSPGOIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
1	1	·	1
L	<u></u>		TINDRSAPRES
5498	2434	1492	ILTHQEIPTGEXPCECGKASIQMSHLSQQKIYSGENPFACKVCG
ł	ł		KVFSHKSNLTEHRHPHTREKPFECNECGKAFSQKQYVIKHQNTH
I	ł.		TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
1	1	!	OKSNLIRHORTHTGERPFVCKECGKTFSGKSNLTEHBKIHIGEK
1	l		PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSQRTS
1	1	1	LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
l	[l	NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH
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No.: nucleotide corresponding to first amino acid corresponding to first amino acid anino acid anino acid anino acid sequence seq	XD.			(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
corresponding to first amino acid amino acid residue of amino acid residue of amino acid residue of amino acid acid cequence codon, /=possible nucleotide deletion, %=possible nucleotide deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, deletion, dele		nucleotide		Glutamic Acid, F=Phenylalanine, G-Glycine,
to first amino acid residue of amino acid sequence sequence 5499 324 926 GROGIGRINITETUREDILE, V=Valline, A-Tryptoplan, X=Tyrosine, X=Unknown, A-possible nucleotide deletion, A-possible nucleotide insertion) QKIRTH SEQUENCE 5499 324 926 GROGIGRINITETYPESPERSGERGMADSQGWVRRYIKAFCKS FVAVFVAVTELDRVACVARVERASMQSGLNPGGSQSSUVIKI MKYNKVPSFWHSGUTSSVBYSNPGBKIKRVILABGIVETIGE NRYVKVPSGHIWSGDHEGISTONSSERPUSIGLHAHATHIL PERBROKLSSVLDPERLPVORSEE 5500 1978 1286 KPDWELDRIVPSERPLVORSESREGEHLKRALGMOPKLEHTWOGE VKHEVPIRINITETYLSVLLCFHGGHULLLISGRRKVWKG PLSFWROKESVLDPERLPVORGEE SERVELPVERPLINDITETYLSVLLCFHGGHULLLISGRRKVWKG PLSFWROKESVLLOFHGGWGGGGGGGGGRPARVEVUDAAARPSSRPPSI AAIMAALISELLDWRSLEWKSRMELITUGGGGGFFFNSWER SERVELPVERPLINDITETYLSVLLOFHGGHULLISGRRKVWKG PLSFWROKESVLLOFHGRAVGGGGGGGGGRPARVEVUDAAARPSSRPPSI AAIMAALISELLDWRSLEWKSRMELITUGGGGGFFFSWMER CRGWALVWHIDAADRKLBASREHMILDREDGGFFSWMER CRGWALVWHIDAADRKLBASREHMILDREDGGFFSWMER CRGWALVWHIDAADRKLBASREHMILDREDGGFFSWMER CRGWALVWHIDAADRKLBASREHMILDREDGGFFSWMER CRGWALVWHIDAADRKLBASREHMILDREDGGFFSWMER REALAKNSHTINTSVLRMNGFARARKSVENENDINKLDDLAGGFF REALAKNSHTINTSVLRMNGFARARKSVENENDINKLDDLAGGFF REALAKNSHTINTSVLRMNGFARARKSVENENDINKLDDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNGFARARKSVENENDINKLDLAGGFF REALANSHTINTSVLRMNG		location	corresponding	H=Histidine, I=Isoleucine, K-Lysine,
amino acid residue of amino acid sequence sequence amino acid sequence sequence 5499 324 926 GROGIGRIHITTYPESPERKSGRRGMADSQRWYRYIKAFCKG FVAVPVAVTLDRVACVARVERGASMQSSLRVGGSSSDVVLLN WKURPEVHRGUVSLVSPKRPEKKIRKRGMADSGLRVGGSSSDVVLLN WKURPEVHRGUVSLVSPKRPEKKIRKRGMADSGLRVGGSSSDVVLLN WKURPEVHRGUVSLVSPKRPEKKIRKRGMADSGLRVGGSSDSVVLLN WKURPEVHRGUVSLVSPKRPEKKIRKVLALEGOLVTITT PPERROKLESVLPPERLYMESSFEGFGHLKKRLALEGOLVTITT 1286 KDDWLLGRLDPELLVMESSFEGFGHLKKRLALEGOLVTITTUDG VKHEVPIRLINGSBRSWMDISARPFROPERLIGENKURKSFER PLSPKYSRGSTKREMALIVENSPENSKREWEVSLGLLEHARTHIL PPERROKLESVLPPERLYMESSFEGFGHLKKRLALEGOLVTITTUDG VKHEVPIRLINGSBRSWMDISARPFROPERLIGENKOM VKHEVPIRLINGSBRSWMDISARPFROPERLIGENKOM VKHEVPIRLINGSBRSWMSPENVIKKRSTLGSBRKS PRISPKYSRGSTKREMALIVENSPENVIKKRSTLGSBRKS PRISPKYSRGSTKREMSKALIVENSPENVIKKRSTLGSBRKS PRISPKYSRGSTKREMSKALIVENSPENVIKKRSTLGSBRKS VKHEVPIRLINGSBRSWMSPENVIKKRSTLGSBRKSPENS DIMLIEKCOI 5501 2927 2726 CREPPUSARVAFGEGGAWGGSGRRBARVEVUNDAARRSSRPPS AANMALISHLDPRSLIPPRKEMERLINLINGOOPPERSHMEN CREVALVIMIDAADREKARSTREHHILDRPOLOGIPPLVLV NKRDLPBALDBRGLIRRMEKARSTREHHILDRPOLOGIPPLVLV NKRDLPBALDBRGLIRRMEKARSTREHHILDRFOLOGIPPLSVIKE RGALENSHTNTEVURINMGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINMGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINMGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINMGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINMGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINGFAARAKSVHENNDINKTOLOGIPTLSTIER RGALENSHTNTEVURINGFAARAKSVLEBHDPKKRATAVKR SPANTILGERVEVS 5503 216. 654 KSVRKGREVENDSBUSHLGYFRMSFLIFKLTSKEVUQAIKST KKVINLERGEBDVCLQLDITISKTSSULSRAARISVLAKVR SPANTILGERVEVS SPANTILGERVEVS SPANTILGERVEVS SPANTILGERVEVS DEPSEMBLIKTERVENDSBURGSPVLESSDLARBATTAVTVR SPANTILGERVEVS DEPSEMBLIKTHANSSELLARGENDARVENSHLENGER GRENGEDCAL PAMYLLCISDLAGKETTOGIHSSSDLIKLARGEN SCHURKEVS CREWNSCHURDSSELLARGENGENDARVENSHLENGENDARMSRRS DEPSEMBLIKTHAN SSELVENGERVENDERVENDERVENDER PESKALENGERVENDERVENDERVENDERVENDERVENDERVENDER PESKALENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDERVENDER	ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
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DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAE EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAV SCIQDPSAEGLSBEVPVFBELPVVFBDVAVYFTRESMGMLDK QKELYRDVMRMNYBLLASLGPAAKPDLISKLERRAAPWIKDP GPKMGKGRPPGNKKMVAVRADTQASAADSALLPGSPVBARAS CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPMLVIDPKBTK FCSACIERPNLHDKSSRLVRGYTGPFKVBTLKYHBVSKAHRLO NTVBIKEDTPHTALVPBISSDLMANMBHFFNAAYSIAYHSRPL DFBKILOLLQSTGTVILGKYRBSTACTQPIKYISSTLKREILB VRNSPCV8VLLDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPFTIVSALDBLDIPFRKPGWVVGLGTDGSAMLSO GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNBLQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGKLKLMRGFH	ļ	ł		LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
EDPGGDGAIPAMYLDCISDLRQKEITDGIHSS9DINILYNDAV SCIQDPSAEGLSBEVPVVPBELPVVPBDVAVYFTREBWGMLDK QKELYRDVMRWNYBLLASLGPAAAKPDLISKLERRAAPMIKDP GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVBARAS CSSSICKEGGOPRRIKRTYRPRSIQRSWFGQPPMIVIDPKETK FCSACIERPNIHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLO NTVBIKEDTPHTALVPBISSDLMANMBHFFNAAYSIAYHSRPL DFEKILQLLQSTGTVILGKYRNETACTQPIKYISSTLKREILB VRMSPCV8VLLDGSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDBLDIPFRKPGWVVGLGTDGSAMLSO GGLVEKPQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNBLQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGFH	Ì	1	1	IEGYTGPFKVETLKYHAKSKAHMPCVNALAARDPIWAARFRSIR
SCIQDPSAEGLSEEVPVVFBELPVVPBDVAVYFTREBWGMLDK QKELYRDVMRMNYBLLASLGPAAAKPDLISKLERRAAPWIKDP GPXMGKGRPPGNKKMVAVREADTQASAADSALLPGSPVBARAS CSSSICEEGDGPRRIKTYRPRSIQRSWFGQPPWLVIDPKETK FCSACIERPMIHDKSSRLVRGYTGPFKVETLKYHBVSKAHRLO NTVBIKEDTPHTALVPRISSDLMANMBHFFNAAYSIAYHSRPL DPEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILB VRNSPCV8VLLDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVGLGTDGSAMLSO GGLVEKPQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCOR IRTVFKPYQSSNKRLMELQEGAAPLEQBIIRLKULMAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGFH	İ	ļ	Ì	DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
QKBLYRDVMRMNYBLLASLGPAAKPDLISKLERRAAPWIKDP GPKMSKGRPPGNKKMVAVRRADTQASAADSALLPGSPVBARRS CSSSLCEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKBTK FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHRVSKAHRLO NTVBIKEDTPHTALVPBISSDLMANMRHFFNAAYSIAYHSRPL DPEKILQLLQSTGTVILGKYRNRTACTQPIKYISBTLKRBILB VRNSPCV8VLLDGSTDASEQACVGIYIRYFKQMEVKESYITLA LYSBTADGYPETIVSALDELDIPFRRPEWVGLGTDGSAMLSO GGLVEKPQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKPYQSSNKRLNBLQGGAAPLEQBIIRLKDLMAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGFH		1	!	EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
GPXWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARAS CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQPPWLVIDPKETK FCSACIERPMIHDKSSRLVRGYTGPFKVETLKYHRVSKAHRLC NTVEIKEDTPHTALVPRISSDLMANMEHFMAAYSIAYHSRPL DPEKILQLLQSTGTVILGKYRNRTACTQPIKYISETKREILE VRMSPCV8VLLDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVGLGTTGSAMLSC GGLVEKFQEVIPQLLEVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNELQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGKLKLMRGFH		į.		SCIQDPSAEGLSEEVPVVFBELPVVFBDVAVYFTREEWGMLDKR
CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETK FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHRVSKAHRLO NTVEIKEDTPHTALVPRISSDLMANMEHFNAAYSIAYHSRPL DFEKILQLQSTGTVILGKYRNRTACTQPIKYISETLKREILBE VRNSPCV8VLLDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVGLGTDGSAMLSO GGLVEKFQEVIPQLLEVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNELQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGKLKLMRGFH	(1		QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
FCSACIERPNIHDKSSRLVRGYTGPFKVETLKYHRVSKAHRLO NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPL DFEKILOLLQSTGTVILGKYRBETACTQPIKYISETLKREILE VRMSPCV8VLLDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVGLGTDGSAMLSO GGLVEKPQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKPYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGKLKLMRGFH		1	1	
ntveikedtphtalvprissdlmanmehffnaaysiayherpi dpekilqllqstgtvilgkyrnrtactqpikyisetlkreile vrmspcvbvildsstdaseqacvgiyirtfkqmevkesyttla lysetadgypetivsaldeldipfrkpgwvvglgtdgsamlso gglvekpqevipqllpvhcvahrlhlavvdacgsidlvkkcdr irtvpkpyqssnkrlnelqegaapleqeiirlkdlmavrwvas rrtlhallvswpalarhlqrvabaggqighrakgylklmrgfh	i '	1 .	1	
DPEKILQLLQSTGTVILGKYRNRTACTQPIKYISETLKREILE VRNSPCV8VLLDSSTDASEQACVGIYIRYPKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVVGLGTDGSAMLSO GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKPYQSSNKRLNELQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGPH	1		1	
VRNSPCV8VILDSSTDASEQACVGIYIRYFKQMEVKESYITLA LYSETADGYPETIVSALDELDIPFRKPGWVVGLGTDGSAMLSO GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKPYQSSNKRLNELQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGPH		1	l .	
LYSETADGYPETIVSALDELDIPFRKPGWVVGLGTDGSAMLSC GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGPH		j	1	
GGLVEKFQEVIPQLLFVHCVAHRLHLAVVDACGSIDLVKKCDR IRTVFKFYQSSNKRLNELQEGAAPLEQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGFH	ĺ	[1	
IRTVFKFYQSSNKRLNBLQBGAAPLBQBIIRLKDLNAVRWVAS RRTLHALLVSWPALARHLQRVABAGGQIGHRAKGMLKLMRGPH	i	1	1	
RRTLHALLVSWPALARHLQRVAKAGGQIGHRAKGMLKLMRGFH	1	ļ	I	
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	!	ſ	1	
VKFCHFLLDFLSIYRPLSEVCOKEIVLITEVNATIGRAYVALE		1	1	VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
			1	LRHQAGPKBEBFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
, , , , , , , , , , , , , , , , , , ,	.			LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
1 1 1	l	1	1	LNLARYFBCSLPTGYSEEALLBEWLGLKTIAQHLPFSMLCKNAL
1 1	1		1	AOHCREPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
1 1 1	'	1	1	SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
CAQVPARSPASARLRKEENGALYVEEPRTQKPPILPSRKAAEV	ı	1	ì	CAQVPARSPASARLRKERMGALYVEEPRTQKPPILPSRKAAEVL
KOCINEPPERLLYPHTSQEAPGMS		[[1
5505 3312 1219 NCSPRSLSAAKNSNRNNNKLPSNLPQLQNLIKRDPPAYIRBFL		 	1210	NCSPRSLSAAKMSNRNNNKLPSNLPOLONLIKRDPPAYIEEFLO
QYNHYKSNVBIFKLQPNKPSKBLAELVMFMAQISHCYPBYLSN	5505	3312	1 1217	
1 1	5505	3312	1219	QYNHYKSNVBIFKLQPNKPSKBLAELVMFMAQISHCYPBYLSNF
FPBLFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNF	5505	3312	1219	QYNHYKSNVEIFKLQPNKPSKBLABLVMFMAQISHCYPEYLSNF PQEVKDLLSCNHTVLDPDLRMTPCKALILLRNKNLINPSSLLEL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S-Soring M. M
i	residue of		S=Serine, T=Threonine, V=Valine,
j	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
i	İ		YTMLRDSNATAAKMSLDVMIBLYRRNIWNDAKTVNVITTACFSK
i	i '	1	VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1			KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
1	1	[BKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
1	l	}	FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
			NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
	1	ł	MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVOEYGELDAK
			DYIPGARVLEVEKERNAENDRDGWESISLSEREDADGEWIDVOH
1	ĺ		SSDEBQQEISKKLNSMPMBERKAKAAAISTSRVLTQEDFQKIRM
i			AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
1	1		PKSDKETRLATAMAGKTDRKBFVRKKTKTNPFSSSTNKKKKKOK
ł			NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKRNK
5506	1	1531	
5500	i	1331	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPEREREREALCPGRS
J			CSGGGGETPGTTPVWSPLEGGGDRELRPNPYVRFPYRWWAVVV
1			LAAFPSLGAGGETPEAPPESWTQLWFFRFVVNAAGYASFMVPGY
1			LLVQYFRRKNYLETGRGLCPPLVKACVFGNEPKASDEVPLAPRT
1			BAAETTPMWQALKLLPCATGLQVSYLTWGVLQERVMTRSYGATA
ĺ	.		TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
i			SFASLSNVLSSNCQYRALKFVSFPTQVLAKASKVIPVMLMGKLV
I			SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
1			LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
j			LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
			GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
			LRVYARGRLKQRGKKAVPVK3PVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
	, ,		VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
			CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
1 1			KLSENTVIVGVVRRVDREELSVMPPISAGFTRRYVENPNIMACY
1			NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIZITSEDRFIQ
1			YANPAPETIMGYQSGELIGKELGKVPINEKKADLLDTINSCIRI
}			GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
}			NGNNKAEKISECVQSDTHTDNQTGKHKORRKGSLDVKAVASRAT
1 1			EVSSQRRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTBA
1			LORVLEILRITELYSPOFGAKDDDPHANDLVGGLMSDGLRRLSG
]			NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
l i			FELEAATHNRPLIYLGLEMFARFGICEFLHCSESTLRSWLQIIB
			ANYHSSNPYHNSTHSADVLHATAYFLSKBRIKETLDPIDBVAAL
]			IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAP
1 - 1	j	•	QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
	j		KPVNSINKPLATLBENGBTDKNQBVINTMLRTPENRTLIKRMLI
{	-		KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
]	j		FDRNTCSIPRSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
	1		KAMKGPDEWKTSWIS555E EDWGICSISSON EDWGICSON EDWGICSO
5508	1151	663	l
~~~	1151	691	LSSVPSRRSASMFAVGCSMGPFLHYWYLSLDRLPPASGLRGFPN
1 1	l		VLKKVLVDQLVASPLLGVWYPLGLGCLEGQTVGRSCQELREKPW
] ]	j		EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
FEAR			KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
ļ l			VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
1 1			RRDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
j (	ļ		LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
1			RDFVTWVDSSKIKRHVLEYNEERDDFDLEA
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
ļ 1	į	Ì	AEGEROPPPDSSEEAPPATONFIIPKKEIHTVPDMGKWKRSQAY
į l	1	ŀ	ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
1 !	ì	į	ETPPVDQPSRFGNKAYRTWYAKLDEBAENLVATVVPTHLAAAVP
. 1			EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
	ļ.	J	
			TAIVFKVFNRYLBVMRKLQKTYRMBPAGSQGVWGLDDFQFLPFI
		į	WGSSQLIDHPYLBPRHFVDEKAVNENHKDYMFLECILFITEMKT
1			GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
L			KFGSLLPIHPVTSG

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	,
ID	beginning	nucleotide	(A=Alanine, C≈Cysteine, D=Aspartic Acid, R=
77O:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ŀ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	<u> </u>	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNI.PPENLITSISAVPISQKBEVADPQLSVDSLLBKDND
1	İ	ĺ	HSRPDIQVQAKRLAEKLRCDTVVSBISTGQRTVNFKINRELLTK
<b>,</b>		<b>!</b>	TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKFHVG
ŀ			HLRSTIIGNFIANLKEALCHQVIRINYLGDWGMQFGLLGTGFQL
l	i	l	FGYBEKLQSNPLQHLFEVYVQVNKBAADDKSVAKAAQBFFQRLE
)		1	LGDVQALSLWQKFRDLSIBEYIRVYKRLGVYFDEYSGESFYREK
1			SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
}		1	SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI
ł	i	Ì	MGYDWAERCQHVPFGVVQGMKTRRGDVTPLEDVLNEIQLRMLQN
ł .		Į.	MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
i	ļ		VFQSRGDTGVPLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
İ			VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
j		1	QIKDSPPBVAGARLHLYKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRRBPITLQDPEAKYPLPL
ļ			IEKEKISHNTRRFREGLPSPDHVLGLPVGNYVQLLAKIDNELVV
	}		RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
:	]		igetiffrgprgrlfyngpgnlgirpdgtsepkktladhlgmia
ł	ł		GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
· .	1	· ·	BIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
1	1		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWKLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
į.	ļ	į	PPTSRGGPGSRDTMSDSEERSQDRQLKIVVLGDGASGKTSLTTC
ł	}	ł	FAQETPGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
1			GKMLDKYIYGAQGVLLVYDITNYQSFENLRDWYTVVKKVSKESB
Ì	Ì	1	TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
J	}		DSVFLCFQKVAABILGIKLNKABIEQSQKVVKADIVNYNQEPMS
1	<b>\</b> '	1	RTVNPPRSSMCAVQ
5514	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
		l l	CYLGSKTLFYRLBILEGITIVGMALTGMAGEQFIPGCPHLMLYD
l .		ł	YKQGHWNQLLGNHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
	1		MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
[	ì	1	EPLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPANDLM
1	l ,	} ·	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS
}	Ţ	}	EVGLLKNAEREOESEREM
5515	1572	260	PVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAP
[	ļ		TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEBLYSYL
	i		KRFIHILYFRHLLVNPRDRRVVIIBSVLCPSHFRETLTRVLFKY
l	1	j .	PRVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
1	1	1	VLNCWGALPLGGKALHKBLETQLLEQCTVDTSVAKEQSLPSVMG
1	1	ł	SVPBGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
{	l .	-	NVDYPLDGEKILHILGSIRDSVVBILFEQDNERQSVATLILDSL
1		1	IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
}			KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
ì	1		YYNQTGRIPDWCSLNNPPLEMMPDVGKTQPPLMKRAFSTEK
5516	3	735	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
1	1	1	IKAMWRVPGTTRRPVTGRSPGMHRPRAMLLLLTLALLGGPTWAG
			KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
Į.			DVKLGALGGNTQEVTLQPGEYITKVFVAFQAPLRGMVMYTSKDR
l	1	ł	YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFRWNY
1	j		PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SELYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
"""	1		TOGTSDLPLKLEALSVKEDAKEKDEKTTODQLEKPONEEK
5518	3	1375	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMRA
] """	1	1 -3/3	FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
	i	1	EPKYVANMHGDETVGRBLLLHLIDYLVTSDGKDPBITNLINSTR
1	1		IHIMPSMNPDGPRAVKKPDCYYSIGRRNYNQYDLNRNFPDAFRY
i	1		NNVSRQPBTVAVMKWLKTBTPVLSANLHGGALVASYPFDNGVQA
ł	1	•	TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
1	1	j	
ĺ	1	1	GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP SFWNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK
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amino acid	1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	J	amino acid	sequence	
HICPYRTHYGEYTIALINGSY TINVTPORHOPHITYKYTTPERS   OMPSALKIOLLIPPER	1	sequence	•	
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S520   117   943   PPERCROVIATETVERSLAMMITTSTETTHEUMSNIPPINNYS SORKINEWRETILAMIAGARMITMALIALICATEVATOLOUTAK RYKOGKOI KPILTAPROLLETTIAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPROLLETTIAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPROLLETTIAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOGKOI KPILTAPPOLETYVENTOLOUTAK RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOKA RYKOK		i	ļ	GVVAVGTVLVALSAMGFTSVGIAASSIAAKMMSTAA1ANGGGVA
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MTLSRARSPSTGTSAGGSSSSQQNSPQMKNSPSPPFHGSRPAGL PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK  5525 105 834 SINTLDFERILFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFLGRVABLNDVTAKVASQQEKHLLFBVQFGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEBPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP TEDDMANYILNMADEAGQPHRP QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTLIKDYQNVPGIBKVDDVVKRLLSLEMANKKEMLKI KQCQFMKKLVANPRDTRSLBARIIALSVKIRSYEBHLEKHRKDK AHKRYLLMSIDQRKWLKNLRNTNYDVFEKICWGLGIEYTFPPL			,	
PGLGSSTQKVTHRVLGPVRGKPVWBPLQHVFGCLGHCMGK  5525  105  834  SNTLDFERHLPIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTTEBFLGRVARLMDVTAKVASGQEKHLLFBVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEBPDBNSSVTSCQASLWMGRVKQLTDEEBCCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP  5526  3  853  RRPCNPVRAAKRTGAARAPERGLKVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGSSAKPPFNQWGLQPRSLLLQAARGYVYKPAQSG LDDDPPPSTLLKDYQNVPGIRKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYBEHLEKHRKDK AHKRYLLMSIDQRKVMLKNLRNTNYDVFEKICWGLGIEYTFPPL	1 1	1		1
5525 105 834 SINTLDFERHLFIMGQQISDQTQLVINKLPEKVAKHVTLVRESGS LTYEEFIGRVABLINDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSEBPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSPCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILINMADEAGQPHRP  5526 3 853 RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGSGSAKPPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTILKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL	į l			
LTYEBFLGRVABLNDVTAKVASGQEKHLLFEVQPGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSBEPDENSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSPCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILNMADEAGQPHRP TEDDMANYILNMADEAGQPHRP S526 3 853 RRPCNPVRAAKRTGAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGSSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTILKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKLVANPEDTRSLEARIIALSVKIRSYBEHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL	l <i>l</i>			PGLGSSTQKVTHRVLGPVRGKPVWEPLQHVFGCLGHCWGK
LTYEBFLGRVAELMOVTAKVASGQEKHLLFEVQFGSDSSAFWKV VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSBBPDENSSSVTSCQASLMMGRVKQLTDEEECCICMDGRAD LILPCAHSFCQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILINMADEAGQPHRP  5526 3 853 RRPCNPVRAAKRTGAAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGSGSAKPPFNQMGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTILKDVQNVPGIBKVDDVVKRLLSLEMANKKBMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL	5525	105	834	SNILDFERHLFIMGQQISDQTQLVINKLPEKVAKHVILVRRSGS
VVRVVCTKINKSSGIVEASRIMNLYQFIQLYKDITSQAAGVLAQ SSTSBEPDBNSSSVTSCQASLWMGRVKQLTDEEECCICMDGRAD LILPCAHSPOQKCIDKWSDRHRNCPICRLQMTGANESWVVSDAP TEDDMANYILINMADEAGQPHRP TEDDMANYILINMADEAGQPHRP S526 3 853 RRPCNPVRAAKRTGAARAPRGLEVTMLRVAWRTLSLIRTRAVT QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAQSR LDDDPPPSTILKDYQNVPGIEKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKLVANPEDTRSLEARIIALSVKIRSYBEHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL	( l	ŀ		
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QVI.VPGLPGGGSAKFPFNQMGLQPRSLLI.QAARGYVVRKPAQSR LDDDPPPSTILKDYQNVPGIEKVDDVVKRLISLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEEHLEKHRKDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIEYTFPPL	اا			
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LDDDPPPSTLLKDYQNVPGIBKVDDVVKRLLSLEMANKKEMLKI KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRXDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIBYTFPPL	į l	ĵ		QVLVPGLPGGGSAKFPFNQWGLQPRSLLLQAARGYVVRKPAOSR
KQEQFMKKIVANPEDTRSLEARIIALSVKIRSYEBHLEKHRXDK AHKRYLLMSIDQRKKMLKNLRNTNYDVFEKICWGLGIBYTFPPL	1 1	}		
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
_	1		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO.	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	1		
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
lj.	sequence		\=possible nucleotide insertion)
· · · · · · ·			RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
352/	3223	363	
j	i .	5	KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
<b>J</b>	1	ĺ	PAKNPSSLPSKEAPKRKAQAVSEEEBBBBGKSSSPKKKIKLKKS
ì	1	ł	KNVATEGTSTQKEPEVKDPELEAQGDDMVCDDPEAGEMTSENLV
i	1	ľ	QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
i	f	f .	AWKDLFVPRPVLRALSPLGFSAPTPIQALTLAPAIRDKLDILGA
	<u>}</u>	Ì	AETGSGKTLAFAIPMIHAVLOWOKRNAAPPPSNTEAPPGETRTE
1	1	ł	AGAETRSPGKAEARSDALPDDTVIBSEALPSDIAABARAKTGGT
1	}		VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN
<b>\</b>	1	ł	LKQBLDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
ļ	1		FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
1	l	1	YHLRNLRQLRCLVVDRADRMVBKGHFABLSQLLEMLNDSQYNPK
1	l	[	ROTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
1	i	i	RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFIMOYPG
	Í	[ '	_
ļ	1	[	RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEQ
1			FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
	Į.		RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVQTK
1 '	1		YMDVVKERIRLARQIBESEYRNFQACLHNSWIEQAAAALEIELE
i	ĺ	i	EDMYKGGKADQQEERRROKOMKVLKKELRHLLSOPLFTBSOKTK
	ļ	j	YPTQSGKPPLLVSAPSKSBSALSCLSKQKKKKTKKPKEPQPEQP
1	ļ		OPSTSAN
5528	3	895	GPFLSACRMNGACKVKVHDSLATISITLRRYLRLGATMAKSKFB
5526	,	695	i .
i i	i i		YVRDPEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
1	l .		QLMCKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
l	l '		FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNCT
1			LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
			AADKNEILFSEFNINYNNEPPMYRKGTVLIWOKVDEVMTKBIKL
			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TPRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
وعدد	10	040	· -
			LSWILSRVLWLSGLSBPGAARQPRIMEEKALEVYOLIRTIRDPE
	· ·		KPNTLEELEVVSESCVEVQEINERRYLVIIRFTPTVPHCSLATL
			IGLCLRVKLQRCLPFKHKLBIYISEGTHSTBEDINKQINDKERV
1		•	AAAMENPNLRBIVEQCVLBPD
5530	4541	2606 .	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
1 1			POPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDINSLGVILFML
j i			VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLOR
( !	ļ		DPKRRASLEEIENHPWLOGVDPSPATKYNIPLVSYKNLSEEENN
[ ]			
, !			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
1		i i	QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
]			ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
j i			PASLKPTASGRKCLFRVEEDEKEDEEDKKPMSLSTQVVLRRKPS
1 1			VINRLISRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
;         !			ASPCTVHKRYHRRKSQCRGSSCSSSETSDDDSESRRRLDKDSGF
1 1	,		TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
ļ J			GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
( )	1		·
1 1			LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQBKSTWKMCISST
			GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNIKNNVLQLPLC
			EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	51.5	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLRHGTVLFARLF
[ [		,	ALEPOLLPLFOYNCROFSSPEDCT.SSPEFLDHIRKVMLVIDAAV
į l		· i	TNVEDLSSLEEVLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
			· · · · · · · · · · · · · · · · · · ·
			LGPAFTPATRAAWSQLYGAVVQAMSRGWDGB
5532	3395	1402	SDWMVVGKRKMIIEDETEPCGEELLHSVLQCKSVFDVLDGEEMR
, ,			RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
ļ <b>j</b>	]	j	KPLVKDRBABLLYFADVCAGPGGFSBYVLWRKKWHAKGFGMTLK
		j	GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN
}	·	}	•
		i	FVLENTDRKGVHFLMADGGFSVEGQBNLQBILSKQLLLCQFLMA
[	ſ	ſ	LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLPAVNIKLNQLRNTDSDVNL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence	ļ	\=possible nucleotide insertion)
	1	ĺ	VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAPVQDTTL
1	Į.	}	SEPROAETRKECLRLWGIPDQARVAPSSSDPKSKPPELIQGTEI
ı			DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAORKI
1		ł	SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
1	}		PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
ì	i	ļ	VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
1	1 ·	ł	IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
1		· ·	MHRA
5533	94	789	MKBRRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
1			TVFENYTACLETEEQRVELSLWDTSGSPYYDNVRPLCYSDSDAV
J	]		LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
}	1		LSTIMBLSHQKQAPISYEQGCALAKQLGPEIYLEGSAFTSEKSI
1	!	· ·	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSBLISPT
			FKKEKAKXCSIM
5534	3	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
			TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
1			CAFILFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
ľ	ĺ		RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTODETOKSDSENEDLKIDCLOESOEL
1	į		NLOXLKNSERILTBAKOKMRELTVNIKMKEDLIKELIKTGNDAK
i i			SVSKQYTLKVTKLEHDARQAKVBLTETQKQLQBLENKDLSDVAM
1			KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
1			ELEQSVDHMKYQKIQLQRKLQEENBKRKQLDAVIKRDQQKIKVI
			LSYXPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
į į			SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
1			DAVYTELQPTSPTPTWFADETPQPQTQTQQLEGTDGPLVTDPET HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
1			FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPOLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
(			PGHPGSWEMGLLTPRDVAVEFSLEEWEHLEPAOKNLYODVMLEN
J			YRNLVSLGLVVSKPDLITPLEQRKRPWNVKSRETVAIQPDVFSH
1			YNKOLLTEHCTBASFOKVISRRHGSCDLENLHLRKRWKREECEG
1			HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
}		•	PTHSSLLNQQEBIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1			EXNYHCNNSEKTLINGSSSPKNHQENYFLEKQYKCKEFZEVFLQS
	i		MHGQBKQEQSYKCNKCVEVCTQSLXHIQHQTIHIRENSYSYNKY
1	j		DXDLSQSSNLRKQIIHNBBKPYKCEKCGDSLNHSLHLTQHQIIP TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1	İ		EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
1	ı		SNLIMHQRVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
	<b> </b>		KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1 1	ľ		RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
			CGKAFSYSSDVIQHRRIHTGQRPYKCKECGKAFNYRSYLTTHQR
1			SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
1	,		FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
FE20			EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLGLIDISQAQLSCTGPPAIPGIPG
]			IPGTPGPDGQPGTPGIRGERGLPGLAGDHGEFGERGDPGIPGNP
			GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
		i	NVPLRRDQTIRFDHVITNMNNYEPRSGKFTCKVPGLYYFTYHA
] ]			SSRCNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMKA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
"		~~~0	IVDGPAALASFPETVPAVPGPYGPHRPPOPLPPGLDSDGLKREK
1 1			DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGOVCS
		,	SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Talousing M. Mahhianina N. Nabysine,
1	to first	amino acid	LaLeucine, Machionine, Nasparagine,
1	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1	1	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	WaTryptophan, YaTyrosine, XaUnknown, *aStop
1	amino acid	sequence .	Codon, /=possible nucleotide deletion,
L	sequence	<u>l</u> .	\=possible nucleotide insertion)
	1	1	BLEKVHOLCONFCHRYITCLKGKMPIDLVIBDRDGGCREDFEDY
1			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
1		ł	SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
į.	•		RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
1	1	İ	QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
1			LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWROHRG
3340	***	1440	
1	<b>l</b> .		PSGAAAPGCALPRGQALBGPRSCRRPQPMARRYDBLPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRBKDEI
			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEUNTAFAKOVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
i i			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQCVGLDTSVASPSSGGED
1 1	ļ		EDILDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSERQKKQ
1			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
1			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWROHRG
ř i			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1 1		•	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHILELE
1 1			
1			KGKMPIDLVIEDROGGCREDFEDYPASCPSLPDONNIWIRDHED
i i			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1 1			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1 1			LAQDTGLTILQVNNWFINAKRRIVQPMIDQSNRTGQGAAFSPEG
			QPIGGYTET3PHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
] ]			PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1			YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
1 1			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
, ,			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
i i	i i	'	SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGRD
1			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEBQKKQ
[ [			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
) ;			QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
j l	, <del></del>		KRPFSDSGAFNSPERRPGVLEAPRRRPVPASFRAVPPRPTRVHG
, ,			SSASRDRVLARTMIVADSECRABLKDYLRFAPGGVGDSGPGEEQ
į j	j	i	
1			RESPARREDESAFIPVEEVLREGAESLEQHIGLEALMSSERV
j }	}		DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
ļ			ARHQCSYLVGSHMAEFLQTGGDPEWLLGLHRAPEKLRKLSBINK
, ,	1		LLAHRPWLITKEHIQALLKTGEHTWSLABLIQALVLLTHCHSLS
	· }		SPVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
į į			ESARDVEALMERMOQLQESLLRDEGTSQEEMESRFELEKSESLL
į ļ			VTPSADILEPSPHPDMLCFVBDPTFGYBDFTRRGAQAPPTFRAQ
ļ ļ	j		DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
1 l	ì		DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
, ,			ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL
[			RAITRYMT
5544	1895	514	LGGLLGRORLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
[ [	ļ		PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
<b>)</b>	1		QRVESLRKKRPLFPWFGLDIGGTLVKLVYFKPKDITAEEREEEV
}	1	ļ	
1 1	1	ļ	ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRRGNLHFIR
[ ]	1		FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
ļ	1	ŀ	LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSBKCQK
	1		LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
ļ J	j		FGLCCLLTGCTTFERALEMASRGDSTKVDKLVRD1YGGDYRRFG
	į		LPGNAVASSFGNMMSKERREAVSKEDLARATLITITNNIGSIAR
} }	Į.	1	MCALNENINGVVFVGNFLRINTIAMRLLAYALDYWSRGOLKALF
	ŀ	Ì	MCALNBNINGVVFVGNFLRINTIAMRLLAYALDYWSRGQLKALF SEHEGYFGAVGALLELLKIP

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine.
}	corresponding	to first	LaLeucine, MaMethionine, NaAsparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	acquence	\=possible nucleotide insertion)
CEAR	802		
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGABLVTCGSVL
ł .	ł		KLLNTHIRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
			GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHPPSPLSNNQEV
}			SAFGEDGEGDDLDLWTVRCSGCHWERBAAVRFQHVGTSVFLSVI
ì		ļ	GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
L	<u> </u>		DRL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
(			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
j			LGVTHFLILSKTETNVYPKLMRLPGGPTLTFQVKKYSLVRDVVS
1			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
1			NVHKVNLNTIKRCLLIDYNPDSQBLDFRHYSIKVVPVGASRGMK
(			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1	}		AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1			FVSKTEERLQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
			RKKSLEGMKKARVGGSDEEASGIPSRTASLBLGEDDDEQEDDDI
			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
			CDQKFPKTKDRSQGAQARRGPRGASRDGGRGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
ł i			RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
			LGVTHFLILSKTETNVYPKLMRLPGGPTLTFQVKKYSLVRDVVS
<b>(</b>			SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
			NVHKVNLNTIKRCLLIDYNPDSQBLDFRHYSIKVVPVGASRGMK
1			KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
1			AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
[			FVSKTEBBLQATLBAKEKKLRLKAQRQAQQAQNVQRKQBQRBAH
ł I			RKKSLEGMKKARVGGSDEBASGIPSRTASLRLGEDDDBQEDDDI
			EYFCQAVGEAPSEDLFPRAKQKRLAKSPGRKRKRWEMDRGRGRI.
1			CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRGRGKRVA
5548	1	2153	DOTGPPETTAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
i I			DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLVLLLAAYFFRF
}			RKQRKAVVSTSDKKMPNGILBEQEQQRVMLLSRSPSGPKKYFPI
			PVEHLEEBIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
i i		,	REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
			FIAAQGPKQETVNDFWRMVWEQKSATIVMLTNLKERKEBKCHQY
j l			WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
1			LVSQLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
}			SAGVGRTGTFIVIDAMMAMMHABQKVDVFBFV9RIRNQRPQMVQ
1			TDMQYTFIYQALLEYYLYGDTBLDVSSLEKHLQTMHGTTTHFDK
			iglbebfrkltnvrimkenmrtgnlpanmkkarviqiipydfnr
Į l			VILSMKRGQBYTDYINASFIDGYRQKDYFIATQGPLAHTVKDFW
			RMIWEWKSHTIVMLTEVQBREQDKCYQYWPTEGSVTHGEITIEI
			KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
			IPARGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTPIAL
			SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYBFCYKVVQ
	,		DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLO
1			CLARGSAGIKGLGRVFRINDDDNNRTLDFKBFMKGLNDYAVVME
			KEEVERLFORFDKOGNGTIDFNEFLLTLRPPMSRARKEVIMOAF
1	'		RKLDKTGDGVITIEDLREVYNAKHHPKYONGEWSEBOVFRKPLD
1	•		NFDSPYDKDGLVTPERFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAPPKVPESYVETSASGTV
2230	2002	7410	SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
			, · · · · · · · · · · · · · · · · · · ·
			TVAMKCQYVGADVLDIAETMVASAIGLVYEPTVFDI.SPQQKENQ
1			RMIQLIQSRLQBEHSLQDVIPKSAFKSTSTALPPREDDSSQSPN
1			ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
[	,		PSHRIDHLSPGBLV9AIINPLDGTBKIAIDHNQMFQYFITVVPT
	:		KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
			MVTVTBEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
			CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	MORDHTMDYKESCPSVSIPSSDEHREKKKRFTVYKVLVSVGRSE

SEQ Predicted beginning mucleotide location nucleotide location corresponding to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	tic Acid, Z= G=Glycine, sine, ragine, ine, nown, *=Stop letion, ) RIFGDNFDPDFIK DSPKHQSDPSBDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence    Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequence   Sequenc	G=Glycine, sine, ragine, ine, , nown, *=Stop letion, ) RIFGDNFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
location corresponding to first amino acid residue of amino acid sequence code, /=possible nucleotide insertion)    Application corresponding to first amino acid residue of amino acid sequence   P=Proline, Q=Glutamine, R=Argini	sine, ragine, ine, , nown, *=Stop letion, ) RIFGONFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
corresponding to first amino acid p=Proline, Q=Clutamine, R=Argini amino acid residue of amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Se	ragine, ine, hown, *=Stop letion, RIFGONFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLLKNYKH LQRERSFPEHRAR
to first amino acid p=Proline, Q=Glutamine, R=Argini amino acid residue of amino acid sequence (Codon, /=possible nucleotide del sequence (P=Proline, Q=Glutamine, R=Argini (P=Proline, V=Tryrosine, V=Valine, V=Serine, T=Threonine, V=Valine, V=Serine, T=Threonine, V=Valine, V=Serine, T=Threonine, V=Valine, V=Valine, V=Valine, V=Tryrosine, X=Unkr (Codon, /=possible nucleotide del (N=Possible nucleotide del (N=Possible nucleotide insertion) (P=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, Q=Glutamine, R=Argini (N=Proline, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V=Valine, V	ine, nown, *=Stop letion, RIFGONFDFDFIK DSPKHQSDFSEDE FLKVIGKGSFGKV MAERNVL1KNVKH LQRERSFPEHRAR
amino acid residue of smino acid w-Tryptophan, Y-Tyrosine, X=Unkr Codon, /-possible nucleotide del sequence wFVFRFYAEFDKLYNTLKKOFPAMALKIPAKE QRRAGLNEFIQNLVRYPELYNHPDVRAFLQM DERSSQKLHSTSQNINLGPSGNPHAKPTDFDF LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHD PFLVGLHYSFQTTEKLYFVLDFVNGGKLPFHI	nown, *=Stop letion, RIFGDNFDPDFIK DSPKHQSDPSBDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
residue of amino acid sequence Codon, /=possible nucleotide del sequence wrvfrryagfokurutkkofpamalkipakk Qrraginerutkkofpamalkipakk Qrraginerutkkofpamalkipakk Qrraginerutkkofpamalkipakk Qrraginerutkkofpamalkipakk Qrraginerutkkofpamalkipakk Qrraginerutkryofpamalkipakkipakkipakkipakkipakkipakkipakkip	nown, *=Stop letion, ) RIFGDNFDPDFIK DSPKHQSDPSBDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
amino acid sequence Codon, /=possible nucleotide del  sequence   possible nucleotide insertion)	letion, ) RIFGDNFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLIKNVKH LQRERSFPEHRAR
sequence \=possible nucleotide insertion) WFVFRYABFDKLYNTLKKOFPAMALKIPAKK QRRAGLNBFIQNLVRYPBLYNHPDVRAFLQMI DERSSQKLYSTSQNINLGPSGNPHAKPTDFDF LLAKRKLDGKFYAVKVLQKKIVLNRKRQKHIN PFLVGLHYSFQTTEKLYFVLDFVNGGELPPHI	) RIFGDNFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVILKNVKH LQRERSFPEHBAR
WFVFRRYABEDKLYNTLKKOFPAMALKIPAKE QRRAGLNBPIQNLVRYPELYNHPDVRAFLOMI DERSSOKLYSTSONINLGPSGNPHAKPTDFDE LLAKRKLDGKFYAVKVLOKKIVLNRKEOKHIN PFLVGLHYSFOTTEKLYFVLDFVNGGBLPFHI	RIFGDNFDPDFIK DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
QRRAGLNBFIQNLVRYPELINHPDVRAFLQMI DERSSQKLYSTSQNINLGPSGNPHAKPTDFDE LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIN PFLVGLHYSFQTTEKLYFVLDFVNGGBLPFHI	DSPKHQSDPSEDE FLKVIGKGSFGKV MAERNVLLKNVKH LQRERSFPEHRAR
DERSSOKLYSTSON INLGESGNPHAKPTDFDE LLAKRKLDGKFYAVKVLOKKI VLNRKEOKHIN PFLVGLHYSFOTTEKLYFVLDFVNGGELPFHI	flkvigkgsfgkv Maernvllknykh Lûrbrsfpehbar
DERSSOKLYSTSON INLGESGNPHAKPTDFDE LLAKRKLDGKFYAVKVLOKKI VLNRKEOKHIN PFLVGLHYSFOTTEKLYFVLDFVNGGELPFHI	flkvigkgsfgkv Maernvllknykh Lûrbrsfpehbar
LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIN PFLVGLHYSFQTTEKLYFVLDFVNGGELPFHI	Maernvllknykh LQRersfpehrar
PFLVGLHYSFQTTEKLYFVLDFVNGGRLPFHI	LQRBRSFPBHRAR
,	
	2AGUAADIDEGGC
1	THE REAL PROPERTY AND THE REAL PROPERTY.
KEGIAISDTTTTPCGTPEYLAPEVIRKQPYD	
EMLYGLP PFYCRDVAEMYDNILHKPLSLRPGV	
EKDRQNRLGAKEDFLE IQNHPPFESLSWADIN	
AGPDDIRNFDTAFTEETVPYSVCVSSDYSIV	NASVLBADDAFVG
FSYAPPSEDLFL	
5552 2748 930 LGPAAGAAMGKKHKKHKAEWRSSYEDYADKP	LEKPLKLVLKVGG
SEVTELSGSGHDSSYYDDRSDHERERIKEKK	KKKKKKSBKEKHL
DDEKRRKRKEEKKRKRERBHCDTBGEADDFDI	
PVRACRTQPARNESTPIQOLLEHFLRQLQRR	
1APGYSMIIKHPMDFGTMKDKIVANEYKSVT	
MTYNRPDTVYYKI_AKKIILHAGPKMMSKQAALI	
EVVPVOVETAKKSKKPSREVISCMFEPEGNA	
ALVEHAADEARDRINRFLPGGKMGYLKRNGD	
DADEBETHPVDLSSLSSKILPGFTTLGFKDE	
ALSMONNSVFGDLKSDEMKLLYSAYGDETGV	
GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRI	
DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSI	
HLNLDETTKLLQDLHEAQAKRGGSRPSSNLSS	
GSPSRLSVGEQPDVTHDPYKFLQSPEPAASAI	
5553 74 1095 LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLI	LBSWALSQVAGMP
VYLKCENVQPSGSFKIRGIGHFCQEMAKKGCI	RHLVCSSGGNAGI
AAAYAARKLGIPATIVLPESTSLQVVQRLQGI	egaevqltgkvwd
EANLRAQELAKRDGWENVPPFDHPLIWKGHAS	SLVQELKAVLRTP
PGALVLAVGGGGLLAGVVAGLLEVGNOHVPI:	IAMETHGAHCFNA
AITAGKLVTLPDITSVAKSLGAKTVAARALEG	CMOVCKIHSEVVE
DTEAVSAVQQLLDDERMI.VEPACGAALAAIY	
PPSLTSVVVIVCGCNNINSRBLQALKTHLGQV	
5554 166 2318 CSGRTGGRGSLRPARNYCLTCKLSGAETRGLI	
GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKL	
WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVRI	
[ ]	
VETPELFORKLINESENSVFQAVYGLQRALQGI	
QRLEALREANIKEETEYMELLAAKKHQVEALI	
DEILEDVRKAADRLEERIEEHAFDUNKSVKG	
ANSKONITKREVEDDLGLSMLIDSONNQYIL	
HFIRDIVTIGHLSLPCGWLCTAIGLPTMFGYI	
SIKSIVQVETLGBFGVFFTLFLVGLBPSPERI	
YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLS	
GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFR	MAVMPTLIQAGAS
ASSSIVVEVLRILVLIGQILFSLAAVFLLCL/	VIKKYLIGPYYRK
LIMESKCNKRILILGISAPIFLMLTVTELLDV	
VSSCGPVVTREIATSIRPIRDFLAIVFFASIC	
TVLVFLTLSVVVMKYLLAALVLSLILPRSSQI	
SEPSPVLGSRARRAGVISREVYLLILSVITLS	
TRCVPRPERRSSL	
	CAND CHARGOTTO
l	
GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKII	
KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAY	
DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFC	
GSDIIVDLEVILEEVYAGNFVEVVRNKPVARG	DAPGKRKCNCRQE
MRTTQLGPGRFQMTQEVGCDECPNVKLVNEE	rtleveie <b>p</b> gvrd
GMRYPFIGEGEPHVDGEPGDLRFRIKVVKHP	
TISLVESLVGFEMDITHLDGHKVHISRDKIT	
PNFDNNNIKGSLIITFDVDFPKEQLTEEAREC	
VYNGLOGY	
	TTKINNAUTUKCO
5556 5835 3346 RTRGMSKNCVPMBFRBYLLRMFQGTFYLLQKI	A ALLIANTERIA VILLANDE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į.	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<b></b>		<del> </del>	LEELDESYIEKFTDFLRLFVSVHLRRIESYSOFPVVKFLTLLFK
1			YTFHQPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
ſ	l		DALVLLLTEVLNRIQFRYNQAQLEELDDETLDDDQQTEWQRYLR
Į.		<b>,</b>	QSLBVVAKVMBLLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
1	i		GHRLNITAENDCRRLHCSLRDLSSLLOAVGRLAEYFIGDVFAAR
ĺ		[	FNDALTVVBRLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
1	1	ł	SLAALQAYSHWLAQYCSEVHRONTOOFVTLISTTMDAITPLIST
l .		ļ	KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
1		{	LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVHSINHASLI
ì	ł	ł	SALSRDYRNLKPSAVAPORKMPLDDTKLIIHOTLSVLEDIVENI
1		1	SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
1			TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
Į.	1	}	VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
]	1	j	PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIABEQMENEP
1		Į	QPSAIMQAPGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
ł	ł	<u> </u>	TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
1	].		APLPEFLTSCDGVDANOKSVLGRNFKMDRVRRERGRAKRRAEWA
1			RKPGTCAARRCHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRIRLSALAGAGRFCILGSEAATR
İ	j		KHLPARNHCGLSDSSPQLWPBPDFRNPPRKASKASLDFKRYVTD
1	ł	i	RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLRAGAKVV
1	l		ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
1	1		AMSSRGLFKNLGIRAVPNTADIPLKVVGMPPSRGEKRALWKLAY
l			DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
			wqlacbikvlhmepwssfdiytrkgplenpkrrblldqlqqkly
ł	ļ	İ	LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
1			LTPLDARDILMQIGKQEDBKVVNMHPQDFKTLFETIERSKDCAY
í	İ		KWLYDETLEDR
5558	1509	96	RAGCTHPQVPADLGAPAEPRRPQKTCVCLLQPQPGGQRGPTTMI
}			TGVFSMRLWTPVGVLTSLAYCLHQRRVALABLQEADGQCPVDRS
[			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
			YTVTNLAGGPKPYSPYDSQYHETTLKGCMFAGQLTKVGMQQMFA
ł			LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
1	,	•	GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1	}		SLQPGISBDLKKVKDRMGIDSSDKVDFFILLDNVAABQAHNLPS
ì			CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
ĺ			NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
}	1		FAVDLTMBLYOHLESKBWVVQLYYHGKEQVPRGCPDGLCPLDMF
<u></u>	]		LNAMSVYTLSPEKYHALCSQTQVMBVGNEB
5559	150	1983	PLAATAHFAKMSRVAKYRRQVSEDPDIDSLLETLSPEEMEELEK
l			ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCBKETKK
]			LMQREMSMDESKQVETKTDAKNGEERGRDASKKALGPRRDSDLG
			KEPKRGGLKKSFSRDRDEAGGKSGBKPKEEKIIRGIDKGRVRAA
1	1	i e	VDKKEAGKDGRGEERAVATKKEERKKGSDRNTGLSRDKDKKREE
	]		MKBVAKKEDDEKVKGBRRNTDTRKEGEKMKRAGGNTDMKKEDEK
	]		VKRGTGNTDTKKDDBKVKKNEPLHBKEAKDDSKTKTPEKQTPSG
	!		PTKPSEGPAKVEBEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
1	!		ITNEILVRFTEALBFNTVVKLFALANTRADDHVAFAIAIMLKAN
1			KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
1	· !		GKTEMELAKLLKENTTLLKLGYHFELAGPRMIVINLLSRNMDKQ
	!		ROKRLOEOROAQBAKGEKKDLLEVPKAGAVAKGSPXPSPQPSPK
1		,	PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
L			GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	9	921	SSVVEPSALSVSMACLSPSQLQKPQQDGFLVLEGFLSAEECVAM
			QQRIGEIVABMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
į l			irppfergvydekgnplvppeksinkighalhahdpvpksiths
j			FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
			EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
			SapgtsplgsepardnslfvptpvqrgalvlIhgevvhkskqnl
]			SDRSRQAYTFHLMEASGTTWSPRNWLQPTABLPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ
	·		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
No:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
İ	amino acid	residue of	S=Serine, TaThreonine, VaValine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	L	\=possible nucleotide insertion)
1			QLLAPTYPSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
1	ł.	ł	QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVT_KPPPPPEVVSRGS
			S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
]	<b>\</b>		LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	ľ		LASPLDFITYSYNIDNVILLITGTLHQRSIAELVPKCHPLGSFE
I.	1		QMRAVNIAQTPABLYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1			INSFGTELSKEDRAKLPPHCGRLYPEGLAQLARADDYEQVKNVA
i	{		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHRVKLNKLAPLNQFHF
5563	342	1385	GVFYAFVKLKEQECRNIVWIABCIAQRHRAKIDNYIPIF SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLBDLKIH
1 3200		1303	LOSTDYCNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1			LASPLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSPB
İ	}		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1			IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1			INSFGTELSKEDRAKLFPHOGRLYPEGLAQLARADDYEQVKNVA
	·		DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
1			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
1	Į.		LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
1		1	VPLTWRCDRDLDCSDGSDEBECRIBPCTQKGQCPPPPGLPCPCT
1			GVSDCSGGTDKKLRNCSRLACLAGBLRCTLSDDCIPLTWRCDGH
ì			PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
1			GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
5565	003	120	TATLLLLSWLRAQERLRPLGLLVAMKESLLLSRQKTSLP
3365	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
1			LALYVFTIATEPLRIIPLIAGAPFWLVSLLISSLVWFMARVIID NKDGPTQKYLLIFGAFVSVYIQEMPRPAYYKLLKKASEGLKSIN
1			PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
			GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
			LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
J		•	LKLCLLCODKNF1LYNORSR
5566	2043	1232	SHIQHHGRGAQAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
1			KNVKBYVRWMYWIVPALYTVIETVADQTVAWFPLYYBLRIAFV
1			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
<b>{</b>			MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
			DEPVGQRPYQPLPRAKKKSKPAPSRSAGYGIPLKDGDEKTDEKA
]	İ		BGPYSDNEMLTHKG?RRSQSMKSVKTTKGRKEVRYGSLKYKVKK
FE22			RPQVYP
5567	1554	233	BFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
			CDSECUTPLHAAATCGHLHLVELLIASGANILAVNTDGNMPYDL
	1		CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ
]	ļ		AGADLHAPLDHGATLLHVAAANGPSEAAALLLKHRASLSAKDQD GNEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDRTPLDVCGDR
1	,	1	EVRAKILEIKHKHDALLRAGSRQRSILLRRRTSSAGSRGKVVRRV
1 1	1		SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR
, ,	ļ		PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
Į ¦	ŀ		STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
1 1	ł	i	GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	ABDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
1 1			SLLVSGPRLFLLQQPLAPSGLTLKSKALRNWOVYRLVTYIFVYE
1	ł	Į	NPISLLCGAIIIWRFAGNPERTVGTVRHCPFTVIFAIFSAIIFL
J [	Ì	Ī	SPEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
	ĺ	[	MVVPSVLVPWLLLGASWLIPQTSPLSNVCGLSIGLAYGLTYCYS
	ł	l	IDLSERVALKLDQTPPFSLMRRISVFKYVSGSSAERRAAQSRKL
1			NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
	Í	ŀ	PTLPPYQPASGLCYVQNHPGPNPTSSSVYPASACTSLGIQPPTP
			VNSPGTVYSGALGTPGAAGSKESSRVPMP
5569	2	835	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	1
1	to first		La Leucine, Mamethionine, Na Asparagine,
i	T .	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	Ţ	\=possible nucleotide insertion)
		1	LKLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
ł	ł	ł	KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
	Ì	İ	PMGIPGEPGERGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
	l	ł	TNPQGDYDTSTGKPTCKVPGLYYFVYHASHTANLCVLLYRSGVK
i	l.	l	1
	j.	{	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
	254		SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1	1	i	MSSPSPGKRRMDTDVVKLIBSKHBVTILGGLNBPVVKFYGPQGT
i		1	PYRGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDBASGTVCL
1		ľ	DVINGTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1	1		RPEBYKOKIKRYIOKYATEBALKEQEEGTGDSSSESSMSDFSED
i		f .	EAQDNEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
1		1	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNBFVVKFYGPOGT
1	1	1	PYEGGVWKVRVDLPDKYPPKSPSIGFMNKIFHPNIDEASGTVCL
1	1	I	
1	1	Ĭ	DVINGTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
I	}		RPRBYKQKIKBYIQKYATEKALKEQEKGTGDSSSESSMSDFSED
			RAQDMRL
5572	2802	2085	RTDYRTGIPGRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
ŀ	i .	!	DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
l .	{	ľ	RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
1	i		RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
{	j	ĺ	KDALRDEYDDLSDLNAVQMESVREWEMQFKEKYDYVGRLLKPGE
	{	[	EPSEYTDEEDTKDHNKQD
5573	2562	219	VPARTPNAKOGGPEARAATATPCOSGGRERAGEAAEDGVKMAAF
	1		SEMGVMPELAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
	į.		1
		1	GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
1	i .		MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYB
	1	[	VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
1 .	ļ	]	NYGERFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
ł	!		QALFPACVLKNABLKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
1	1	}	SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
1	1	ì	IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
1	<u> </u>	ì	GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR
1	]	ł	LQVIVCSATLHSPDVKKLSEKIMHPPTWVDLKGEDSVPDTVHHV
1	1	1	VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
1	l .	ļ ·	IKILKGBYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQQGGG
1		l	PDKKGHQFSCVCLHGDRKPHERKONLERPKKGDVRFLICTDVAA
1	l	}	RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
	•	[	
	1	ľ	TEKEKVNYHVCSSRGKGCYNTRIKEDGGCTIWYNEMQLLSEIEE
1	1	]	HINCTISQUEPDIKVPVDRFDGKVTYGQKRAAGGGSYKGHVDIL
<b></b>	L		APTVQBLAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
1		Į	LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
i	l		TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
i	[	·	RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
i	ĺ		FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCORN
i	1		RSNYYDAYQAQPLATRSSPRPGQPPKVKSEPNSYSLTGYV
5575	456	766	LLNALPCPPPTAAAVILSSTGLMELLEKMLALTLAKADSPRTAL
1 -5/5	-30	,00	I
1	l '		LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
<b></b>	ļ		SPDIGRNSPHYLMFP
5576	249	2146	RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
1	ĺ		BEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
1			QOTLFSINGSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
1			SKWTPLBTQEKBEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
1	ſ		DOKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
			EIILVDDASTEBHLKEKLEQYVKQLQVVRVVRQBERKGLITARL
1	1		
1			LGASVAQAEVLTYLDAHCECFHGNLEPLLARIAEDKTVVVSPDI
			VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFCWBTLPPHEKQRR
L	L		KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNOMBIWGGENVEM
_			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<b>!</b>	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ĭ	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	o o quanto	\=possible nucleotide insertion)
<del>                                     </del>	Joquoneo		SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNOVR
ł	ł	Į.	LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC
1	į.	•	HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNOCLDVGENNRG
Í	í		GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
j .	]		LGSCHPTGKNSQVPKDEEWELAQDQLIRNSGSGTCLTSQDKKPA
l	1		MAPCNPSDPHOLWLFV
5577	3	1275	RNSDCSCGRISVHCLPWVLFILDLKVRSSMFCPLKLILLPVLLD
\			YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
İ	ſ	[	SPGEHAKDBYVLYYYSNLSVPIGRPONRVHLMGDILCNDGSLLL
	}	}	QDVQEADQGTYICEIRLKGESQVPKKAVVLHVLPEEPKELMVHV
			GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
ŀ			SVEYSOSWGHFONRVNLVGDIFRNDGSIMLOGVRESDGGNYTCS
l	1	'	IHLGNLVFKKTIVLHVSPBBPRTLVTPAALRPLVLGGNQLVIIV
<b>1</b>	(	<b>{</b>	GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK
1	1	1	EXPCHPERCEGEKHIYSPIIVREVIEEREPSEKSRATYMTMHPV
1	1		WPSLRSDRWNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMAS PCACRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
ł	,	1	WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
ĺ			TSVDYSSVVVAAMQARYAHVPQLRWETMDVRKLDFPSASFDVVL
j		j	EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRF1
l	İ		SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
į.		1	LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMRGLLTR
[	[		CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL
ì	}	,	REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
	·	}	RAMEKLVRVIDQEMQAIGGQKVNMPSLSPARLWQATNRWDLMGK
	ł	ł	BLLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
· ·		`	VTRKFRDBPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
( .	1	{	DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
}		ł	ICPRCSYSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
1			KYSSIFNAQFTNVCGKPTLAEMGCYGLGVTRTLAAATEVLSTED
•	ľ		CVRWPSLLAPYQACLIPPKKGSKBQAASELIGQLYDHITEAVPQ
1	<u> </u>	<b>.</b> .	LHGEVILDDRTHLTIGNRLKDANKFGYPFVIIAGKRALKDPAHF
5580	<u> </u>	454	EVWCQNTGEVAFLTKDGVMDLLTPVQTV
3360	1681	450	ADAGTRCIPGFVVPSGAGYSAPAQRGRRSSGRMRAAAAPGLTAP WRLLQCCKLRAGELGMAVPAAAMGPSALGOSGPGSMAPWCSVSS
	[	ł	GPSRYVLGMQELFRCHSKTREFLAHSAKVHSVAWGCDGRRLASG
1	ł		SFDKTASVFILEKDRLVKENNYRGHGDSVDOLCWHPSNPDLFVT
]	1	Į	ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGGTIAVGNK
	1		DDVVTFIDAKTHRSKABBQFKFEVNEISWNDNNMFFLTMGNGC
}	I	Ì	INILSYPELKPYOSINAHPSNCICIKFDPMGKYFATGSADALVS
1	Í		LWDVDBLVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
[	[		EVETGDXLWEVOCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
<b>j</b>	<b>j</b>	]	RAGTVKLPGLPNDS
5581	54	947	GGGSGPRAPSATLLDTGESVAAVASGEDKGTAASAAAAAVFACS
	]		CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA
	ļ	]	YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG
	ŀ	i	TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY
Į į	1	}	SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
			TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
	1		TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	IITNNNNVIIPLVIAYHLSGSAQARGERSPAFRLMEROKRKADI
			BKGLQFIQSTLPLKQBEYEAFLLKLVQNLFAEGNDLFREKDYKQ
		}	ALVOYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
			EKALEDSEKALGLDSESTRALFRKARALNELGRHKEAYECSSRC
	{		SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
			TAAGVADQGTSNGLGSIDDIKTDCYVDPRGSPALLPSTPTMPLF
(			PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPBLDTLLDSLSL
}			VQCGLSGSGVPSELPQLIPVPPGGTPLLPPVVGGSIPVSSPLPP
			ASPGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL
	<u> </u>	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alamine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
] No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į			Codon, /=possible nucleotide deletion,
ł	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
[	1		DSFGSTRGSLDKPDSFMBBTNSQDHRPPSGAQKPAPSPEPCMPN
	]		TALLIKNPLAATHBFKQACQLCYPKTGPRAGDYTYREGLEHKCK
Į.	1		RDILLGRLRSSEDQTWKRIRPRPTKTSFVGSYYLCKDMINKQDC
!		]	KYGDNCTFAYHQEEIDVWTEERRGTLNRDLLFDPLGGVKRGSLT
{	<b>{</b>		IAKLLKBHQGIFTPLCEICFDSKPRIISKGTKDSPSVCSNLAAK
J	)		HSPYNNKCLVHIVRSTSLKYSKIRQFQKHFQFDVCRHEVRYGCL
{	<b>4</b>		REDSCHFAHSFIELKVWLLQQYSGMTHEDIVQESKKYWQQMEAH
Į.		]	AGKASSSMGAPRTHGPSTYDLQMKFVCGQCWRNGQVVEPDKDLK
1		}	YCSAKARHCWTKERRVLLVMSKAKRKWVSVRPLPSIRNFPQQYD
ł	l	1	LCIHAQNGRKCQYVGNCSFAHSPEBRDMVTFMKBNKILDMQQTY
1	l	· ·	DMWLKKHNPGKPGEGTPISSREGEKQIQMPTDYADIMMGYHCWL
l	1	1	CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
1	1	1	LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
I	1	1	KDMLLCPRDDDFGKYNFLLQEDGDLAGATPRAPAAAATATTGE
5583	3	1265	SSGCROGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEB
1	1	1	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
l			QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
l		ļ	HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
1	ļ	Į	CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
ł		İ	SGAKVIREKKIIEVHVEKGMKDGQKILFHGEGDQEPELEPGDVI
ł	ł	ł	IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF
1	1	[	PEKHWLSLEKLPQLEALLP?RQKVRITDDMDQVELKRFCPNEQN
)		l	WRQHREAYEBDEDGPQAGVQCQTA
5584	3	1265	SSGCRQGRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE
}		1	IKKAYRKLALKYHPDKNPDEGEKFKLISQAYBVLSDPKKRDVYD
		1	QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
1	1	1	HOLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL
			CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC
l	İ	Ī	SGAKVIREKKIIEVHVEKGMXDGQKILFHGEGDQEPELEPGDVI
	}	1	IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI
i	1.	ĺ	LVITSKAGEVIKEGDLRCVRDEGMPIYKAPLRKGILLIQFLVIF
i	ļ ·	ļ	PEKHWLSLEKLPQLEALLPPRQKVRICDDMDQVELKEFCPWEQN
		ļ	WRQHREAYERDEDGPQAGVQCQTA
5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
1		1	YHSLTYATILEMQAMMTFDPQDILLAGNMMKBAQMLCQRHRRKS
l .	ŀ		SVTDSFSSLVNRPTLGQFTEESIHABVCYAKCLLQRAALTFLQD
1		1	RIMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
{			VELGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
	1	}	GHSFRSVLCVMLLLCYHTPLTFVLGTGNVNIEBABKILLKPYLNR
I		ĺ	YPKGAIFLFLAGRIEVIKGNIDAAIRRFRECCEAQQHWKQPHHM
1	ļ	)	CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
İ		1	SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
Į		}	RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTDGILEIITX
			AREMLEKGPENRYSVDDECLVKLLKGLCLKYLGRVQEABENFRS
l	1	1	ISANEKKIKYDHYLIPNALLELALLIMEQDRNERAIKLLESAKQ
	<u> </u>		NYKNYSMESRTHFRIQAATLQAKSELENSSRSMVSSVSL
5586	2619	915	LPAGTPESSLHEALDQCMTALDLFUTNQFSEALSYLKPRTKESM
1	i	1	YHSLTYATILEMQAMMTFDPQDILLAGNMMKBAQMLCQRHRRKS
l	1	1	SVIDSFSSLVNRPTLGQFTEKEIHAEVCYAKCLLQRAALTFLQD
1		I	ENMVSF1KGG1KVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG
ĺ			VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS
1		]	GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIBEABKLLKPYLNR
1	ŀ	l .	YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM
	}	j	CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL
1	ì		SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS
l		1	RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILBIITK
1	1		ABEMLEKGPENEYSVDDRCLVKLLKGLCLKYLGRVQEAEENFRS
1	1	1	ISANEKKIKYDHYLIPNALLELALLIMEQDRNERAIKLLESAKQ
L	L	<u> </u>	NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL
5587	1768	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T-Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	begaence	\=possible nucleotide insertion)
	acquence		CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKOSRI
1	· ·		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIBKNGKLRYE
ł		l ·	IDTGEETKFVKPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
	ļ		DFGEKOKNALGEAARAAGFNVLRLIHEPSAALLAYGIGODSPTG
ŀ		<b>{</b>	KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
ļ	]		TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAKVAKHSLSTLGS
l		}	ANCPLDSLYEGODFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
l	ł	ſ	NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
ı	İ	<b>,</b>	VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
ľ	· ·	1	SRFTVLFPSGTPLPARROHTLQAPGSISSVCLELYBSDGKNSAK
1		ļ	EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDQET
1			
FERR	<u> </u>	500	GKCHAISIBIAS TPPPPEQAMVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGK
5588	3	589	LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
1	1	1	VLAFPCNOFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
1	1	ł	AHPAPKYLAQISGKEPTWNPWKYLVAPDGKVVGAWDPIVSVEEV
<b>!</b>		1	RPQITALVRKLILLKREDL
5589	1884	553	LROAWHEGGIGOTDKERGAAALPGEEGDPTRGRSLGRASWESGS
5589	1884	553	PRRPRSPPSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1			GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
		1	ATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLF
l .			RPPAQWSSILGAAHSSDYSMWRKNQYVSNGLRDFAERGEANALM
ſ	Í		KETEAAGEALQSVHAVPSAPAVPSGTGQTSAELEVQRRHSLVSF
1			VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSG?
			TFSSPNFATIPODTVTBITSSSPSHPANSFYYPRLKALPPIARV
1		ľ	TLLRLROSPRAFIPPAPVLPSRDNBIVDSASVPETPLDCEVSLW
1			SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEERABCVP
	•		DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
3350	/*	)	EDAVKETSSVKOPWDHTTTTTNRPGTTRAPARPPGSGLDLADA
{	ſ	1	LDDODDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
) .			LADALDDRNDRDDGRRKPIAGGGGPSDKDLEDIVGGGEYKPDKG
ì		ţ	KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
1	`	ł	QQKKPCFSIQQGLNADYVKGENLEAVVCBBPQVKYSTLHTQSAB
1	,	j	PPPPPBPARI
5591	68	1494	AGSSRRAAABRILLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
555.	1		LRVTRNSKINAKNKAKINMAGAKRVPTAPAATSKPGLRPRTALG
	1		DIGNKVSROLOAKNPMKKRAKPSATGKVIDKKLPKPLEKVPMLV
1	1	1	PVPVSEPVPEPEPEPEPEPEPEPEPEPEPELVDTASPSPMETSG
]	]	ļ.	CAPARROLCOAFSDVILAVNDVDAEDGADPNLCSRYVKDIYAYL
1	Ì		ROLEBEOAVRPKYLLGREVTGMMRAILIDWLVQVQMKFRLLQET
1	{	1	MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPBI
	1	1	GDPAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
1	i		KIGEVDVEOHTLAKYLMELTMLDYDMVHPPPSQIAAGAFCLALK
1	1		ILDNGEWTPTLQHYLSYTERSLLPVMQHLAKNAAMVNQGLTKHM
	1		TVKNKYATSKHAKISTLPOLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
4		1	VGKSALVVRPLIKRFIWBYDPTLESTYRHQATYDDEVVSMEILD
	{		TAGOEDTIOREGHMRWGEGFVLVYDITDRGSFBEVLPLKNILDE
]	1	Į	IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
	1		ACTGEGNITEIFYELCREVERREMVOGKTERESSTTHVKQAINK
	ł	ł.	MLTKISS
5593	<del>                                     </del>	7777	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
5533	3	1113	
	i	1	SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1	1		DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
1	1	t	BLDLYDNOIKKIENLEALTELEILDISPNLLENIEGVDKLTELK
1		i	KLPLVNNKISKIENLSNIHQLQMLELGSNRIRAIENIDTLTNLE
{	1		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1	1	1	RLYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
.}	L	1	BFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ	Predicted	Predicted end	I Amino acid noment containing cional
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	1	
110:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
j		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S-Scrine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
Ţ	j	`	SSGIVADLSEQSLKDGEERGEEDPEEEHBLPVDMETINLDRDAB
ľ	1		DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLRELOSLR
ŀ		Ì	ELDLYDNQIKKIENLBALTELEILDISFNLLRNIEGVDKLTRLK
ı	1	ļ	KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1	1		SLFLGKNKITKLONLDALTNLTVLSMOSNRLTKIEGLONLVNLR
(			RLYLSHNGIRVIEGLENNNKLTMLDIASNRIKKIENISHLTELO
1	!	ļ	EFWINDNILESUSDLDELKGARSLETVYLERNPLQKDPQYRRKV
i	<b>1</b> '		MLALPSVRQIDATFVRP
5595	3	1476	
	] 3	74.0	ARWINGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
ļ	<u>'</u>		PIALAMSPPLYLFPIPLPSWAVSQPTPTIGTMFADLDYDIEEDK
Į.	[		LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVPDNTP
1	]		AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
1	]		NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
1	1		NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
1	}		VFSVIGVRBPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
	J l		DINTYLNKAIPDTRLTIKKYLDVKFRYLSYCLKVKEMDDREYSC
i	[		IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
ł	}		LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
}	j		HTTLAYGLNQEEFTDGREEEEREDTAAGEPSRDTRGAAGPLDKG
			GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISPIFP
1			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
			FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
			KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
1	!		VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQRPR
1			PCGGPHTAVGTKYGMPSSHSQFMWFPSVYSFLFLYLRMHQTNNA
1			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSQVLYGGIAG
	ļ		GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
			FRYTVTRAKARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
}			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFRG
			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVINNTECGKLLEE
] .			IKCALCSPHSQSLPHSPEREVLERDLVLPLLCKDYCKEFFYTCR
<b>j</b>			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
} !	j		LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1 1	1		NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM
	]		ITLDDMBEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHPNS
	ì		TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
(	ĺ		SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1	ļ		YGSYVFGDRNGNFLTLQQSPVTKQWQBKPLCLGTSGSCRGYPSG
4 1	ŀ		HILGFGEDBLGBVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
	Į.		CRATVQPAQTLTSECSRLCRWGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
	(		DAKFGERNEGSGARRRCLINGNPPKRLKRRDRRMMSOLELLSGG
j 1	}		EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
} I	ļ		· •
	Í	i	IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1	Ì	į	GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1	ļ		QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
	ţ	ľ	LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1	j		SLAPHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
	\	j	NPHQVDLRTARVFLEVABLHRKHLGGQLLFGPDGFLYIILGDGM
[ [	į		ITLDDMEEMDGLSDPTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
L1			TNOPPRVPAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS

SEO	Predicted	Predicted end	Design and government and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO	II.	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
· ·	sequence	1	\=possible nucleotide insertion)
	† · · · · · · · · · · · · · · · · · · ·		SARTLOTIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCOSERL
l .	1		YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
Į.	į	•	
ì	I	]	HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEK
			CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQB
i		ļ	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLBDPNGSF
İ		1	SNARMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
			FPNCKFARKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	ļ		AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
	1		TFYHPTINVPPRHALKWIRPQTSB
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
1	I		EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
1.	1		SNAEMSELSVAOKPEKLLERCKYWPACKNGDKCAYHHPISPCKA
1	1 ·		
1	1	ĺ	FPNCKFARKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
i	1		AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
5602	<del></del>		TFYHPTINVPPRHALKWIRPQTSB
3602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
			NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
i	1		AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
	1		IPGYRABBAVBMLKTFYKQENPNAPKSKVRKKBCQQILNMF
5603	1	565	FRGRTPISGGRRGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
			WIGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
l			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
ł			TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLOHHA
İ	i		TIPLOVVDRRMO
5604	1	1506	BDIFPAQLLKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
			DOGOVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
į	·		GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
			RLDGILSETIPIHGRGNFPTLBLQPSLIVKVVRRRLAEKRIGVR
1	<b>}</b>		DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFOTVKDV
İ	1 .		
ļ.			V-DCLLDPLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
ŀ	l t	•	SLSNNSGKNVELKFVDSLRRQPEFSVDSFQIKLDSLLLFYBCSE
l	1		NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
1	]		LLKYCNLLVRGFRPASDBIKTLQRYMCSRFFIDFSDIGEQQRKL
			ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
1	]		ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
	<u></u>		QPVFTCQQQTYSTWLPCN
5605	35	1821	SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
		'	MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRPVFQ
]			KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
			GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
			ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKS PRVAP
1		•	GSARPWPALRSLLHRNLVLRTHOPARYSLTPEGLELAOKLAESE
1			GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
1			GEYRVLLCVDIGETRGGGHRPELLRELORLHVTHTVRKLHVGDF
ì			
1	ļ		VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ
			KFRLKRCGLERRVYLVEEHGSVHNLSLPBSTLLQAVTNTQVIDG
			FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
			SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
[			VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
			QRNLGPALSRTLSQLYCSYGPLT
5606	3	1099	GRSRCPGPGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
]			LSSVGSISEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
			IBECQYQFRNRRWNCSTLDSLFVFGKVVTQGTREAAFVYAISSA
į (			GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
			VAFSOSFVDVRERSKGASSSRALMNLHNNRAGRKAILTHMRVEC
			KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
			SSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGR
]			TCNKTSKAIDGCELLCCGRGFHTAQVKLAERCSCKFHWCCFVKC
			TCMKTSKAIDGCELLCCGRGFHTAQVKLABRCSCKFHWCCFVKC RQCQRLVELHTCR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Guidelding T Tallandine, G=Glycine,
1	corresponding		H=Histidine, I=Isoleucine, K=Lysine,
Ĭ		to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
ì	sequence	1	\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMI.WLDLAMAGSSFLSPEHQRV
1	1	}	QQRKBSKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
1		i	COMMONAL PARTICIPATION DEPRING QUARTER DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DEL COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DEL COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DEL COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DEL COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DEL COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE LA COMMON DE
5608	2		FDVGIKLSGVQYQQHSQALGKFLQDILWBEAKEAPADK
3608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
	i		RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
1		}	VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
1	i	1	SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPRP
1			KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
1			VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
1			QADGQGQRRYRGLLHCMVTIVREGPRVLFKGLVLNCCRAFPVN
1	1		MVVFVAYBAVLRLARGILIT
5609	1628	304	
1 5005	1020	204	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
1	•		KRIRBAKRSARPELKDSLDWIRHNYYESFSLSPAAVADNVERAD
i			ALQLSVEBFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
1			RNOKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
			EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
			GTGIHIDPLGTSAWNALVQGHKRWCLPPTSTPRELIKVTRDEGG
			NQQDEAITWFNVIYPRTQLPTWPPEFKPLEILQKPGETVFVPGG
			WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
1			ILKQEHPELAVLADSVOLQESTGIASDSSSDSSSSSSSSSSSDSD
1 1			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
1			R
5610	54	1196	LERTPASADMAWTKYQLFLAGIMLVTGSINTLSAKWADNPMAEG
	• •	1130	CCCCVETCEOUDD OF WHAT ORDER AS THE TREE TO THE
			CGGSKEHSFQHPFLQAVGMFLGBFSCLAAFYLLRCRAAGQSDSS
]			VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
1 ' 1			VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
1 1	1		DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
í .			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
1			VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
i 1			TVVIWALSLALGWRAFHALQILGFLILLIGTALYNGLHRPLLGR
1			LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACAESSSLAASAKPGAGGSPALAMSG
			ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDRENLPE
ł I			KLTAPKEKYMBPDLNNEGBIDLMSLKRMMEKLGVPKTHLKMKKM
1. 1	1		ISEVTGGVSDTISYRDFVNMMLGKRSAVIKLVMMFEGKANESSP
		í	KPVGPPPERDIASLP
5612		721	ASRDGYMDATIAPHRIPPEMPQYGEENHIPRLMQAMWLCKHLNS
	~	, 67	
[ ]	İ		SLLTLENLILNEFSYTATRARRLYLQRKTVPSALLVQLIQERLA
j	. !	]	EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
1 1	1	ļ	IERNLGKRIDPQTGBIYHTTPDWPPBSBIQNRLMVPBDISKLBT
{	i		AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
<u>                                     </u>			NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKODKYKPPKFNLFGKISGWFRSILSD
Į [	i	1	KTSRNLFFFLCLNLSFAFVRLLYGIWSNCLGLISDSFHMFFDST
1 '	ŀ	1	AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIPTAF
		1	FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
1 1	1	l	GRSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
] ]	ļ	1	ANCHEUPUCUDOBOL VERTICIDADO COMO COMO COMO COMO COMO COMO COMO CO
] [	}	İ	AHCHCHFHSHDGPSLKETTGPSRQILQGVFLHILADTLGSIGVI
j i	, [	į	ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
l i	<i>'</i>		TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
II			IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNBHACPLOAGLGLTQRKPKAIRGREGRATNQGQGETQNER
ļ Ī	i	ſ	APWGARQRLGVMAELQQLQBPEIPTGREALRGNHSALLRVADYC
ļ į	Í		EDNYVQATDKRKALEETMAFTTQALASVAYQVGNLAGHTLRMLD
		}	LQGAALRQVBARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
!		j	QKVIAPBNLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
ļ <b>l</b>			LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
	ľ	1	SLASAGSAEGVGGAPTPKGQAAPPAPPLPSSLDPPPPPPAAVEVP
! [	İ		QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
			GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY
			· · · · · · · · · · · · · · · · · · ·

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	l ·		Harristidine, I=Isoleucine, K=Lysine,
į	location	corresponding	
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			SDGWCRGVSSEGTGPPPGNYVEPSC
5615	9	1558	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEONF
"""	_		DGTSDREHEOKLLPVOKHYOLDDQEGISFVOTIMHLLKGNIGTG
<b>!</b>	I	}	LIGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
1		ì	FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
ł			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
Ì	1	1	LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYO
Į.	ļ ·		YVVRNMPDPHNLPIVAGWKKYPLPFGTAVFAFEGIGVVLPLENQ
	1		MKESKRFPOALNIGMGIVITLYVILATLGYMCFHDBIKGSITLN
i	}	į	1 · · · ·
1			LPQDVWLYQSVKILYSFGIPVTYSIQFYVPARIIIPGITSKFHT
1		1	KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
1		<b>!</b>	LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
		ļ <u></u>	reityptpkvvagtpospfininstcltsglk
5616	ī	719	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
1	]	1	LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
1	1	1	HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
1	1	1	IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD
i			KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
J		1	YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAKEQVNRSAGLAPDCEASATAETTVSSVG
Í	1		TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
l l		1	KDIKPAATHHYLVVPKKHIGNCRTLRKDQVBLVENMVTVGKTIL
i		İ	ERNNFTDFTNVRMGPHMPPFCSISHLHLHVLAPVDQLGFLSKLV
1			YRVNSYWFITADHLIBKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
1 3020		]	LFLNSGGDSLKSIRLLSBIEKLVGTSVPGLLBIILSSSILEIYN
1		1	HILOTVVPDEDVTFRKSCATKRKLSNINGBRASGTSLHQKAIMT
1			FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
i		t	OTNIONLKGLNSPVLIGKSKDPSCVAKVSEBGKPAIGTQKMELH
1.		}	VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
	1	] .	SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1	1		EKYMMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
1		1	VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
Į.	į.		KHSCGKPLFSSPQCCSQYICIGCVDGHLLCFTHFGEQVWQFSTS
1	ł		GPIFSSPCTSPSBQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
			<u></u>
1	1	1	YATPPAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYKLP GBVPSSPVVLRSMLIIGCRDNYVYCLDLLGGNQK
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVRAALRSLGSPPGAGRGCPCP
			AGSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
1	}	1	RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSPLGHCSVL
1		1 .	LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQFPLGP
	1	1	TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
		<u> </u>	ECSPPATP
5620	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
Į		1	AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
Ī		1	LIADAKTLIDKARVETONHWFTYNETMTVESVTQAVSNLALQFG
	1		REDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
1	1	i	AIGSASEGAQSSLQRVYHKSMTLKRAIKSSLIILKQVMEEKLNA
1		1	TNIELATVQPGQNFHMFTKRELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
1	i	[	ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF
1	1	1	MIMLGDKEKTFOFLHOFSRLLTSAFLWLPRLHISSYLPNDTVES
1	1	1	GIHPVYFCSTHYIKMLLKAELPLVFSAFHMSGFAPSQICLQWIT
1	İ	Į.	OCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLQQDILQ
1	1		HTOTODLOVFLKEBALHGPRVSDYPEYMEILEQNYRTVLLRDMR
1	1		
F633	<del> </del>	<del></del>	NIRLQST
5622	1122	456	AASTKOAVSRKRSHSASEKSGTGTSISKRLMMPQIRNPMKAMY
1	1	1	PGTFYFQFKNLWRANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
{	1	1	QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
	l	L	GEVARFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV

Section   Predicted on mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucleotide   Coation of mucle				
No:   nucleotide   location   corresponding   to first   amino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   residue of   maino acid   sequence   sevente, G-Suprine, X-Unknown, *-Stop   Codon, /-possible nucleotide deletion;   Sevente, T-Thronine, V-Valine,   maino acid   sequence   maino acid   sequence   maino acid   sequence   maino acid   sequence   maino acid   sequence   maino acid   maino acid   sequence   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   maino acid   ma	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first and cold weight and cold amino acid weighted of amino acid sequence   epicline, Gellutamine, Rearginine, sequence   epicline, Gellutamine, Rearginine, sequence   epicline, Gellutamine, Rearginine, sequence   epicline, Gellutamine, Rearginine, sequence   epicline, Gellutamine, Rearginine, September   epicline, Gellutamine, Rearginine, sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Rearginine, Sequence   epicline, Gellutamine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, Rearginine, R				
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to first wand acid residue of amino acid sequence solvenie, "L-Thronoine, V-Valine, "second of amino acid sequence sequence sequence "Sosonine, T-Thronoine, V-Valine, "second sequence "Sosonine, T-Thronoine, V-Valine, "second sequence "Sosonine, T-Thronoine, V-Valine, "second sequence "Sosonine, T-Thronoine, V-Valine, "second sequence "Sosonine, T-Thronoine, V-Valine, "second sequence "Sosonine, V-Valine, V-Valine, V-Valine, "sequence "Sosonine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Valine, V-Vali				
amino acid residue of amino acid sequence  codon, /-possible nucleotide deletion, /-possible nucleotide insertion)  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence			to first	
residue of amino acid sequence (Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion)  5623 3 954 RIBDEROFYCHREFOYNDREFEFFERGLETBELLGERILGESL O		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence codon, /-possible nucleotide deletion, /-possible nucleotide insertion)  SIDVEDFEXCHERFYTHINEEFEPHKELKERERES.  1 Section   SIDVEDFEXCHERFYTHINEEFEPHKELKERERES.    1 Section   SIDVEDFEXCHERFYTHINEEFEPHKELKERERES.    1 Section   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION   SECTION		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
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CRPVPADRERKKIAVLENIABOSCULTGEDDSLADKHACPAYUGPE ILSSRASYSGKAADVWSLGVALFTMLAGHYPPQDSEPVILFGKI RGGYVALPAGLSAPARCLURCLLERRPASRITATGILLHPALRG DPMPLAPTESILLWRAAQUVPDGLGJDEARERSBOREVULVG  5626 3123 2011 PPRALGSVAMERQVZTPPVYWAQGHELVIRGESDDEVVLLYG PPRALGSVAMERQVZTPPVYWAQGHELVIRGESDDEVVLLYG EBERLIKKLBLSSEGSPETLINLRKGLIRFUNFUNGULGFSWIFFW LTVQKKVSQWWBRITTKQBKRP LFLAPDPDRWIDGSDAEMELRAK EBERLIKKLBLSSEGSPETLINLRKGLHYMYNUVQLGFSWIFFW LTVRFCILGKSSPYDTEHTVADMWYFCOMLAVVBTINAAIGVTT SPVLPSLIQLIGRNFILPI I FGTMEEMQNKAVVPFVPYLWSAIE IPRYSFYMITCIDMDWKULTWLBYTLWI I PLYPLGGLARAVSVIQ SIPIPMBTGREFFTLPYVKIKVRFSFFLQIVLIMI FLGLYINF RHLYKORRRRYGQKKKIH  FRAULHFKAQGHGAKGDNVYEFHLEFLDLVKREVYKLTCRQVN I TYOKKVSQWMBRITTKQEKRP LFLAPDPDRWIDGSDAEMELRAK EBERLMKLRLSSEGSPETLINLRKGVLFPYNVLOVPLGFSWIFFW LTVVRPCILGKRSPYDTPHVVADMWYPCQMLAVVETINAAIGVTT SPVLDSLIQLIGRBFILF I I FGTMERMQMKAVVFPVYFLASAIE IPRYSFYMITCIDHDWKULTWLRYTLWI PLYPLGCLABAVSVIQ SPIPMBTGREFFTLPPVKIKVRFSFFLQIVLIMI FLGLY INF RHLYKQRRRYGQKKKIH  5628 75 1455 VAGAMASKCLKGGFSSGSLTRVSAMYSSSPCKLP SLSPVMASFSSACSUGGSSYRTSCLPALCLPAGGFATSYSGG GGMFGGGILTGMEKETMQSLINDRLAGYLEKVRQLEQKNASLESR IRENCEQQVPYMCDDYQSYPTTIERLQKKTLCSKAENARLVVBI DNAKLAADDFRTKYETTSVISGLUTEDDINGGRRILDDLTLCKSD LKAQVESLKBELLCLKKNHEBEVNSLRCQLGGBINAVBVDAAPPV DLNRVLERRRCQVFSTLVENNRRDAEDHLTDGSEELMQQVVSSSE GGMFGGGILTGMERKTVBALEI ELQAGHSMRDALESTLAETRARY SSQLAQVQCMITNVBAQLABIRADLERQMGECQVQLLDVRARLEC . KINTYRGLLESSDSLEDLPNPCAPDYSPSKCCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF 5629 2287 938 GRPRSSSDNRMFLRERRAGLSSAAVQTRIGNSAASRRSPAARPFV PAPPALFRRFROTESSTSLAAPAVVAVAVAVVVAVSAVANAMN NYIHVPPGSPSPPKLNTVQDQBERGRCRGGLICHGRADDFRHVCM NYIHVPPGSPSPPKLNTVQDQBERGRCRGALLGLICHREPWDD QRVTLQLFTDGITMKLLGCVANTMEDVVLVRIYGNKTELLVDR DBEVKSFFRVLQAHGGGAPGLYCTFNNGLCYEFTQGEALDPKHVCM DBEVKSFFRVLQAHGGGAPGLYCTFNNGLCYEFTQGEALDPKHVCM DBEVKSFFRVLQAHGGGAPGLYCTFNNGLCYEFTQGEALDPKHVCM		]	1	1 · · · · · · · · · · · · · · · · · · ·
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DPMPLAPTRSHLWEAQUVPDGLGLDEAREEEGDREVVLYG  5626  3123  2011  PPRALGSVAMENQUITPHYMAQRHERLY,RUELSDVQNPAIST TENVLHERAGGRAGHAVY BPHLEFIDLVKPEPEPYYKLTQRQVN ITVQKKVSQWBERLTKQEKRPLPLAPDFDRWLDESDAEMELRAK EEERLMKLALESEGSPETLTINLRKGYLWYMINQPLGFSWIFVAN LTVRFCILGKESFPOTFHTVADMWYCQMLAVVETNARAGVTT SPVLPSLIQLLGRNFILPIIFGTMEEMQNKAVVFPVPYLWSAIE IFRYSFYMITCIDMDWKULTWLRYTLWILVFLGCLARAVSVIQ SIPIPMETGRESFTLPYPVKKARFSPFLQIYLINIFLGCLARAVSVIQ RHLYKQRRRYGQKKKKIH  5627  3123  2011  PPRALGSVAMENQVITPHYWAQRHERLYRAVELSDVQNPAIST TENVLHBYRAQGHGAKGMVYBPHLEFLDLVKQEBVYYLLTQRQVN LTVQKKVSQWMERLTKQEKRPLFRAPDFDRWLDESDAEMELRAK EEERLNKLALESEGSPETLITHLRKGYLFWHIVQFLGFSWIFVM LTVRFCILGKESFYDTPHYVADMWYCQMLAVWETIMAAGVTT SVVLPSLIQLLGRNFILPIIFGTMERMQNKAVVPFVPYLMSAIK IFRYSFYMLTCILMDNKVLTWLRYTLMTPLYPLGCLARAVSVIQ SIPIPMSTGRFSFTLLPYPVKI KVRFSFFLQIYLINIFLGLY INF RHLYKQRRRYGQKKKKIH  5628  75  1455  VAGAMASKGLKRGFSSGSLKSPGGASGGSTRVSAMYSSPCKLDP SLSPVARSFSACSVGLGRSSYRATSCLPALCL-PAGSFATSYSGG GGWFGEGILTGMEKETMGSLNDRLAGYLEKWRQLEGENASLESR IRBNCCQQWPYMCDDYQSYPRTIERIQKKTLCSKARMARLVVBI DRAKLAADDFRTKYBTBVSLRQLVCBDINGLRRILDDLTLCKSD DRAKLAADDFRTKYBTBVSLRQLVCBDINGLRRILDDLTLCKSD DLRAVLEEMRCQYBTLVENNRRDAEDHLDTGSEELNQQVVSSSE QLQSCOABILELRRTVNALELELQAGHENDALESTLAETEARY SGLLAGMQCMITHVRAGALASTRADLBRRDALESTLAETEARY SGLLAGMQCMITHVRAGALASTRADLBRRDALESTLAETEARY SGLLAGMQCMITHVRAGALASTRADLBRRDALESTLAETEARY SGLLAGMQCMITHVRAGALASTRADLBRRDALESTLAETEARY PARPALFREGRESTELSARAVVIVAVAVVVVVVSAVANAMA NYTHVPPGSPBVPKLNVTVQDQBEHRCREGALSLLGHLRPHWDP PAPPALFRGRESTESSTBLSARAVUVVAVAVVVVVVSAVANAMA NYTHVPPGSPBVPKLNVTVQDQBEHRCREGALSLLGHLRPHWDP QBVTLQLFTDGITNKLIGCVVGNTWEDVALVTYRGKTELLVDR DEKVKSFRVLQAHGCAPQLYCTFYNGLCYYETVGCBALDEKHVCN	ŀ	Í		
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TENVLHFKAQGHQAKGDNYYEFHLEFIDLVKPEPVYKLTQRQWN ITVQKKVSQWBERLIKDGKRPLFLAPDFDRWLDESDAEMELRAK EERRIMKIALLESEGSPETLTINLKRGYLFWININQFLGFSRIFVN LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT SPVLPSLIQLLGENFILPIIFGTMEERQMKAVVFFPYLWSALE IPRYSFYMLTCIIDNDWKUJWALKYTUNIPLYPLGCLARAVSVIQ SIPIPNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYGGKKKKIH  5627 3123 2011 PPRALGSVAMENQVLTPHVYWAQRHERELYLRVELSDVQNDPAISI TENVLHFKAQGHGAKGDNYYEFHLEFIDLVKPEPVYKLTQRQW ITVQKKVSQWWRRLTTQBKRPLFILADLVKPEPVYKLTQRQW ITVQKKVSQWWRRLTTQBKRPLFILADLVKPEPVYKLTQRQW ITVQKKVSQWWRRLTTQBKRPLFILADLVKPEPVYKLTQRQW LTVRFCILGKRSFYDTPHTVADMMYPCQMLAVVETINAAIGVTT SPVLPSLIQLLGRNFILFIIFGTWERWQNKAVVFFVYLWSAIE IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLABAVSVIQ SIPIPWSTGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF RHLYKQRRRYCQKKKKIH  5628 75 1455 VAGAMASKCLKAGFSSGSLKSPGGASGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLFAGGFATSYSGG GGWFGGILTGNEKETWQSLNDRLAGYLEKVRQLEQENASLESR IRBWCQQVPYMCPDYGSYFRTIERLQKTLCSKABNALUVEII DNAKLAADDFRTKYBTEVSLRQLVESDINGLKRILDDLTLCKSD DKAKLAADDFRTKYBTEVSLRQLVESDINGLKRILDDLTLCKSD LKRQVESLKEBLLCLKKNIEBEVNSLRCQLGDRLANVEVDAAPPV DLMRVLEBWRCQYBTLYBNNRRDABNIDTGSEBLMQQVVSSSE QLQSCQABIIELRRTVNALEIELQKRTLCSKABNALUVEI SSQLAQMQCMITTVRAQLABIRADLERQNGEYQVLLDVRARLEC - BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVOPGGRP GPRESSDMRPLRERGAGJSSAAVGTRIGNSAASRRSPAARPPV PAPPALFRGRPGTEGSTSLSAPAVLVAVAVVVVVVSAVANAMA NY1HVPPGSPBVPKLMVTVQDQKBHRCREGALSLLQHERPHWDP PAPPALFRGRPGTEGSTSLSAPAVLVAVAVVVVVVSAVANAMA NY1HVPPGSPBVPKLMVTVQDQKBHRCREGALSLLQHERPHWDP DEKVKSFRVLQAHGCAPQDYCTFNNGLCKRFIQGRALDPKHVCN				
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5627  3123  2011  PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPATSI TENVLHYRAQGHQAKGDNYYEYHLEFIDLVKPEPVYKLTCRQVN LTVQKKVSQWWRRLITKQEKRPLFFLAPDFDRWILDEDAAMELRAK EBERLNKLRLESEGSPETLITNLRKGYLFMYNLVQPLGFSWI PVN LTVRFCILGKRSFYDTFHTVADMMYDCQMLAVVBTINAALGVTT SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVPFVPYLWSAIB IFRYSFYMLTCIDMDWKVLTWLRYTTLWIPLYPLGCLABAVSVIQ SIPIFNBTGRFSFTLLPYPVKI KVRPSFFLQIYLIMIFLGLYINF RHLYKQRRRYGQKKKKIH  5628  75  1455  VAGAMASKCLKAGFSSGSLKSPGGASGSTRVSAMYSSSPCKLP SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG GGWFGGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIEBLLKKTLCSKAENARLVVEI DRAKLAADDFRTXYBTEVSLRQLVESDINGGRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV DLNRVLEEMRCQYBTLVENNRDAAEDNLDTQSEBLNQQVVSSSE QLQSCQABIIELRRTVNALEIELQAGHSMRDALESTLAETEARY SSQLAQMQCMITNVENQALEIRADLERQNQEYQVLLDVRARLEC RINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRP  5629  2287  938  GRPRSSDNRNPLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAAPPALFRGPGTESSTLSAAPAVLVVAVAVVVVVSAVANAMA NYIHVPPGSPEVPKLNVTVQDQEBHRCREGALSLLQHLRPHWDP QBVTLQLFTDGITNKLIGCVVGNTMEDVVLVRIYGNKTBLLVDR DEEVKSFRVLQAHGCAPQLYCTFNNGLCYBFIQGEALDPKHVCN	<b>!</b>		l	· ·
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GCWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR IREWCEQQVPYMCPDYQSYFRTIERLQKKTLCSKAENARLVVEI DRAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD LEAQVESLKEELLCLKKNHEEEVNSLRCQLGERLNVEVDAAPPV DLNRVLEEMRCQYETLVENNRRDAEDNLDTQSEELNQQVVSSSE QLQSCQABIIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC . BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALFRGRPGTEGSTSLSAPAVLVAVAVVVVVSAVANAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN	1	1	1	
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DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD  LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV  DLMRVLEEMRCQYETLVENNRRDAEDHLDTQSEELNQQVVSSSE  QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY  SSQLAQMQCMITTVVEAQLAEIRADLERQNQEYQVLLDVRARLEC .  EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA  ARTNCSARPICVPCPGGRF  5629 2287 938 GRPRSSDWRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV  PAPPALFRGPPGTEGSTSLSAPAVLVAVAVVVVVSAVANAMA  NYIHVPPGSPEVPKLNVTVQDQEBHRCREGALSLLQHLRPHWDP  QEVTLQLFTDGITMKLIGCYVGNTMEDVVLVRIYGNKTELLVDR  DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN	1	}	I	
LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV  DLMRVLEEMRCQYETLVENNRRDAEDNLDTQSEELMQQVYSSSE QLQSCQAELIELRRTVNALEIELQAQHSMRDALESTLAETEARY SSQLAQMQCMITNVBAQLAEIRADLERQNQEYQVLLDVRARLEC . BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF  5629 2287 938 GRPRSSDNRNPLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALFRGPGTESSTLSAPAVLVVAVAVVVVVSAVANAMA NYIHVPPGSPEVPKINVTVQDQEBHRCREGALSLIQHLRPHWDP QEVTLQLFTDGITMKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN	ļ		Į.	
DLNRVLBEMRCQYBTLVENNRRDAEDNLUTGSEBLNQQVVSSSE QLQSCQABIIELRRTVNALBIELQAQHSMRDALESTLAETBARY SSQLAQMQCMITNVRAQLABIRADLBRQNQBYQVLLDVRARLEC . BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRP  5629 2287 938 GRPRSSSDNRNPLRBRAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVANAMA NYIHVPPGSPBVPKLNVTVQDQBBRRCRBGALSLLQHLRPHWDP QRVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTBLLVDR DBEVKSFRVLQAHGCAPQLYCTFNNGLCYBFIQGBALDPKHVCN	1	J	1	<u> </u>
QLQSCQABIIELRRTVNALBIELQAQHSMRDALESTLABTBARY SSQLAQMQCMITNVBAQLABIRADLBRQNQBYQVLLDVRARLEC . BINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA ARTNCSARPICVPCPGGRF  5629 2287 938 GRPRSSSDNRNFLRBRAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVANAMA NYIHVPPGSPBVPKLNVTVQDQBBHRCRBGALSLLQHLRPHWDP QRVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTBLLVDR DBEVKSFRVLQAHGCAPQLYCTFNNGLCYBFIQGBALDPKHVCN				_ "
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5629 2287 938 GRPRSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV PAPPALFRGRPGTEGSTSLSAPAVLVVAVAVVVVVSAVANAMA NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR DEEVKSFRVLQAHGCAPQLYCTPNNGLCYEFIQGEALDPKHVCN				ARTNCSARPICVPCPGGRF
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	b=Leucine, M=Methionine, N=Asparagine,
]	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
Į	4		
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence	1 -	\=possible nucleotide insertion)
	boque	<del>                                       </del>	ADEDINKRPLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
i		Ī	1
	l .	l .	LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
1			DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
ŀ		ŀ	NQFALASHPFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP
1	ì	i	EVTALKVPB
5630	1194	278	GFWAIAOTCAHHLPPGSPWLVPASPNRLPEMSSFGYRTLTVALF
3630	1134	270	_ · · · · · · ·
	ł	İ	TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
ļ	1	l .	GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
}	Ĭ	}	KSNVSVYQPPRQVILTLQPTLVAVGKSPTIBCRVPTVBPLDSLT
J		1	LFLFRGNETLHYETPGKAAPAPQBATATFNSTADREDGHRNFSC
1	1	1	LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
ŀ			LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
		ļ <u></u>	
5631	1053	290	SRVDDFVRPEPSRAEPSRSGRRPARKAATMSVFGKLFGAGGGK
l			AGKGGPTPQEAIORLRDTEEMLSKKQEPLEKKIEQELTAAKKHG
1	}	1	TKNKRAALQALKRKKRYBKQLAQIDGTLSTIBFQREALBNANTN
ì	ł	1	TEVLKNINGYAAKAMKAAHDNINDIDKVDBLMQDIADQQRLAEBIS
<b>!</b>	[	1	TAISKPYGFGREFDEDBLMARLEBLEQEELDKNLLEISGPETVP
ŀ	1	l .	
	<u> </u>		LPNVPSIALPSKPAKKKEBEDDDMKELENWAGSM
5632	3	952	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
l	l .	1	SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
1	<b>\$</b>	1	FTFVSSADAKDLSGS1ASPDVKLNLGGDF1KESTATTFLRQRGY
l	1	ı	CWLLEVEDDDPEDNKPLLEBLDIDLKDIYYKIRCVLMPMPSLGP
{	ł	t .	NROVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
l	I	Į.	LTIPLLARVICGEVAYGOVLGVIGYSLLPLIVIAPVLLVVGSPB
		ľ	
1	1	l .	VVSTLIKLFGVFWAAYSAASLLVGREFKTKKPLLIYPIFLLYIY
I			FLSLYTGV
5633	771	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
j	1	1	CLPENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
1	İ	f .	LLLLLSGHRPWGSSMV
5634	1446	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
2634	1446	833	ARNTLSSRFRRVDIDEFDENKFVDEQEEAAAAAAEPGPDPSEVD
1	1	}	
1	1	ł	GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
ļ	1	Į.	SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLIQWHEK
i	i	1	ALAVGGLGSIIRVLTARKTV
5635	3	· 943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1 2000	1	1	RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
1	1	1	1 1 1 - 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1	1	1	GVRRAVLQLPGLTQVRWSRYSPEPKDPLIDXEYYRKPVEELTEE
1	1	1	RKYVRBLKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
l	l .	Į	LARSLMIQTLEAVKRKQFEKYHAASABBQATIERNPYTIFHQAL
1	1	ſ	KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
1			KKHORTLMPEKLSHKLLEAFHINGGPVIKRKHDLHKMARANRALA
1	1	1,	HYRWW
L	<del></del>	<del> </del>	
5636	2253	1143	LEDTICQHPPAEKKLYLYHRKLREVKRNGIPRLPKDVPMDTHQG
1		1	LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
I	1		ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
}	}	}	YGSERDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMQSSGFD
f	ĺ	l .	ALLHEIQEIRETQARLEESPETLKEHYQRDYSLIMQTLQEERYR
1	1	•	
ł	1		CERLBEQUIDLTBLHQNEILINLKQELASMEEKIAYQSYERARDI
1	l .		QEALEACOTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
I	1	į .	LLAVMAVLLVFUSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
i	1		HWDALFSYVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
3037	240	2334	1
	l .	1	HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG
ł		t	QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
	Ì	L .	
			QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFQNL
			VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFERIYVVTE
			VSCKRVPRELKMLCPPKHDNVLSALDIIQPPHIDYPERIYVVTE LMQSDLHKIIVSPQPLSSDHVKVPLYQILRGLKYLHSAGILHRD
			VSCKRVPRELKMLCPPKHDNVLSALDIIQPPHIDYFERIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
			VSCKRVPRELKMLCPPKHDNVLSALDIIQPPHIDYFEBIYVVTE IMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA PEILMGSRHYSNAIDIWSVGCIFAELLGRRILPQAQSPIQQLDL
			VSCKRVPRELKMLCPPKHDNVLSALDIIQPPHIDYFERIYVVTE LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA

Prediction   Prediction   Proceedings   Prediction   Processing   Prediction   Processing   Prediction   Processing   Prediction   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Processing   Pr		1 2 37 5 3	The Hotel and	Lamino hold commont containing cional poptide
No.	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding   corresponding   corresponding   cofirst   amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   residue of amino acid   resid				
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1092   QQGKKTMLSHTMKKQKQQATAIMKZVIGNVDGMDLGKKVS   IPRD_MLBELSHLSNRGARLFKMRQRRSDKYTFENFQYQSRAQI   MRSIAMQNGKVDGSNLBGGSQQAD-LTPFNTEPPRSPPNPNIA   GYSGPLKEIPPEKPNTTAVPKYQSPHBQAISNDFELLBALYPK   LFKPBGKARLPYNFRYSPRNAQIFSEKASRWYKKVPDFELLL   LTDPRFMSFVNPLSGRRSFNRKPKVDFFELL   LTDPRFMSFVNPLSGRRSFNRKFVKDFFELL   LTDPRFMSFVNPLSGRRSFNRKVKVDFFELL   LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT   VPRSRDL   CRINCREDVKLLSNQMDKLFAFHLFTFHGLLEFLDGSIQKLIQA   EIILSDNSSILVLENNFLFFKVKSKQFIHLIAKKFYISITIVSAS   NGBSFVLSMIVTO   TERCHDFILVELFYLASVLMGLVLICVCSKTHSLKGLARGGAQ   IFSCI_PRCLQRAMIGGLHTJFHTRHTTFIVLHLVLQCMVTTEY   TWEFFGYCOBLEISLHYLLBYLLVHLUNGFFFTLTCSTNPGIIT   KANELLFLHVYEFDSVMPPKNVRCSTCDLRKRARSKHCSVCTMC   VHRPDHHCWWNNCIGAWNIRYFLIVLTLTASAATVAIVSTTF   LYBLVWMSDLYQETYIDDLGHLHWDTVFLLQYLLTFFRIVPM   LSPUVILSFLLGGYLLFVLYJLAATNQTTMEWYRGDWANCQRCPL   VAMPPBAEPQVIRRI HSHGLISBLYGTJFYDRFCHRKQB   TWERGFYTLASGRAPQVATGHTBHGKLGSNJGVDFFFTLIGTRRQB   RVQGDMCATIGVDPJASKGFFFRGYBFTLAPBFCHERKQB   RVQGDMCATIGVDPJASKGFFRGYBGYDGYTLAGGYLTVS   EIKASLKWBTERARQVLEHLLKGGLAWLDJQAFGARHWLPALF   TDLYSGETTABERGPTLAGGLAGGTAKKKLAAAK   ALGTGFGI IPVGGTYLLQSVPARLNMDHTVVLQLABKKQYDTVS   EIKASLKWBTERARQVLEHLLKGGLAWLDJQAFGARHWLPALF   TDLYSGETTABGSVQLATTSVGSTGTLSSVGJWLAPFTAGISLSITAAGY   GLGLASATAGIASSIVENTYTRSAELFAGRLYTATSTDQLEARLRD   TEKNHGGCVIANVSGSTGTLSSVGJWLAPFTAGISLSITAAGY   GLGLASATAGIASSIVENTYTRSAELFAGRLATATSTDQLEARLRD   TVLYIRVFRVILSFRADPRIVRKNARATGRPLIANG   GLGLASATAGIASSIVENTYTRSAELFAGRLATATSTDQLEARLRD   VOSVRDLKRLSFPDPDFGGSGRAVITLRRASGQVPTL   VOSVRDLKRLSFPDPDFGGSGRAVITLRRASGGVPTLANG   STAGGGAQ   AGKPAPCTYTLIRAB IPPAFKRASSGVIATIADP   AGKPAPCTYTLIRAB IPPAFKRASSFFYCTFRELEYLIGF   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYSAICHPQKEGTGNSRSFTCTPELFPRLQTHL   LSLLKFHVHVSVSYS	İ		ſ	
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BHSIAMQNGKVDGSNLEGGSQQAPLTPPNTPDPRSPPPNTALP GYSGPLKEIPPEKPNTTAVRYQSPBQAISNDPELLBALYPK LPKPBGKARLPDYRSFNRVATPPGGFEKASRAVKKVEDFELLL LTDPRFMSFVNPLSGRRSFNRTPKGWISENIPIVITTEPTDDTT VPBSEDL  5641 27 332 CRINCAGDVKLLSNOMDKLFAFHLPTFHGLLHFLDGSIQKLIQA EIILSDNSSILVLENNFLPKVKSKQFIHLIAKKFYISITIVSAS NGBSPVLSMIVTG  199 1247 ITPCRMDFIVJEIPYLASVLMGLVLICVCSKTHSLKGLARGGAQ IFSCI-PECLGRAMIGGLHTJFHYRNHTFIVJHLVLQGMVTTBY TWEVFGYCOBLELSLHYLLDFYLLFYRNHTFIVJHLVLQGMVTTBY TWEVFGYCOBLELSLHYLLLBYLLJFPHLAGNAUFFFFILTGATNPGIIT KANKLLFLHVYEFDEVMPPKNVRCSTCDLRKPARSKHCSVCNWC WHRDHHCWWNNCIGAWN IRYFLIVJUTITASAATVALVSTTF LYHLVWADSLYGETYIDDLGHLHMVPFLIGVYLFTPRIVFM LGFVVVLSPLLGGYLLPVLYLAATNQTTNEWYRCDWAWCQRCPL VAMPPSAEPQURRN HEHHGLRSMLGHIFLFAPCHERKQB FRUGFDDMCATIGVDPLASGKGFWSEMIGVGDPYRSLGVQIIEVC LALKHRNGGLTTLEBLHQQVLKGRAPQDVSGDDLIRAIKKLAEAK YKKRGTVLAEDQLAQMSKQLDMFKINLEEFASKHKQEIRRNPEF RVQFQDMCATIGVDPLASGKGFWSEMIGVGDPYRSLGVQIIEVC LALKHRNGGLITLEBLHQQVLKGRAPQDVSGDDLIRAIKKLA ALGTGFGIIPVGGTYLIQSVPABLIMDHTVVLQLAEKGGVVTVS BIKASLKWBTERRRQVIEHLLKEGLAWLDLQAFGBAHYWLFALF TDLYSGLSTTABERRAED  5644 83 1138 PRRWGSWQLITSVGVQQNBCWTVAGQYGBKRRFTEEVIEYFQ KKVSPVHLKILLTSDRAWKRFVRVAELPREADALYBALKNLTP VANIBUKMQCKBQOFREWFLKRFPQIRKKIQESIERLRVIANS IEXWHRGCVIANVVSGSTGILSVIGWALAPFTAGLSIITAAGV GLGASATAGIASSIVENTYTRSAELTASRITATSTDQLEALRD LIEDITPNVLSFALDFDEATMIANDVHTLRRSKATVORPLIAM RYVPINVVSFALDFDEATMIANDVHTLRRSKATVORPLIAM RYVPINVVSFALDFDDEATMIANDVHTLRRSKATVORPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYVPINVSTALDFDDEATMIANDLHTLRSKATVGRPLIAM RYPPINVLSFALDFDDEATMIANDLHTLRSKATVGRPLIAM RYPPINVSFALDFDDEATMIANDLHTLRSKATTSDLYCHLDSLKGG UNDATTSDLYCHGDEATMIANDLHTLRDSLKGG SGGASATGRTYTTALLRASIPPATRASFLSSFIRMFPBELVSLTTADD AGKRAPCRYTTALLRASIPPANGRAFSLSSFIRMFPBELVSLTTADD AGKRAPCRYTTALLRASIPPATRASFLSSFIRMFPBEL	5640	280	1092	QQGNKKTMLSHNTMMKQRKQQATAIMKZVHGNDVDGMDLGKKVS
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S642   199   1247   ITPERMOFIVITE, FYLASVIMOLIVLICVCSKTHSLKGLARGGAQ   IFSCI.PSCI, PSCI, CRAMIGLILHYLEHTRINHTF IVLHILVLAGMYTRY   TWEVFGYCOBLELSHYLLLPYLLLGVNLFF FTLTCGTNPGI IT   KARKILJEHHYVEFDEVMPPKNVRCSTCOLRKBARSKHCSVCNMC   VHRPDHHCVWVNNCIGAWN IRYFLI YVLTITASAATVAT USTTF   LVHLVVMSDLYQETYIDDLGHLHVMDTVPLIQYLFLTFPRIVPM   LSFVVVLSFILGGYILLFVLYLAATMOJTTMEWYRGDMAWCQRCPL   VAWPPSAEPQVHRN HSHGLRSNLQBI FLPAPPCHERKKQB   YKBRGTVLAEDQLAQMSKQLDMFKINLBEFASKHKQEIRKNPEF   RVQFQDMCATIGVDPLASGKGFMSMIGVGDFYYELGVCII LBC   LALKHRNGGLTLTLEELHQVLKGRGKPAQDVSQDDLIRAIKKLAEAK   YKBRGTVLAEDQLAQMSKQLDMFKINLBEFASKHKQEIRKNPEF   RVQFQDMCATIGVDPLASGKGFMSMIGVGDPYYELGVCII LBC   LALKHRNGGLITLBELHQVLKGRGKPAQDVSQDDLIRAIKKCAEAK   YKBRGTVLAEDQLAQMSKQLDMFKINLBEFASKHKQEIRKNPEF   RVQFQDMCATIGVDPLASGKGFMSMIGVGDPYYELGVCII LBC   LALKHRNGGLITLBELHQVLKGRGKPAQDVSQDDLIRAIKKCAEAK   YKBRGTVLAEDQULKGRGKPAQDVSQDDLIRAIKKCAEAK   YKBRGTVLAEDQULKGRGKPAQDVSQDDLIRAIKKCAEAK   YKBRGTVLAEDQULKGRGKFAQDVSQDDLIRAIKKCAEAK   YKBRGTVLAEGGLAWLDLQAFGGBAHYWLPALF   TDLYSQEITABEARKADVLEHLIKEGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLIKEGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLIKEGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLIKEGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLIKEGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLKGGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLKGGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLKGGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLKGGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARQVLEHLKGGLAWLDLQAEKNGYUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETBERARGAEKNGUTVS   EIKASLKNETS   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EIKASLKST   EI	5641	27	332	CRHNCNGDVKLLSNQMDKLFAFHLFTFHGLLHFLLGSIQKLIQA
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5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVITKAATPPPLVLSLTTADP AGKPAPCRVTLITLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKPHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	5645	537	799	
5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVITKAATPPPLVLSLTTADP AGKPAPCRVTLITLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKPHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ  5647 288 800 GVINATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	}	YLCLONSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD
AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ  5647 288 800 GVIMATSELSCEVSERNCERREAFWAEWKDLTLSTRPEEGCSLH	5646	3745	3328	AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP
LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSERNCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	1	AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFERLEYILGF
RAEGGAQ  5647 288 800 GVIMATSELSCEVSERNCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	1	LSLLKFHVHVSVYSAICHFOKEGTGNSRSFTCTPELFPRLOTHL
5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	Í	
EESTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY	EFAT	1 200	800	CHIMATERI.SCRUSERNORDREARWARWEDI.TI.STRORRICCSI.H
PERIODE LINGUE CONTRACTOR TO THE PERIODE CONTRACTOR TO THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE PERIOD OF THE	304/	200	1 300	DEDITODRICTY/UOCOCOUT. UOD COUT. MADMCTT CDCI.ORVOT.DV
	L		<del></del>	DDTAMETTINKOACATAKINE INTERPRETATION

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
•	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		<del> </del>	ORVLPLPIPTPAKMGATKEEREDTPIQLQELLALBTALGGQCVD
	1		ROBVAEITKOLPPVVPVSKPGALRRSLSRSMSQEAQRG
5648	1 7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLQQAGNTDWSLTM
50.0			APOSLPSSRMAPLGMLIGLLMAACFTFCLSHONLKEFALTNPEK
		Ì	SSTXETERKETKAEEBLDAEVLEVFHPTHEWQALQPGQAVPAGS
	}		HVRLNLQTGKREAKLQYEDKFRNNLKGKRLDININTYTSQDLKS
	İ	l .	ALAKFKEGARMESSKEDKAROAEVKRLFRPIEELKKDFDBLNVV
		İ	IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
	1	j	LLSPGGLQVVINGLNSTEPLVKEYAAFVLGAAPSSNPKVQVBAI
		į.	EGGALOKLLVILATEOPLTAKKKVLFALCSLLRHPPYAORQFLK
		1	LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEREAELT
			QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPRHDAREKV
	1	1	LOTLGVLLTTCRDRYRODPQLGRTLASLQAEYQVLASLBLQDGE
	Ĭ	]	DEGYFOELLGSVNSLLKELR
5649	1172	3006	MIQEQLDAINEEIRMIQEEKESTELRAEBIETRVTSGSMEALNL
5012			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
1		İ	MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
	l .	1	TLRLEKLGHPALSQEBGKSALEDQGSNPSSSNSSQDSLHKGAKR
}	1	1	KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
			VPAKLGTQAKKDRRLKKKHQLLEDARRKEMPFAQWDGPTVVSWL
	İ	<b>.</b> .	ELWVGMPAWYVAACRANVKSGAIMSALSDTBIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
}	ļ	{	TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
	(	ĺ	DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
1	·	}	LEKRREESQHBIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
		1	HGALLALDENFOHNTLALILQIPTONTOARQVMEREFNNLLALG
1		<b>!</b>	TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASABTLPA
	}	1	GFRVSTLGTTQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINERIRMIQEEKESTELRAERIETRVTSGSMEALNL
1			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
ţ	· ·	1	MGVMTLPSDLRKHRRKLLSPVSRBENREDKATIKCETSPPSSPR
			TLRLEKLGHPALSQEBGKSALEDQGSMPSSSNSSQDSLHKGAKR
{		1	KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQRPM
	<u>'</u>		V?AKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
ļ	Į.		ELWVGMPAWYVAACRANVKSGAIMSALSDTEIQREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
l	}		TDSEBGSWAQTLAYGDMNHBWIGNEWLPSLGLPQYRSYFMBCLV
	ì		DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCDKRLNYDRKE
ĺ			LEXRRESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
ŀ	İ		HGALLALDENFOHNTLALILQIPTONTQARQVMERBFNNLLALG
ļ	1		TDRKLDDGDDKVFRAPSWRKRFRPREHHGRGGMLSASAETLPA
	<u> </u>		GFRVSTIGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5651	646	1869	ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
1	1		AWGEGAGIR+ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1			WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
l	ł	ľ	ADP+LPGHSSQSPPRG+RWGRSRSAPAPAHPEHPAPAGSASASQ
ļ	ļ	Į.	QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
ļ	ļ	•	PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
	l .		PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
l	1		GWRAGISPBLLGAAGLSDNWARCPGPGPAR*GGQPGCRTIPASA
1	i	1	CMPSPPVEGSLGLSRKGHGDLPSQAR+GWHECRRARHLVPLPRL
		<u> </u>	LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
l		1	CEPCARSFRISSNLVIHRRIHTGEKPLOCEICGFTCRQKASLNW
L	<b> </b>		HORKHABTVAALRFPCBFCGKRFBKPDSVAAHRSKSHPALLLA
5653	66	1401	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
	İ		CFPQPCQPGTRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
	1		GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
l		1	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SEDVIQ
L	L	<u> L</u>	GWLLBLQPRRSLYRGHLVR+FARRSRKSSEV+YCHQRGKSHGMQ
L		<del></del>	X

SEQ	Predicted	Predicted end	Drive acid compart containing signal postiling
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	
I NO.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
			H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ES*IKERTQSCVHRPHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
ľ			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
		•	PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSOSTY
1	ł		LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
İ			ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIQHOK
1	•	1	THAANV
5654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINORRDSVRMSAL
	}	1	NWKPFVYGGLASITABCGTFPIDLTKTRFQIQGQTNDAKFKRII
í	ļ	j	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
I	1	i	
	1		PRLHRSQVKSLRCV+KEQIA++/MFSLLISTLISKYIYYAADVL
5655	ļ		KKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPRQLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
1		1	PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGGDPELC
1	1	1	ATDEMIPFKDEGDPQ\REKIFABIVNPEEEGDLADIKSSLVNES
	1	l	EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
1	1	1 -	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
	ŀ		AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
			PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
1	1		LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
			PSNMNAFMENLKKNIHLRTSYSELVGF%SVBFGGRTNKVPHIWK
İ			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
i	İ	j	NSKLQKPPKRGVYELAVFQMKPGGPALWGDAPERATNAHVNLGY
	<b> </b>		TKVVGVPHTEYGELNRVHVLWWNRSADSRAAVRHKSHEDPISWG
ŀ	<b>\</b> .	•	GVRBSVNYL\VSQQNM
5657	105	1052	GORLOSPRVOMPVOPPSKOTEEMEAEGDSAARMNGEEEKSEEER
1	•	1	SGSQTESEEESSEMDDEDYERRRSECVSEMLDLKKQFSELKEXL
]		Į	FRERLSQLRLRLREVGAERAPEYTEPLGGLQRSLKIRIQVAGIY
		1	KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
ł	ł	ľ	LEEDROSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
l			PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1 .			GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
ŀ			ALVWTPPL
5658	2346	3541	
1 2020	2340	3247	TERRVYNPWPBPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
ł			NOLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
1	l		RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
l .			RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIBGSRQA
1			LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
1			PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
1	1		TAVKIDQLIRPINA_DELCRLMKSFVHPKPGAAGSVGAGLIPIS
1			SELCYRLGACOMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
1			IMQATDIMRKQGPRVEILAKNLRVKDQMPQGAPRLYRLCQPKMN
			GDL
5659	2	696	wkrsgevspkgelgawrgnsgrpkligraabaenedrtlgrllp
1			GNERSQPRSPLRLLAPQLKARAAADKGLAPVPPPPFSSGHSGPC\
			EREGEGORGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPAEVA
1			AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
1			BDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
1			FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
		-	CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
j l		•	QRKAFPHHRFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
†			TAASLPLLMVYFINFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
<b>,</b>	•		
5661	2	477	PYGTYPREPFLVLHILLQVFLFCLCVFPDPFW
2007	4	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAKAPLPVTVRGSGL
	1		AGMAVTCDPKAFLSICPVTLVFLQLPLASICQN*GTDSCASRGK
			ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
			SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRERGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
L			PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ı	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
I	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	i -	\=possible nucleotide insertion)
	<del>                                     </del>	· · · · · · · · · · · · · · · · · · ·	LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
	I		QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
			NVLGSILRIRSRATAAIHSFFKDSGFVHIHTPIITSNDSEGAGE
1		-	LFQLEPSGKLKVPRKNPFNVPAFLTVSGQLHLEVMSGAFTQVFT
1	ĺ	İ	FGPTFRAENSQSRRHLAEFYMIRAEISFVDSLQDLMQVIBELFK
f	[	<b>{</b>	ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
			AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGPQELEGSVA+HSLGLMILLSIVVIGOP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
1.			VQSYFEKGPLTFRDVATEFSLEBWQCLDSAQQGLYRKVMLRNYR
Į.			NLVFLGIALTKPDLITCLEQGKBPWNIKRHEMVAKPPVICSHFP
			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDRCKVH
			KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTQKEAALRALVQRTGYSLVQENGQRKYG
İ			GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
ŀ			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYBIRNGRLLGV
			CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLI ILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
i .			ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
<u></u>			ANGHPQQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNQDQPVPFNSSHPDEYKIAALVFYSCIFII
			GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
			PYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
i	· !		ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMPAYACQR
1	<b>,</b>		PTPLTHHNTGLSEALBILABAAGFEGSEGRLLTFCRAASVLKAL
			PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEERAVLVGGRWSPSLDGLDPQADPQ
5669	407		VLVRTAIRCAQAQTGIDLSGCTKW
3669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
·			ADSRFNDRYAHKSAQLYFLYFVCWIFQDVYYFTIKEKNHFFFPK
i			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMQLQKL NSO
5670	3	373	1
3070	,	373	SSECLTMAWIPLILIPLLILCTVSVASYRLAQPSSVSVSPGQTAK ITCSGDVLAKKYARWFQQKPGQAFVLVIYKDTERPSGIPERFSG
ł	1		
5671	280	524	STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
20/1	200	3 <b>24</b>	KFPPKKTPPHLGMESAITLWQFLLQLLLDQKHEHLICWTSNDGE FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRILLFMT
5672	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNLPAKDITGS
1 -50.2		331	SDPYCIVKVDNBPIIRTATVWKTLCPFNGEEYQVHLPPTFHAVA
			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLPSHTGLPSP
1	j !		1
			WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS   OAWLLLPLP
5673	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
	J/	0,70	KLSSOTLIQAGDDEKNORTITVNPAHMGKAFKVMNELRSKOLLC
			DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
5674	17	984	GGGSMEGESTSAVLSGFVLGALAFOHLNTDSDTEGFLLGEVEGE
		J	AKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYNSSGEVNEQA
	l l		LKKILSNVKKNVVGWYKFRRHSDQIMTFRBRLLHKNLOEHFSNO
	ļ		DLVFLLLTPSIITESCSTHRLEHSLYKPOKGLFHRVPLVVANLG
			MSEQLGYKTVSGSCMSTGFSRAVOTHSSKFFEEDGSLKEVHKIN
	i i		EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
j	]		MFLKVAVTTTTISM
5675	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
			KSGVPVSAPGSDGKWWBERPGMFSLMASCCGWFKRWREPVRKVT
			LLMVGLDNAGKTATAKGIQGEYPEDVAPTVGFSKINLRQGKFEV
	.]		TIFDLGGGIRIRGIWKNYYABSYGVIFVVDSSDEERMEETKEAM
	L		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
		1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
		İ	HKCL
5676	2	930	FVSSPPPRPVOPARPGGFGLSGRRSLLCOVASTPAHVGVMRSPV
	}		RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
			PPIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
	i		HNOTGKKYOWDAETOGNILGSFFYGYIITQIPGGYVASKIGGKM
i		l	1
			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
	1	1	MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	1		WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
	<u>                                       </u>		L
5677	ī	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
1		1	VTARTHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
l			GRSLPGLTAATMSSFSESALEKKLSBLSNSQQSVQTLSLWLIHH
		1	RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEP
	1	ĺ	TREFESVLVDAFSHVARRADEGCKKPLERLLNIWQERSVYGGEF
		l	IQQLKLSMEDSKSFPPKATEEKKSLKRTFQQIQEEEDDDYPGSY-
	1	· ·	SPODPSAGPLLTERLIKALODLENAASGDATVROKIASLPOEVO
j	1		DVSLLEKITDKBAABRLSKTVDBACLRNRGPGTS
5678	3	593	SSSPESTPSLPLPFYLLLGOLRLOLLMGTAHLSGAGEAAPCPG
5678	3	593	
	Į	ł	GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
	1 .	j	SLAEFTEOFNOLHNRRNENLOLGPLGRDPPOECSTFSPTDSGEB
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
			AAALQPDFDVSKRLSLPMDI
5679	2	623	LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGR
			DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
			LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
			FDPRKADSIFTEEGETPAWLBOMIAHTTWRDLFYKLABAHPDCL
	l	}	MINFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLONRNSHTPLESLIHPQPSYKGFGIMFGKKKKKIE
3000	1	]	ISGPSNFKHRVHTGFDPQKQKFTGLPQQWHSLLADTANRPKPMV
-			DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
2091	45	869	
		}	ROTRPORLRKRAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
	i	İ	FTSAGLWIVYFIAVKDDKILPLNSAERKPGVKHAPYISIAGDDP
	į		PASCVFSQVMNMAAFLALVVAVLRYIQLKPKVLNPWLNISGLVA
	1		LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
			QGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
		1	QKINGTIHCQVCPGAPANPGSPWHEEMGLLLLVPLLLLPGSYGL
			PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYO
			GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
		1	LRHRSPGDYQGRVHLRQD
FC03		720	
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
	1	İ	HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
			ATYCTVCSKKPASPNAYENHLKSRRHVELEKKAVQAVNRKVEMM
			NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
			EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
	ļ		SEDREHDLC
5684	195	677	TWCFRGYLGPRVIMKALDBPPYLTVGTDVSAKYRGAFCEAKIKT
		1	AKRLVKVKVTFRHDSSTVBVQDDHIKGPLKVGAIVEVKNLDGAY
			OBAVINKLTDASWYTVVFDDGDEKTLRR99LCLKGERHFAESET
	į.		
	<u></u>		LDQLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLQQPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
			VKQEHPHTDSDLMHVKPQHEQRKEQEPKRPHIKKPLNAFMLYMK
			EMRANUVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
	1		RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWOVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
			PHEAKLMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF
ı	d		THE SHOW A A CAT DOWN THE WASTON STATE AND THE TA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
MO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
)	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ŀ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible mucleotide insertion)
			QNLPFVAEVLEGIPAGVSIYQVVAIDLDEGLNGLVSYRMPVGMP
}			RMDYLINSSSCVVVTTTELDRERIAEYQLRVVASDAGTPTKSST
		l	STLTIHVLDVNDETPTFFPAVYNVSVSEDVPR\GSGWSG*AARN
i		Í	NDVGLNABLSYFITGGNVDGKPSVGYRDAVVRTVVGLDRETTAA
L		L	YMLILEAIDNGPVGKRHTGTATVFVTVLDVNDKRPIILQSSYV
5687	17	917	AAPPAPPDG/PPP/PPPAPPT/PGPAA/APASSCQPRLSAGRAA
			QGDGGAAAVGHVLVVPAVGPVRVNPGLQTPVPRPBLLPGP\SSS
)		i	LHSDSSYPPDAGLSDDEEPPDASLPPDPPPLTVP/ADA/PMPVT
			SGCRMPSTSASE/AAGCQGACTHAKGSETPPPASPQTSEPAPSP
1		1	LPPHLTCGPGMYSSEAKLPNSFSCLGLAGTGAGI*GTASAHGTG
[		i	PPVLPHVCTPSLANPQP\AVGPBASSLPLGVSGIGMSA/SAPIS
1		1	SSPFVAIGSCWLRGIPPPGSGFLCPGRAPGPVPITTHGQEGQGP
l		<u> </u>	VLDI
5688	1	420	LTKWDLFGRCYRLLKTGIEHGAMPEQVGVYWYS/CLYDSRKLFP
l		1	+SHMIIRSLL+KVIDDSLGQLPLLRELLL++LNVIDRCIILAYV
ſ		}	LRVEKTFAITYLKNFTVKVDFSLLGBIPLISMAAILKLWIMKID
F600		ļ	DGYIPAVF
5689	1504	3	HRLSGKHISMVSGNTCNWHPGGHSPGGGCQGEITSKDRGEIPAL
			TWA/RKPIGTWTATKPTHRAG*GGAEEYQPPFQPCBGPRSTSRG
<b>\</b>	1	<b>5</b>	GEG*GHAVGPGREIGKEGSLPFLGPKALGF*SASCQRAFEGGAH GSTARKPAPATPGTRHPRTMETREVAQGWPAGPRSQFWDQHPHS
	ļ	1	PGEHRPSG\SPLPACPPRAWPKAGAVASATGTG\PQLPGSRGKQ
			KLPRTREPPLLQAGWAVRKPPWSEAKEGLGQAGRPSGMDSSAS\
ļ			POTPGGRGSLEWGLPLYLGPHHDVK*RSDRLG*PP*GGQGGGGH
1		,	GAPSTPGPGGEAW*LPQQTSRPKPGPQAY*GE\GSPGLQCPCSK
		· ·	EL*RVPPGSLGPSTQCMYEPTDKHS\GGADAQLEVSTAGSRSTF
	1	4.4	GOELKGPLDAGRLWPGAPSASSSHR*GG*ERARAGAGHRGST*A
ļ ·			SSKIEGGRPRPGPTSDALADVEGGAES/GPHPWPLPGTLPNR/P
<b>!</b> .	· ·	1	GSPPPA*ASAGRKGTVSTLGGGLL
5690	1424	58	PSPPAGVCAAPAPLPLLALARRDRRPCSPGARAAPWQTGGPAID
1			GAWRTSVSALRRGATG/APCSPGARAAPWQTGGPAIDG\DGELP
1			*VRSBEAPRGCGAEGGGPGSGPVRRPGAGRGAHAGQGRQQDPEP
{	i		DGLRHRQHGAASHARHRLQRLRPGHHQNRHVRRDPQAPPGGPAP
1		1	GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPRH
1		<b>{</b>	PTFQGRAGS\GQPGYQPPNPHPGPSSPPAAP\GPRGA*GNPQLE
1	1	1	KAPRSDRNPSQGLRTRIRRPETPDCGPPSPAGSSASASTFRCTS
1	1 .	1	SLSLLGP/PGAHNLDTAPQDR+HGP+GDKRGAPGVAGEDPRPP+
1	1	ĺ	GNFVR+LLLMP/GVA+RHGTSPFLGPSLGENGCQWDSGNLFGTP
1	1	<b>!</b>	kg*shpaftkst*smearksywnhphr\drgrogvrinclrvge
1		1	SEMWGPYSAPRPGTVFLSSPLSPASEEH\PEGSSSFNTPFPPAG
			PEGDPGLNSPGLLP
5691	107	550	ISNDPSPGYNIEQMAKRGKKLVELPYTVKGMDVSFSG-LSFIED
İ	i	ł	VAHRMLATGECTPEDLCFSLQVMQ*KTGTESWG*RFYIVEQN*S
ł	ſ		GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG
L		L	GVGVYVLLRSVPLSYS
5692	1193	548	TQAWTRAEKDRKGSVRALRLHLRRGPPT*RGSHPL\QSVPCIQK
1	l'	ļ	PSIPSSYPI/GLPQSGGEPGPVGEQQPVRRPEQPSCGPASRMPL
Ī	1	J	TSRSVPPGRGALPPDSLSTRRGLPRPSTAGHRVRESGHKVPVSQ
ļ	ļ	l	RLNLPVMGATRSNLQPPRKVAVPGPTR*RDQDSKQDFSSKPLQS
L			VPGLASTQQTLTPADSGPGTGGRDATRAGLPGVBTMGNGVD
5693	1258	1330	ALTVVPVRKGTTWWAQPHGCSNLVSRARLDLSSRPSQNTEPQAP
1		1	*QAGPPSSLRPP\SRRR*APEWPKRATGSRCRGLSAPPWPWPAA
l	Į.	l	RGE/PGSAPSHAP/PNSPRPSGTRHP/PGPSSRVLYSPSLPRNS
1		l	PEAIVWRSSRFPLWFPLRCCFWVSGFKDPNPVLRFF
5694	3	1338	GSKRPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
		1	QRCL\nnlssbefnassslnslpstptasrrnstivlrtdsbkr
Ì		I	SLAESGLSWESESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES
ł		l	CDDSSKEGELKKPISLGHPGSLEKGKTPPVAVTSPITHTAQSAL
ļ	1	1	KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
]		}	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
	<u> </u>		<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W-Trustophon V-Truston V Tolerand
	amino acid	sequence	W-Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
1	sequence	bequence	
	bequence		\=possible nucleotide insertion)
	İ		KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1		ŀ	VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
i			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
ł			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5695	3	1338	GSKBPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLARSGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1		•	CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKBPTKVASGRTT
i			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
i l			PTATKLABLPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
1 1			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1			SLABSGLSWFSESERKAPKKLEYDSGSLKMEPGTSKWRRERPES
1			CDDSSKGGBLKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
			KVACKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
			IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1			VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKRPTKVASGRTT
l i			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1 1		i	PTATKLAKLPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
1 1			DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
1 1		ı	QGPATVQSVBDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
1 1			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
1 1			SSEKEAKVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
1 1			RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
] ]	1		EGPIAAQMLSFVMDDPDPESEGSDTQRRADDFPVRDDPSDVTDE
1 1	•		DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
ļ		·	EGKTPSKENKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEER
1	i		RRQQRPPRSRERTAA
5698	2	666	GARAABPORDLPPLSQSSRFFOROOKMNKSLGPVSPKDVAVDFT
1 }	i		QREWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEO
1 1			GREPWIVEGRPLLQSYPDEVWQTDDLIERIQERENKPSRQTVPI
į l	1		ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
	ł	J	NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
1	<b>;</b>		FNO
5699		1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
	- 1		ENTINES CONTROL AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST AND CONTROL DESCRIPTION OF TARREST
1	i		EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA RPS/GRTNAPPPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
	. I	•	DSQRSSSKGSGWBTPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
j (	·		THIS CARCER CONDUCTION OF THE PROPERTY AND THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE
1 1	ĺ		TWLVCGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS+HLDPNT
, ,	l		WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
			VPILFONPSGALRSRRTEPAGWVPPTRHE+DDG+TAAPASGGAP
1 1			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
1		j	GGSLGCR/SMLPASSGPPPAPGPRRLAAGAUTSASARCPPAAAA
[ [	ł	Į	GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
[		<b>_</b>	HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
<u></u>			FPPGRG
5700	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSPPPPTPNSARS
		]	KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSB
5701	59	410	IFEKICSDTORFISPKINPOICSWLIFDKGAK/NHATGKDSLFN
ļ J		1	KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
<u> </u>	1	1	LEENTGENLHDTGLGNVPLDMTPKTQPTKQK

Beginning   mucleotide   location   corresponding   to first   amino acid   residue of   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   amino acid   residue of   residue of   amino acid   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   residue of   resid	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Docation   Corresponding				
location   cofirst   anino acid   maino acid   maino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino acid   anino ac				Glutamic Acid. F=Phenylalanine. G=Glycine.
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SIDNVAPRRP+LPPQPQMEVPPQPIMAVSPQPPMEASLQPLMGE SPQP  5705  23  562  GDVEFDSPYMDDISQAAKDLVTRLMEVEQDQRITAEEATSHEMI SCRAASDANIKDGVCAQIERNFARAKNKKAVRVTTIMKRIRAPE QSSTAAAQSASATDTATPGAAGGATAAAASGATSAEGDAARAA KSDNVAPRRP+LPPQPQMEVPPQPLMAVSPQPPMEASLQPIMGE SPQP  5706  1161  610  QJGRFXAQDTVAIRKVKEVFGTGAMEHVVILFTHKED*GQQALD DYVANTINCSLKDLVRECERRYCAFNNWGSVEEQRQQAELLAV IBELGREREGSPHENDLPLDAQLLQRTGAGACQBDYRQYQAKVE WQVEKKKQELRENESSWAYKALLRVEHLMLLHYEIFVFLLLCSI LFFIITLF  5707  28  609  GSPAPTFGFRRPGRGTPSFGTRHHQGRAEPEPDAPBRAPLRR* MFAIQRGLABGCQFLGDPPPGLCOPBLQFDSKSAMFMASAKDANR NMHGMGRGVUPILRRSSSESPSDNQAFQARGSFEEGVRSPPEGA RIPGAEPERWGGASTVCSPLEDNGYASSSLSIDGRSSSPEPACG TPRGPGPPDDLLBVAQA  5708  44  1925  SSEMETISFCPFKMFAEPWHLSPVSLGAGMEGGPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTDGGGAGSDPQARPKP PRCPFTAMPSPRTKQRVRNKVCLLIAIRTSDLPSDVSKAP\GPA GNPHDRSSTAA*JHJRRAGACLSASLLPSFSSLGARGAPGL RVSPASGGPRKEGQGGG*AGGGQP\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SGGGGGGGAMPPVCSSDLLRPPTSVSGTG RAG*CSWQPAACCTFRCS*Q*NAVARSPSRCSRN*RQSGR*RG*S* SGRRRGP*AAGRSTPAVP*PCS*CGAGRRAYACRTGWGYAPSR* LEPSOPTSGSAL*TWASHSTGA**SRLCTAGTGPLCSGSSRS* GGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AARSELSPRGSGSSSY*SHDNINGTWPAPPSACHLLVGG*NS QRTSSDH*YTGTREPAAGPSTRCSTAPSRAPPVSRCRPPPPP PPRPPRLPAAAS/SGGASGSPAASCSCCRAPAKPASS/GBAPA PPPRPSEPPPPARRP  5709  2 2031  TILCPLPQTEKCINVVTEAATPLGIYLKARVEAGGLKKLEISWG LHQIVVRNGAVVWRAGAVVFRAAMPAPPAPN/NALSFLVNDCS	l .			SGNAASDKNIKDGVCAQIEKNPARAKWKKAVRVTTLMKRLRAPR
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5705  23  562  GDYEFDSPYWDDISQAAKDLUTRLMEVEDDQRITAEEAISHEWI SGMAASDKNIKDGWCAQIEKNFRARKNKKAVRYTTIMKRIKRAFE QSSTAAAQSASATDTATPEDAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP*LPPQPQMEVPPQPIMAVSPQPPMEBSLQPIMGE SPQP  5706  1161  610  OLGEPXAQDTVAIRKVKEVFGTGAMEHVVILFTHKED*GGQALD DYVANTDNCSLKDLVRECERRYCAFNNWGSVEEQRQQAELLAV IERLGRERGSFHENDLFLDAQLLQRTGAGACQBDYRQYQAKVE WQWEKHKQELRENESNWAYKALLRVKHIMLLHYEIFVPLLCSI LFFIIFLF  5707  28  609  GSPAFTGFRRRPGRGTPSPGTRHGGRABPEPDAPBRAPLRR* MPAIQPGLAEGGQFLGDPPPGLCQPELQPBSNSNFMASAKDANR NHIGMGRGRVBFILRRSSSESPSDNQAPGAPGSPESGVRSPPSGA EIPGABPERWGGASTVCSPLEDNGYASSSLSIDGRSSSPBPACG TPRGGBPDPLLPSVAQA  5708  44  1925  SFSWERTISPCFPKMPARFWMLSPVSLGAAGWPGQPRPYLDLPA QASVSRPHDRA*GRAVSLSLSSGDVCGHTDGGGAGSDPQARKPP PRCPFTAMPSPRTKQKVNIKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSFSLGAGASPPL RVSPASGGPRREGRGSGG*AGGGD\ARTHADLPCVGFVCSPP LLK*SDSPVKQLPA\SQGGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACTTPRSQ*MAVARSPSRCSRW*RQSGR*RG*S SRRRGG*AAGGSPRFSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACTTPRSQ*MAVARSPSRCSRW*RQSGR*RG*S SRRRGG*AAGGSPSPSSPSAHCLSWSGGRTPGAESH*L AG*RCCCTAASPCGGSGPSFSPSSPSAHCLSWSGGRTPGAESH*L ARSELSPRPGSGSRGSY*SHINDNWGTWPAPPAPSAGHLLVGG*NS GRGRSDH*YTGTRRPWAGGTRCSTAPSTAPPAPPAPSAGHLLVGG*NS GRGSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLVGG*NS GRGSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLUVGG*NS GRGSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLUVGG*NS GRGSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLUVGG*NS GRGSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLUVGG*NS GRTSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHLUVGG*NS GRTSSDH*YTGTRRPWAGGTRCSTAPSRAPPVSRCHCRPPPPP PPPPREPPPARRP PPPREPPPARRP  PPRPSPPPARRP S709  2  2031  ITLCPLPQTRGCWCMAPFAPK/RALSFLVNDCS			•	KSDNVAPRRP+LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGR
SGNAASDKNIKDGVCAQIEKNFARAKMKKAVRYTTIMKRLRAFE QSSTAAAQSASATDTATTGAAGGATAAAASGATSAPEGDAARAA KSDNVAPRRP * LPPQPQMEVPPQPIMAVSPQPPMEASLQPIMGE SPQP  5706 1161 610 OLGEFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD DYVANTDNCSLKDLVRECERRYCAFNNWGSVEEQRQQAELLAV LERLIGERREGSFHENDLFLDAQLLQRTGAGACQBDYRQYQAKVE WQVEKHKQELRENESNWAYKALLRVKHIMLLHYEIFVPLLLCSI LFFIIFLF  5707 28 609 GSPAPTSGFRRPGRGTPSPGTRHHQGRABPEPDAPBRAPLRR* MFAIQPGLABGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANR NNHGMPGRVBPILRRSSSESPSDNGAPQAPGSPEBGVRSPPPGA EICABPRHWGGAFVCSPJEDNGYASSLSIDGRSSSPBPACG TPRGPGPPDPLLPSVAQA  5708 44 1925 SSEMERTISPCPFMPARPFWHISPVLGAAGMPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTGGGAGSDPQAKPKP PRCPFTAMPSPRTKQKVMKVCLLIAIRYSDIPSDVKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPPSPSLGAAGAPPC RVSPASGGPRKGRGCGGGACMPPVGSSDILPPRPTSVGGTG RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACCTGWGYAPSR* LEPSGPTSGSAL*TWASHSTGA**SRLGGTATGGPLCSGSRS* AG*RCCCTAASPCGSGSPSHPGSPSAHCLSWSGGRTGPRAPSAH GGGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGFTGAGRSHTLK AARSRLSPRGSGSGSY*SHNDNWGTWPAPPSAGHLLVGG*NS GRRSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP PPRPRILPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GRAPA PPPREBPPPPARRP  5709 2 2031 ITLCPLPQTBRCLMVVTGAATPLGTYLKARVEAGGLKKLEISWG LHQIVVNWGAVVMRACMGGCKCWWAPPAPN/NALSFLVNDCS	į .			SPQP
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KSDNVAPRRP*LPPQFQMEVPPQPLMAVSPQPPMEASLQPLMSE SPQP  OLGREYXAQDTVAIRKUKEVFGTGAMEHUVILPTHKED*GGQALD DYVANTDNCSLKDLVRECERRY CAFMINGSVEEGRQCQAELLAV IEBLIGERENGS FHSHDLPLDAQLLQRTGAGAQBDYRQYQAKVE WQVEKHKQELRENESHMAYKALLRVKHLMLHYEIFVFLLLCSI LFFIIFLF  5707 28 609 GSPAPTPGFRRPGRGTPSPGTKHQGRAEFEPDAPERAPLRR* MFALQPGLABGGGTLCQBLQPDSSSMFMASAKDANR NINGMPGRVEPLLRSSSESPSDNQAPQAPGSPEEGRVESPPEGA EIPGAEPEKMGAGTVCSPLEDNGYASSSLSIDERSSSPEPACG TPRGPGPPDFLLPSVAQA  5708 44 1925 SFSWEETISPCFPKMPAEPWMLSPVSLGAAGMPGQPRPYLDLPA QASVSRPHDRA*GEAVSLSLSSGDVCGHTUGGGAGSDPQARFNP PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA GNPHDRSSTAA*LHRRAGAGSLCLSASLLPSPSSLGAPGAPSPL LLK*SDSPVKQLPA\SGGGSGAMPPVGSSDILRPRPTSVSGTG RAAG*CSWQPAACCTPRSQ*NAVARSPSRCSRM*RQSGR*RG*S SRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR* LEPSGPTSGSAL*TMASHSTGA**SRLCGTAGTGPLCSQSSES* AG*RCCCTAASPCGGSGPSPPSSAHCLSWSGGRTQPRAPSAH GGGRAMGSRCVCTCTGLPCPGIPLSGASPGSGETGAGRSHTLK AAPSRLSPRPGSGSRGY*SHNDNWGTWPAPPSAGHLLVGG*NS QRTSSHM*YTGTRRPWAGPGTRCSTAPSRAPPVSRCRPPPPPP PPRPPRLPAARS/SGGASGSPAASCSCSCRAPAKPASS/GRAPA PPPRPPPPAARP  5709 2 2031 ITLCPLPQTBKCLMVVTRAATPLGIYLKARVEAGGLKELEISWG LHQIVVRMGAVVMRAGMGGCRCWGWAPPAPK/NALSFLVNDCS	<u> </u>			SGNAASDKNIKDGVCAQIEKNFARAKNKKAVRVTTLMKRLRAPE
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Section   Predicted on mucleotide   Cocation   Corresponding   Corresponding   Control   Cocation   Corresponding   Corresponding   Corresponding   Control   Cocation   Corresponding   Corresponding   Control   Cocation   Corresponding   Control   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Cocation   Coc			19715	
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S710   1   562   IPGSTISCEVELMARMAKTIDSPTQNQTELVVIIDGLDACEONK   VIQMLDITVRUIPSKEPITALFASDPHILIIKAINQMIANSVESGFK   VIQMLDITVRUIPSKEPITALFASDPHILIIKAINQMIANSVESGFK   VIQMLDITVRUIPSKEPITALFASDPHILIIKAINQMIANSVESGFK   VIQMLDITEPHRATIALGK*(NIJVASQE)IDG*DAIGEFLIVV   CIAIQPNINKDDAT   CIAIQPNINKDDAT   CIAIQPNINKDDAT   REPEPENTATORORASHIDVAFTSTFVLFYFDSAQFFIVKSESS   SQLAKAVLSQQRESLFHECAPHPFS*SLQRHTINLDQGIP*LLM   LSEBRQHLFBSS/IWTTPHNLK*/PEHHEHLGSHEGIWTLFFTL   QIL   CIAIQPNINKDDAT   CIAIQPNINKDDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT   CIAIQPNINKDAT	j	l		
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VLQMLDTVRULPERIGRETAL FRASDPILITIANIONIANSVESEK (LAGRIBLYRM VVLLPUPLINSKEL), FOO /LORDET LAGOMET FLA QUILOGYRMLTEEPHRTALGR *QNLVARQPS IDG* DAIGPELVV CIAIQPNINKDDAT  5711 1526 1130 REIPPOWITTVORARSHIBUVAFTSTPVLFYPDSAQPFIVKSESS SQIAKAVLSQQRPSLFHECAPHPFS* SLQRIFTINLDQGIP* LLM LSERRQHLFBSS/ INTTHINLK* / PSIHERIGSHSGHTLFPLL QIL  5712 3 1391 GRKLFQSILDISKELKFLLGLDCVDUTLI VILAREHGCLDITKELD ETVIDI.INKCLTPHPSKRPTPDELMRDKVPSEVSPLYTPPTKDA SLPSSSLRCADITLPBDISQLCTORINDYLARSI LERVYLINCL AGGDLEK KLUNKEI ITRSKPD CILINENTYLARSI LERVYLINCL AGGDLEK KLUNKEI ITRSKPD CILINENTYLEBGISFROQGRORSS/  TFR* YHNDIVUNBAKK* 1ERCMGRS ILD ITLKHTSLLFYSNIN NELSAAATLPLITERDTEVQLART ILLDYSNIN NELSAAATLPLITERDTEVQLART ILLDYSNIN NELSAAATLPLITERDTEVQLART ILLDYSNIN NELSAAATLPLITERDTEVQLART ILLDYSNIN NELSAAATLPLITERDTEVQLART ILLDYSNIN NELSAAATLPLITERDTEVGLART PROTICEMEN FOR STOPPLITER PILINENTYD FLORING EVOIPPCIGVORELLSSPREGARKFRULKAWVSHPDLVYNGGLD SLCAPPLVIANFNERALVYACHSPLAYDAINCHYD FUNDRELLSPART PROTICEMEM TARCKGRRGAQVOHLPRBIARAVSHINDLKAVPKGGLIGK EVOIPPCIGVORELLSSPREGAKKFRULKAWVSHPDLVYNGGLD SLCAPPLVIANFNERALVYACHSPLAYDAINCHYD FUNDRELIFYDD FLORING EVOIPPCIGVORELSSPREGAKKFRULKAWVSHPDLVYNGGLD SLCAPPLVIANFNERALVYACHSPLAYDAINCHYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUNDRELIFYD FUND				
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SQIAKAVLSQQPSLIFIECAPHPES*SLQRIPINLDQGIF*LLM LSERQHLFBSS/INTPRINLK*/FBIHRHLGSHBGHWTLFFLL QIL  5712  3 1391 GRKLFGSLDISERLKFLLTLDCVDDTLIVLAERHGCLDIIKELP KTVIDI.INKCIT-PIPEKRPYPDEBLKMDKWFSLVSPLYTPFTKPA SLPSSLRCADLTLPEDISQLCKDINNDYLAERSIEBVYVLWCL AGGDLEKELVNKEIIRSKPPICTLENFIFIEBGSFQGGBRSS/ TFF*YWHDIVVNPAKK*IERCKGPSLPFTLKMTSLLILPYSNSN NELSAAATLPLIIREKDTEYQLNRIILIPRLLKAYPVKNQUKK EARVDIPPLMRGLTWAALLGWEGATLEVTLKMTSLLILPYSNSN NELSAAATLPLIIREKDTEYQLNRIILIPRLLKAYPVKNQUKK EARVDIPPLMRGLTWAALLGWEGATLEVATLKWAVVSHPDLVYWQGLD SLCAPPLYINFNNRALLGWEGATLEVATLWFFLKDNSHVIGEY LTVFSGMIAPHIPPELSSHHLBEIGFPIDLYATEWHETHVPFL HKIFHLW\DTTLLGEFLPPILYWE  5713  634  284  PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGFMEGH TACKGSRRGAQVQHLPREDIRABE*DPHLREWNFGLPTSSATSP *RAVITSPCSHIGSADAASSHHLCGVSPH TACKGSRRGAQVQHLPREDIRABE*DPHLREWNFGLPTSSATSP *RAVITSPCSHIGSADAASSHHLCGVSPH *RAVITSPCSHIGSADAASSHHLCGVSPH SSRGSSGSGGGBWAGESADKATAAAAASLLANGHDLAAA MA  5715  131  1979  ESASQGRRSKCILILTLKLELSGSAPKKTSARPGSSLWLPPHSOR QTPPASKLQGGGGLQTGMGHENPTAASPLPRICLFGAVAX' GLRGP*LCPSGAA/GGLQRGFGLSPLGAAGKVSCHPPSMVRNN DSTCHEHRIEGILAARVTPVF\SGKCGRVLKFPFRVCHPPHPAAS PRPPS/SDLLGGERQDHLRAPPAHGGFWTPHGGERKTFMSS QIRRKETKDL*RKTPAG\NNYQSNSIPUSQSPOLTVDLLPSAGR TQAPSGRGDAKKPTFGHG\LPKASVILTPNCPCSLAGGQ*PPGL PRITTCRGSGHVALQAGHDSARPVSGGRVALQACHDSTQVLGSPT PKYTACGSGHVALQAGHDSARPVSGGRVALQACHDSTQVLGSPT PKYTACGSGHVALQAGHDSARPVSGGRVALQACHDSTQVLGSPT PKYTACGSGHVALQAGHDSARPVSGGRVALQACHDSTQVLGSPT PKYTACGSGHVALQAGHDSARPVSGGRVALQACHDSTQVCRG*PCTUPSTCPSULQFTD*E GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGRACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRRPGGSGCGCACGGREGGACCRE/GG*DPT GLIT/GYDGTDPKRGGRACGGREGGACCRE/GG*DPT CHAPACTESSEWUSENGKGGGRGGACCRE/GG*DPT STOM **CPELLCEGPHGCOGNICLTINTSTNILS	l .	1		CIAIQFNINKDDAT
LSBERQHLFESS/IWTTPHNLK*/PEIHEHLGSHEGHWTLFP*LL  S712  3 1391  GRILFQSLDISERLKFLLTLDCVDDTLIVLAERHGCLDIIKELP KTVIDI.INKCI.FFRPSKRPTDELMKDKVPSSVSPLYTPFTKPA SLPSSLSRCADLTLPRDISQLCKDINDVLAERSIEBEWYLWCI. AGGDLEKELVWERI IRSKPPICTLPNFLFEDGESPGQRDRSS/ TFR*YHWDIVVWPAKK*IREKMORGILPITLKMTSLLLPYSMSN NELSAAATLPLIIREKKDTEYQLMR ILLFYGRLKAYPYKROLUKK EARVDIPPLMRGLTWAALLGVEGAIHAKVDATDKOTFIPTDRQI EVVDIPRCHQYDELLSSPBGHAKFRRVLKAWVSHPDLVYMQGLD SLCAPPILYINFNRBALVYACMSAFT EKYLYMFFLKDMSHVIQEY LTVYSQMLAFHDPELSNHLMBIGFTPDLVAIFWETMFTHVPPL HKIFHLW/DTLLLGEVLFPTLYWE  5713  634  284  PVCAVPVDRWPVLPREDQRGQQL*AKLPRDFRR*FQILGFMEGH TACRCSRRGAQVQHLPREDIRAB*DPHILRERWEGLPTSSATSP *RAVLTSPCSHLGSBADASSHHLCGVSFH  5714  212  613  WGLGLGPTMSSLGGGSQDMGGSSSSSTMGSGSGSSGSKGKAGAAD KSAVVAAAAPASVADDTPPPERRNKSGIISENFAKSIRSRFPLS HYSSFGSSGSGGSGMWGGSSADKATAAAAASLLAMGHLAAA MA  5715  131  1979  SSAQQKRSKCLILTLKLLELGSAPKKTSARPGSSLWLFPHSQR GTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRMCLFGAVAK\ GLRGP*LCPSGAA/GGLQRGFGLSPLGAARGVSCHPPSWYRNN DSTCHKHHIGGILAARVTPVP\SGKPGRVLKYPGRVCEPPIPAAS PRPPGS/SDLGGPRQMHLRAPYBAHGGPVNTPHGGEEKTFMSS QIRRKETKEL*RKTPAG\NNYQSNSTPVSQSPOLTVULLPSAGR TQAPSGRGBAKKPTPGKS\QFRGVSGPPSGPSDLTVULLPSAGR TQAPSGRGBAKKPTPGK\QFRGVALQAEHDSTQVVGRP VHRHIPLS*LGLSRRTQAGHDSARDVSGRVALQAEHDSTQVVGRP VHRHIPLS*LGLSRRTGAGGSGPRGAAACVACQAQLE EGPIRLPGQDRGAQPCSCHCGS*DPT GTT/GVPGTDPRRGGSRRQCGSPAGAAACVACQAQLE EGPIRLPGQDRGAQPCSCHCGS*DPT GTT/GVPGTDPRRGGRRRQGSCGTTCPTVWSGPESPLQDRT*E RQR/VCAGASSGVGLSRGRAGGPSAWWAMMLLLLRHGSHSEL TDLTEAQTSQH  5716  1711  1370  RVPSLLCEGPGHCTQGAVCRRACAAASPGLDSAAEPHRLCEHTD *LPKAGGFIQHEMDSNILCILYNTISMILPSYSF*GVARYAC* RCPLVL*SGFPTIVGGYSCCMPLKT  5717  44  1489  LPTEALRESEWUSEVGKCGFRGLVPEGSSTSPLPSSVDTRDSLD  5717  44  1489  LPTEALRESEWUSEVGKCGFRGLVPEGSSTSPLPSSVDTRDSLD	5711	1526	1130	RRHPFOWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
LSBERQHLFESS/IWTTPHNLK*/PEIHEHLGSHEGHWTLFP*LL  S712  3 1391  GRILFQSLDISERLKFLLTLDCVDDTLIVLAERHGCLDIIKELP KTVIDI.INKCI.FFRPSKRPTDELIMGDKYPSUSPLTTPFTKPA SLFSSLRCADITLFEDISQLCKDINDVLAERSIERVYLWCI. AGGDLEKELVWREI IRSKPPICTLPNFLFEDGESPGQRDRSS/ TFR*YHWDIVVMPAKK*IRKCMGRSILPFTLMTSLLLPYSMSN NELSAAATAPLIIREKUTTPUDARI LLPFYSMSN NELSAAATAPLIIREKUTTPUDARI LLPFYSMSN NELSAAATAPLIIREKUTTPUDARI LLPFYSLMSHULPYSMSN NELSAAATAPLIIREKUTTPUDARI LLPFYSLMSHULPYSMSN EARVDIPPLMRGLTWAALLGVEGAIHAXVDATBOFTPITPGQI EVVDIPRCHQYDELLSSPBCHAKKFRVLKAMVVSHPDLVYMQGLD SLCAPPILYINFPINABLUVYACMSAFTPIKYINFFIKDNSHUIQBY LITVFSQMLAPHDPELSNHLMBIGFTPDLYAITPWFLTMFTHVPPL HKIFHLM\DTLLIGEPLPPILYWR TACKCSRRGAQVQHLPREDIRAB*DPHILRERWBGLDTSSATSP *RAVITSPCSHLGSBADASSHHLICTGVSPH  5713  634  284  PVCAVPVDRWPULBREDIRAB*DPHILRERWBGLTTSSATSP *RAVITSPCSHLGSBADASSHHLICTGVSPH  TACKCSRRGAQVQHLPREDIRAB*DPHILRERWBGLTTSSATSP *RAVITSPCSHLGSBADASSHHLICTGVSPH  *HYSPGSSGGGGGSMWGGSSADKATAAAAAASLLAMGULAAA MA  5714  131  1979  ESASQQKRSKCLILTLKLLELSGSAPKKTSARPGSSLWLPPHSQB CYPPASKLQGGGGGLQTGWGLHPVPVTAASPLPRMCLFGAVAK\ GLEGP*LCPSGAA/GGLQRGFGLSPLGAARGVSCLHPPSWVRN DSTCHKHHIGGILAARVTPVP\SGKPGRVLKVPPHPAAS PRPPGS/SDLLGGPPQMHLRAPYAAHGGPVNTPHGGEEKTFMSS QIERKETKPL*RKTPAG\NNYQSMSIPVSQSPGLTVULLPSAGR TQAPSGRGBACKPTPGK\QLAPBAADASSHLICGGPPTQUVGRP VMRTPLIS*LGLSRENTQATRRGLWSGRVALQACHDSTQUVGRP VWRTPLIS*LGLSRENTQATRRGLWSGRVALQACHDSTQUVGRP VWRTPLIS*LGLSRENTQATRRGLWSGRVALQACHDSTQUVGRP VWRTPLIS*GRIVALQACHDSTQUVGRP VWRTPLIS*GRIVALQACHDSTQUVGRP VWRTPLIS*GRIVALQACHDSTQUVGRP VWRTPLIS*GRIVALQACHDSTQUVGRP VWRTPLIS*LGLSRENTQATRRGLWSGRVALQACHDSTQUVGRP VWRTPLIS*LGLSRENTQATRRGLWSGRVALQACHDSTQUVGRP VWRTPLIS*GRIVALQACHDSTQUVGRP VRTACIGSGRIVALQACHDSTQUVGRP VRTACIGSGRVALQACHDSTQUVGRP VRTACIGSGRVALQACHDSTQUVGRP VRTACIGSGRVALGACHSAGQPSGRAACVACQADLE GGPILLPGQDGRAQPCSCCGR*CDTTCTVWSGEESPLQPKP*E RQB/VGAGASSSVGLSRGRGGPSSAWKVAAMLLLLERGSHSEL TDLTEAQTSQH  5716  1711  1370  RVPSLLCEBPCHCTQGAVCREACAAASPGLBSAAPRRLCCHTD *LPKAGGFGIOHFEGDSNILCILIYNISMLFSYSF*GVARYAC* RCPLVL*SGPPTIVGGYSCCMPLKT  TALLFRAGTSCH  **LPKAGGGGGM**CREACAAASPGLBSAA		1		· · · · · · · · · · · · · · · · ·
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TILTEAQTSQH	1	1	Ī	GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
TILTEAQTSQH	I		I	RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSRL
5716 1711 1370 RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD  *LPK*GPGY1QHFHCDSN1LCILYNISFNLPSYSF*GVARYAC* RCPLVL*SGFFTI1VGGYSCCMPLKT  5717 44 1489 LPTRALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	i		I	
*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYAC* RCPLVL*SGFFTIIVGGYSCCMPLKT  5717 44 1489 LPTRALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	5716	1711	1370	
RCPLVL*SGFFTIIVGGYSCCMPLKT 5717 44 1489 LPTRALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	3/10		1	
5717 44 1489 LPTRALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD	ŀ	1	Ì	
		<del> </del>	1.22	
EGPGALVLESDILLGQDLEFEREEREERGDGNSDQLMGFERDSR	5717	44	1489	
	L	<u> </u>	<u></u>	RGPGALVLESDHLLGQDLEFEREEKEEGDGNSDQLMGFERDSB

( and	F8-37-4-3	1 - 31 - 3	
SBQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=Glutamic Acid, F=Phenylalanine, G=Glycine,
, NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	*amino acid	sequence	Codon, /=possible nucleotide deletion.
1	sequence	} "	\=possible nucleotide insertion)
	1		GDSLGARPGLPYGLSDDESGGGRALSABSEVEEPARGPGEARGE
1		1	RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
1			SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
1	Ì	ĺ	EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
ľ	ļ	i	RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
1	ļ	ļ	Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQKLERGEGSRLG
	1		AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
}	1		RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGEKPYKCPL
5718	120	284	CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
2,79	120	284	VAHALSLPABSYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT S**STADPLHL
5719	48	428	BLNNGPFQMPLCNGGNLAVTGSMADRSPLHRAASQGRLLALRTL
1 3/13	30	740	LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLEAGANVNAIT
1			IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	1	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
			\RCT\YYE\TCGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
Ī	[		GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE/SGGGSAFSD
			Y\SSSVPSTPSISQRELRIETIAASSTPIPIRKQSKRRSNIFTS
}			RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
l	<u> </u>		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
1			KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
ļ.			LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
5721	97	492	QHPASG
3/21	]	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
	l i		QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
1			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
ŀ			PPPPPHLGALTAGSGEERQSQPRAKTLRLGRGAPLP\PRAERGG
			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGMAGAILGPRVHGTRAVLRVARGGVQAPGAP
}			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRGPRFP
			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
			GRPRRAAAAPGRAPADPQPPAPRPAPADVRPPADAPAPAPA
ĺ			PPPPPHLGALTAGSGEERQSQPRAETLRIGGGAPLP\PRABRGG
[			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
			KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLINFK
			KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVABBAADLDGBID
			LSACYDVTBYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
			MKHVHPTTAPDVTSSLPBEKNKSSCSFETCPRPTEKQEAELGEP
			DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP
			ADTH\DPWRPEARHGELERBRARREBRRKRFGMLDATDGPGTE
			DAALRMEVDRSPGLPMSDLKTHNVHVKIEQRWHQVETTPLREEK
			QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSQKEASDLLEQ
	i		NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHQKKIE
			DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME RELEKSQRSQISSVNSDVEALRRQYLERLQSVQRELEVLSEQYS
		:	QKCLENAHLAQALBABRQALRQCQRBNQELNAHNQBLNNRLAAB
		I	ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTOLC
			TORPOGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEO
5725	3	1049	VNGHSEBTSQSPNRTEPHDSDCSVDLGISKSTEDLSPOKSGPVG
		*****	SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLOPLK/FTSAVEG
			KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
			PB/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA
	· · · · · · · · · · · · · · · · · · ·		

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i .	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNPSNHN
		Ĭ	NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
	ĺ		SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
1			SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
ı		1	TSP
5726	2	486	SRSLSMWWNSGLPASSHSSKLPVTVGFSGCVKRLRLHGRPLGAP
3,20	_	900	
İ			TRMAGVTPCILGPLEAGLPFPGSGGVITL/ESVGAGIPGPSRAG
İ	}	1	QGSPGGSGEGPPLSSPSQPLPADLPGATLPDVGLELEVRPLAVT
F222	ļ		GLIPHLGQARTPPYLQLQVTEKQVLLRADDG
5727	21	221	RPILILKETRRLPWATGYAEVINAGKSTHNEDQASCEVLTVKKK
			AGAVTSTPNRNSSKRRSSLPNGE
5728	2	877	GTRNGQFEPRRGRAWEGSAGGLRAPGAAAGGPGVQPRGSG/LPG
1		1	NAIRAGVNPGRGPASPFWDLSLPWDLWPPPTDHAPGAPDPPAVE
1	!	1	GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
[	1	]	GGPAGAGGDAG/LPGRCPSAPWRAGSRPAASCPDWIPGPQGLWL
	į		HRNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
1	[	ł	BPPQVPRAGEEDAVPAKEGPGGTPETQADQVRERPKAHLAEGGA
L			KGSPRRLADPQDLPAGQMSLAPPFPPVAAVIRSNK
5729	1	1525	AGGAREVLTLQLGHFAGFVGAHWWNQQDAALGRATDSKEPPGEL
<b>1</b> 1	i	Í	CPDVLYRTGRTLHGQETYTPRLILMDLKGSLSSLKREGGLYRDK
1			QLDAAIAWQGKLTTHKBBLYPKNPYLQDFLSAEGVLSSDGVWRV
			KSIPNGKGSSPLPTATTPKPLIPTEASIRVWSDFLRVHLHPRSI
i			CMIQKYNHDGEAGRLEAFGQGESVLKEPKYQEELEDRLHFYVEE
			CDYLQGFQILCDLHDGFSGVGAKAAELLQDEYSGRGIITWGLLP
Į.			GPYHRGBAQRNIYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR
			PEPPVSFPYLHYDATLPFHCSAILATALDTVTCS\YRLCSSPVS
			MVHL\ADMLSFCGKKVVTAGAIIPFPLAPGQSLPDSLMQFGGAT
			PWTPLSACGEPSGTRCFAQSVVLRGIDRACHTSQLTPGTPPPSA
1 1			LHACTTGERILAQYLQQQQPGVMSSSHLLLTPCRVAPPYPHLFS
			SCSPPGMVLDGSPKGAAVESVPVFG
5730	1258	1713	KKFQAPARETCVECQKTVYPMERLLANQQVFHISCFRCSYCNNK
1			LSLGTYASLHGRIYCKPHFNQLFKSKGNYDEGFGHRPHKDLWAT
			KIETEGFWERPRNFENCGRPLKSPGGEDCPSC*GGCPGSNY*AQ
			GSSSREKGGQASWNPKLRVA
5731	122	443	RSHRGELIPKDSCYMRKPPRRPKKRRQG/CALPQGCLTFKDVAI
			BFSLBEWKCLNPAQRALYRAVMLENYRNLESVGLTSKDSWYMRK
1 1		•	KPGRGRGKQRRQEWFFLRVY
5732	226	772	PPSRSCQSPRRKSRRRAHVTVTLVCGFTSFSFSLPLYLCGCLRF
	İ		PERTCSQLQQADWAPDFGPSSFVPSWGATATGARKFLIAFNI\N
]			LLGTKEQAHRIALNLREQGRGKDQPGRLXKVQGIGWYLDEKNLA
			QVSTNLLDFEVTALHTVYRETCREAQELSLFVVGSQLVGLVPLK
			ALLDAA
5733	1	460	PALQEVNANALAWGKQYENDARTLFEFTSGVNDTESPIIYRDES
			MRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYM
			AQVQYSMWVTRKNANYFANYDPRMKREGLHYVVIERDEKYM\AS
			FDEI\VP\EFIGKMDEVLSRDPM
5734	3	968	RCNSPESLTSLLVLLTTANNLFVLIPAYSKNRAYAIF?IVFTVI
	-	200	GSLFLMNLLTAIIYSQFRGYLMKSLQTSLFRRRLGTRAAFBVLS
			SMVGEGGAPPQAVGVKPQNLLQVLQKVQLDSSHKQAMMEKVRSY
}			
			GSVLLSAKEFQKLFNELDRSVVKEHPPRPEYQSPFLQSAQFLFG
			HYYFDYLGNLIALANLVSICVFLVLDADVLPAERDDFILGILNC
			VFIVYYLLEMLRVFALGLRGYLSYPSNVFDGLLTVVLLVLEIS
	ļ		TL\VCTDCHTQAGGRRWW/RLLSLWDMTRMLNMLIVFRFLRIIP
- case			SMKPMAVVASTVLGL
5735	2	540	PFTPCVARAFNFPDQATVKKAAYSLPRVGGGTSCGLPQARRISL
	i		ATPRQLYK/SSNMTQRWQRREISNFEYLMPLNTLAGRTYNDLNQ
			YPVFPWVLTNYESBELDL/TLPGNFRDLSKPIGALNPKRAVFYAE
			RYETWEDDQSPPYHYNTHYSTATSTLSWLVRIVSIFIBLACLWY
			LKILT
5736	1	382	GTRPSTKKSGYSPQQVAVIHCKGHQKENTAVAHSNQKADSAAQV

SEO	Predicted	Predicted end	Amino poid garment containing signal news in-
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	ведиелсе	ļ	\=possible nucleotide insertion)
			TARLSVTPPNLLPTVSFPQPDLPDNPVYSTTTRKLASDLRANKN
			QES**ILPDSGIFIP*T*TSYLQSTTHLRRAKLPQLLRR
5737	290	1041	KACLHLLSSFLTSNFLFNPLLPDSLYSVRARSQRANLGPCRRKR
ł	1		LQTLMRLAAGFQYSSHKDPSLSAKEKETDYHNEARGPWPGWVG*
1			RTADGSCGRGPDGAHHPGPKSSSWRASRLLPGLGGSHHLDAYVG
	ľ		RDLECGTPAPLQLEIPPQPRGHPAPIPTGQAGPRDSGPGASP*V
			BTRPLTDGRR*PGVRPVGWTPAHPAGTLRPRGAVEPSVSACGKW
5020			APSPTSQGCCEGRCDAVPKHRAWRTPLCSQ
5738	8	460	DTLSINCTLPETLPMTPSF*LSFL*FPGLARAKSIPTKTYSNEV
Į.	l	}	VTLNYRPPDILLGSTDYSTQIDMN*GQVEVWQGPCGKGGGLVTT
1			ATQPAAFLFTVPSLPRGVGCIFYEMATGRPLFPGSTVEEQLHFI
5739	1	1222	FRILSERAWALCAVETHR
",5"	1 -	1 22	SFORRGIRWNVHTLHPHPRAVWAGIGRGHGS*ALLGRARAPALC PPTLLEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISD'LLAEV
			SAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKI
	I	i	LQCQGFYQLCGVHQKDVIYLALPLYHMSGSLLGIVGCMGIGATV
1	1		VLKSKPSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPPSKAKRG
1	l		HKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINY
			TGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATS
İ			PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
1			TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFRALDF
L			LQRVNVYGVTV
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
		ı	YVYERVYN*DISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
			LQSELHKLYDBETQSWVSGSACGGYP
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
			YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
			EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAORYVV
Į .			ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	TQSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVQDLLDAG
	_		TYVNIPDRSGDTVLIGAVRGGHVBIVRALLQKYADIDIRGQDNK
			TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	GKTPEGIDAIKEIBIDLBETERKISPQENGLKEVKPLGEMQTDL
[			KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE
		•	VKPVDEMETDLKTTGREGSSREKTREVIDAAEVIETDLEETERE
L			ISPQE
5744	3	703	TRRTTTTSPTTTRQMTTTPAALPTTVVTTPDLTTGTPLQMTTIA
1			VFTTANTCLSLTPSTLPERATGLLTPEPSKEGP1LTARSETVLP
]		į	SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
			POPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMITAP
	i		SIGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
ETAE	1400		QHGREDEDGLFTL
5745	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
<b>i</b> .	İ		KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
]			VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
j l			YICGSHGVEHRVYKHFSSINSTSTHQASHKQIHQKRKRHPERGR
			EKSEEBRSKHKRKKSCBEIDLDKHKSIQRKKTEVBIETVHVSTE KLKNRKEKKSRDVVSKKBERKRTKKKKEQGQERTEEEMLWDQSI
]			LGF
5746	3	821	SPASGRLTPSSPAFDGELDLORYSNGPAVSANSLGMGAVSWSRS
	-		RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARILLE
į		1	LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP
[			YCKGKPRTSABRERHLHILHRPWKCGLCSFGSSQBEELLHHSLT
	ľ		AHGAPERPLAATSAAPPPQPQPQPPPPQPKPRSVPQPEPEPQPER
[			BATPTPAPAAPERPPAPPEFRCOVCGOSFTOSWFLKGHMRKHKA
			SPDHACPV
5747	2	1328	DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
3,3,			
3,4,			PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTBPQKRNTE
3,4,			PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTBPQKRNTE BSSSPVRKESSRGRHREKEDIKITKERTPESEEENVEWETNRDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
í	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	bequence	\=possible nucleotide insertion)
	Bequence		SDNGDINYDYVHELSLEMKROKIQRELMKLEQENMEKREEIIIK
1	1		KEVSPEVVRSKISPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
i	j	J	AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKE
1		1	KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
İ		l	ISSRHHSSSSOSGSSIORHSPSPRRKRTPSPSYORTLTPPLRRS
i			ASPYPSHSLS89ORKOSPPRHRSPMREKGRHDHERTSQSHDRRH
1			ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
ĺ	1		RR
5740	934	473	SEGPOVFYKGLAPTLIAIFPYAGLOFSCYSSLKHLYKWAIPAEG
5748	934	1 4/3	KKNENLONLLCGSCAGVISKTLTYPLDLFKKRLQVGGPRHARAA
ł	i	}	· ·
1			FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
L			FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLARRPRGMIRSGSFRDPTDDVHGSVLSLAS
1	1	I	SASSTYSSAEERMQSEQIRKLRRELESSQRKVATLTSQLSANAN
1	1	[	LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
		1	SRAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
	<del> </del>	L	GSSKDADA  IFISICLWNAHLCFLLLPKDCIDQVMKLQNLFVDDSGRYLAIQF
5750	22	866	
ļ .		Ì	IILEWAYVFLYYYBYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
1		i	QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
1			ILNDIKLADCEQFQMPDLCABEIAIILGICTNFQKNNPVHTLTE
1			VELLAFTSCLLSQPKFWAIQTSALILRTKLBKGSTRRVBRAMRQ
			TOALADQPEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIFEKLEMWK
5751	3	751	SCGSALRAWRCGAAALATFPAPALFGLMYRALYAFRSABPNALA
1			PAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLQGLEQ
		1	DVLQAIDRAIBAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
I		[	SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPPVKRRDREA LMASGSGGHNTMPSGGNSVSSGSSVSSCI
F350	<u> </u>	471	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGARLPCLSGAAT
5752	3	4/1	VEREMELRHKNEMLRVETEARARAKAERENADIIREQIRLKASE
1		:	HROTVLESIRTAGT_FGEGPRAFVTDRDKVTATVNIFIKQGWQV
	1	ł	AEROHVGASWSPRSCPCRLCTAL
	<u> </u>	102	
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
		ľ	GOEAFKKINYIDIGEIKKRPMEVVNTRVKPVIHSRINVSARFRK
l	ļ		PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
L			TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEFAGEHARATASREQEVLQGWKELLSACEDARLHVSST
		1	ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
	<u> </u>		WPTPATPSPLTAPFSME
5755	3	888	LGDQFYKBAIBHCRSYNSRLCABRSVRLPFLDSQTGVAQNNCYI
1		1	WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
l			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
1	1	1	RVLENDENVERGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
l	1		AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDBAQ
1	1	1	DOETRSPPNHRNENHRPOKGPDGTVTPNNYCDFCLGGSNMNKKS
		·	GRPEELVSCADCGRSAHLGGEGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPERPPLLGAEDSLLASQEALRYYRRKVAR
1		]	WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
1			SSPVVSKLLQDMRHFPTISADYSQDBKALLGACDCTQIVKPSGV
1	1	l	HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
	L		AAFHLDRILDPRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
1			LSISQSVHVAVKVPPLIQPFEPPPASIGQLLYIPCVVSSGDMPI
i	1		RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
1	1	!	ASNAAATVSRRRQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGBFKVHRVRFFNYVPSGIRCVA
	[		YNNOSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
	1		WARGORLFSAGLNGRIMEYDLQALNIKYAMDAFGGPIWSMAASP
<u> </u>	<del></del>	·····	L

	<u> </u>		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to Eirst	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	
			SGSQLLVGCEDGSVKLFQITPDKIPV
5759	2	1240	GNAAFAGQGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
	[	1	MARSSPYPTDVARVVNAPIFHVNADDPBAVIYVCSVAAEWRNTF
	İ		NKDVGADLVCYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA
		ļ	DKLIAEGTVTLQEFEEEIAKYDRICBRAYGRSKDKKILHIKHWL
	i		DSPWPGFFNVDGRPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
	1	1	KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
	1	ļ	NGODVERGTFSHREHVLHDOEVDRRTCVPMNHLWPDQAPYTVCN
	ļ	<b> </b>	SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
		ł	ISTGQAKWYRHIGIYLLLPHGMEGMGPEHSSARPERFLQMSNDD
	1	}	
		<u> </u>	SDAYPAFTKDF3VSQL
576C	1	1221	VRDITSDSLSLSWTVPRGQFDHFLVQFKNGDGQPKAVRVPGHED
		I	GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
	]	]	PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
	1	)	LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
		}	CRVGPVSAIGVTAABBETPTPTBPSMBAPBPPBEPLLGELTVTG
	ł	(	SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGBESEVT
	į.		VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
	1		TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
	ł	1	VOYKORDGRPOAVRVGGQESKVTVRGLBPGRKYKMHLYGLHEGR
	1	i	RIGPVSAIGVT
			SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
5761	3	1275	
	ľ	ŀ	VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
	4	<b>,</b>	RALGAQIBKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
	İ	1	AEKEQKRLERLORKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
			GMQAASSKMVSAEISENRKRQWPTKSQTDRQASAGKRRCFWLGM
		,	EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
		1	FPSGSQRARVVNTDHGSPRQLQIPVTDSGRHILEDSCAELGESK
		1	KHMESRMVTETEETOEKKAESKEPIREEPTGAGLNKDKETEERT
	1	1	DGERVAEVAPRERENVAVAKLORSOPGNAVIDKETIDLLAFTSV
	1		ARLELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGOTPLHSQGGGGGGGGGRRTPRGMPKEKYEPPDPRRMYTI
3/02	1	233	MSSEBAANGKKSHWABLEISGKVRSLSASLWSLTHLTALHLSDN
	Į.	1	SLSRIPSDIAKLHNLVYLDLSSNKIR
	<u> </u>		
5763	3	129	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGERTTGRVRINV
	1	1	LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
	1	ł	ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
	l		TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEBIVSVRGFSLEEK
	1		LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
	1	i	MPDPDPTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
	1	1	TPEAORDKL
5765	3	825	QKILRLNNSHQPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
3,05		""	VOASAPOGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
	1		STGKROKYOGRPGRATGMNSALGQSVSSGGSGNPNSNSTSTSTS
	1	1	
1	1	Ī	AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
Ī	1	1	GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
ł	1	1	GEVSKSAPDSGLMONSMLVKKBEREEBSHRRIKKLKTEKVDPLF
1	1	1	TVPAPPPHV
5766	1608	663	SGLFSVDPASSQAMBLSDVTLTEGVGNKVMVVAGVVVLTLALVL
1			AMLSTYVADSGSNQLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
!	[		PTELPHPSEGNDRKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
	1	Ì	IOGLPKROAGAGSSSPHAPLRSEDSTCLPPSPGLITVRLKFLND
	Ī		TERLAVARPEDTYGALKSKYFFGQESQMKLIYQGRLLQDPARTL
]	l .	1	
}	1	1	RSINITONCVIHCHRSPPGSAVPGPSASIAPSATEPPSIGVNVG
	ŀ		SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVPPSFLV
1	}	i	FGMYGR
5767	2	892	NPRATPRPPTRPELRTGTEVILWYLDWRALMKRKRMKANIKLVG
1	1	į	SGPPLPSSDLDDSLTEBIDEKIGFRNDANFDWQNVADFRDAGGS
l	J		LTEVKVEREERDPQSPBYEIEEEBEMLSSVIPDSRRENBLPDFP
	•	1	

SEO	T D 31 3	Predicted end	
ID	Predicted		Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyxosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<b></b>		<del> </del>	HIDBFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
ľ	1	<u> </u>	
		}	LQVEKERLQIEKERLRHLDMEHERLQLEKERLQIEREKLRLQIV
t		<u> </u>	NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
			FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
		i	AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAREPSNKRVKPL
1			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSBSRPDILAPRP
j	}	}	WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
1		• • • • • • • • • • • • • • • • • • • •	TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
	1	ļ ·	
1			DRCVEVIAKEGONLKELYLVSCKITDYALIAIGRYSMTIETVDV
}	1		GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
<u> </u>	<u> </u>		PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
I	[		FASQLKKTSLSLTPDVPEADLSEVDPKLVSNLMPFQRAGVNFAI
1			AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
I	1		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYNVTLRSKLGPLEIOOPAMLLRE
]			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
l	1		LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
Į.			AFHRLLADITHDIB
5772	148	202	
3772	146	383	RFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
L			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
Į.			KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
			DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
1			LROYNIVGLHTNIDFLLNLSGHPEFRAGNVHTDFIPQHHKOLLL
ļ. ·	l i		SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSSG
ŀ			RRLNISYTRNMTLKDGKNSK
5774	· 2	592	FVERENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
	_		VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
			KLPKSSSQRVEAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
FREE			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPV8KCPKKSBSLWKGWDRKAQRNGL
j l			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
i i			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
			BGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
1			RP
5776	2	484	REPODCYCONESESECTECPSKGLEFVPPDIDRRTVELREGGNF
i i			IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
]			DSNRLPSLGEDTLRGLVNLQHLIVNNNQLGGIADEAFEDFLLTL
] .			EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	
~′′′	-	747	GODPEPGODLFOPEREVDPSWGRGREPRIGKLRFONDRISVLKO
1			VXKLEQALKDGSAGLDPQLPGTCYSPHCPPDKARAGSTLPENLG
ļ			GGSGSKVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
1			YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
·			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYBFE
			DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
ł			YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFPRQ
		i	MSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
	-	1210	
			GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1		•	WAPLGAPERPEHLINRVLERLAGGATRDSAASDILLDDIVLTHS
			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
			YQGLLQEBEGAGHIIKDLYLLIMKDBSLYQGLREDTLRLHQLVE
			TVELKIPBENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
			CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
	•		LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYRALV
	<del></del>		

ama	1 6 37		
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ	sequence		\=possible nucleotide insertion)
			PLPKEIQVSPGDTEIHRVEPEDVANHLTAFHWELFRCVHELEFV
į.		•	DYVFHGE
5779	138	1671	RAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCAEVIIPLLS
1			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
1	ł	1	ALHWAAYMGHLDVVALLINHGABVTCKDKKGYTPLHAAASNGOI
i	j		NVVKHLLNLGVBIDBINVYGNTALHIACYNGQDAVVNELIDYGA
		ļ	NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
i		1	SPLHMTAVHGRFTRSQTLIQNGGEIDCVDKDGNTFLHVAARYGH
Ī	ļ		RLLINTLITSGADTAKCGIHSMFPLHLAALNAHSDCCRKLLSSG
1			QKYSIVSLPSNEHVLSAGFEIDTPDKFGRTCLHAAAAGGNVECI
			KLLQSSGADFHKKDKCGRTPLHYAAANCHFHCIETLVTTGANVN
1			ETDDWGRTALHYAAASDMDRNKTILGNAHDNSEELERARELKEK
			EATLCLEFILLONDANPSIRDKEGYNSIHYAAAYGHRQCLELLLE
5780	154	624	RTNSGFEESDSGATKSPLHLAVSEMP
3/60	124	6.24	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGERKSEPVS
			BIRTSVVKGSHFPVGVVPPRAKSPTPBSSTIASYVTLRKTKMM
			DLRTERPRSAVEQLCLAESTRPRMTVEEQMERIRRHQQACLREK
5781			KKGLNVIGASDQSPLQSPSNLRDNP
2/81	19	941	RGSLGGHPWRPPMRAASQGCLPVSFVTGPHQBRAYGGRGPGGAF
1 :			PAPPVSGTCPPDLIYAPTPEKAEGGSQKNHQPPPGERAAHRDGE
1			QAPCRAGPTRKVAVAPRPPSCP*GPE\PGEEPRRPLDRSPPLGQ
1			VQPHFTSQDAKSAKDRAPSRHLGKHQPRSAQVGSRLDALQGPKT
1 !			QHSIHTVTCKSPRQKEDRSPKPPQAPKHPERHGRQS\QAPPPLP
			VAPSRTCGGC*TWDPALLVSP/PQGDSTPELPAP\QQPTGGPSR
1			CROALPPOG*ROOPRORPR/PTGASRSHPAKAKGCOGPPKIRNY
			NIMD
5782	5176	1237	DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE
			PPMTPPLPPREPPEGPALPTEQSALTAENTWPTEVPSLPSEESV
}			SQPEPPVSQSEISE?SAVPTDYSVSASDPSVLVSEAAVTVPEPP
			PEPESSITLTPVBSAVVABBHEVVPBRPVTCMVSETPAMSAEPT
)			VLASBPPVMSBTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA
1			ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL
i i			EPSVVTVPEPPVVARPDYVTIPVPVVSALEPSVPVLEPAVSVLQ
			PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVALESTPM
		i	ILESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGKEPHAR
1			EHLKGDFYESEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE
1 1			IGEEKILPTSETKORTVLDTYPGVSEADAGETLSSTGPFALEPD
1 1			ATG\TSKGI3FTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP
]	ļ		SGGSEADIEGPLPAKDIHLDLPSNINLVSSDINEPLPVKRD\DQ
j i			TLAALI\SLKESSGGEKEVPPPS+REHLPDSGFSANIEDINRAD
j )			LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV
			\SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG
<b>!</b> [			BKEKKRDSSLRSRSKRSKSSKHKSRKLTSESRSRARKRSSKSKS
; I			HRS\QTRSRSRS/RDRRRRSSRSRSRSRSRGRRSVSKEKRKRSPKH
1			RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRRRSR
į į			SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRS
1 1			RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS
1 1	•		RSPIRRKRSRSSERGRSPKRLTDLDKAQLLETAKANAAAMCAKA
1 1			GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE
, 1		ľ	DDDVIVNKPHVSDEBEEEPPFYHHPFKLSBPKPIFFNLNIAAAK
1	ľ	1	PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGREN
1 1			KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAPDLEAMSM
1	l		LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQBQLANTGAQAWI
1	ļ	•	KKDQFLRAAPVTGGMGAVLMRKNGWREGEGLGKNKEGNKEPILV
	ļ		DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN
1 I	ļ	!	KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR
	İ	j	Y
5783	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
1		0.70	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ
	1		
į į	1		
	1		KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL NDLIEB/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHQEKKL

CEO	Predicted	Predicted end	Amino and company and delicated and and a
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, FaPhenylalanine, GaGlycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
I.	corresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1 - 1 - 1 - 1	\=possible nucleotide insertion)
<u> </u>	Codenias	<del> </del>	LHGDIKSSNVVIKGDFRTIKICDVGVSLPLDENMTVTDPEACYI
1	1	•	
1	}	ł	GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS
ľ	Ì		NDDDDEDKTFDESOFDDEAYYAALGTRPPINMEBLDESYQKVIE
L		<u> </u>	LPSVCTNEDPKDRPSAAHIVBALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
ı	}	i	GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1	ì		RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
1	i		QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
1			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVBLQMSKITNISAVEM
			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
1	1		VDSGCPBESKERMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
1	l		E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1	1		HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
L			WPANKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGP\$D\$A\$RDLWVNIDQMBKDKVKIH
1			GILSNTHRQAARVNLSFDFPFYGHFLRBITVATGGFIYTGEVVH
1	ļ		RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
ı			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
1			GLSDAFVVVHRICOIPNVRRRTIYEYHRVKLOMSKITNISAVEM
1	!		TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
1	<b>(</b>		VDSGCPEESKEKMCKNTEPVET\FLEPPQP*ERQPPSSGS*LPP
			B/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAKKKGGTL
1	'		FAGLIVGILLVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
1	] '		WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5786	2532	1674	
5/86	2532	15/4	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP
1			APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M
			S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
			SPPLACSFCQAAQKSQSLSSGRSTR+PERMSFRP\SPPGNPAIP
			SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
1	i		GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
L			TGGSTATAPPKRFPRNWNPMMAE
5787	2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
i		•	T\RYCEIP\GPD\LEBSP\TCP\LCKEPFRP\GSFRPNWQLANV
			VENIERLQLVSTLGLGERDVCQEHGEKIYFFCEDDEMQLCVVCR
1		·	EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKBREBIQBIQS
ì			RENKRMQVLLTQVSTKRQQVISBFAHLRKFLEEQQSILLAQLES
1			ODGDILRORDEFDLLVAGEICRFSALIERLEEKNERPARKLLTD
I			IRSTLIRCETRECREPVAVSPELGORIRDFPQQALPLOREMEMF
			LEKLCFELDYBPAHISLDPOTSHPKLLLSEDHQRAQF9YKWONS
ł		-	PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
1 .	}		BDVORKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEOP
1 .			ROVRVSLDYEVGWYTFTNAVTREPIYTFTASFTRKVIPFFGLWG
		!	<u> </u>
<del></del>			RGSSFSLSS
5788	2	6860	PHSVSGRSSAYGDATABGHPAGPGSVSSSTGAISTTTGHQEGDG
1			SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR
1			AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV
1			SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
			ATAAALLSSGAVDYCLHVLKSLLKYWKSQQNDEKPVATSQLLKP
}			HTTSSPPDMSPFFLRQYVKGHAADVPEAYTQLLTEMVLRLPYQI
ì			KKITDTNSRIPPPVFDHSWFYFLSEYLMIQOTPFVRRQVRKLLL
1			FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
1			SPOSALQYDTLISLMEHLKACAEIAAQRTINWOKFCIKDDSVLY
ļ l			FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
			1
1			SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQEDQ
1			LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
			IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
l i			TPQTBKKLKEYSQKAVBILRTQNHILTNHPNSNIYNTLSGLVRF
[			DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI
1			GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
]			RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIBFADPYENYQAS
1			TETLOCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF
<b>L</b>			**************************************

CEC	Predicted	Predicted end	Imino haid compat containing signal nortide
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	N=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
<u> </u>	- Bequence		LCNACGECKYAREDEMLYAKECCAVDELENEEDRKKAVSNINTL
1		i	
	1		LDKADRVYHQLMGHRPQLENLLCKVNRAAPEKPQDDSGTAGGIS
		ļ	STSASVNRYILQLAQRYCGDCKNSFDRLSKIIQKVFASRKELLE
1			YDLQQREAATKSSRTSVQPTFTASQYRALSVLGCGHTSSTKCYG
1			CASAVTEHCITLLRALATNPALRHILVSQGLIRBLFDYNLRRGA
			AAMREEVROLMCLLTRDNPEATOOMNDLIIGKVSTALKGHWANP
·	İ		DLASSLQYEMLLLTDSISKEDSCWELRLRCALSLFLMAVNIKTP
1	1	l	VVVENITLMCLRILOKLIKPPAPTSKKNKDVPVBALTTVKPYCN
1			BIHAQAQLWLKRDPKASYDAWKKCLPIRGIDGNGKAPSKSKLRH
1	j		LYLTEKYVWRWKQFLSRRGKRTSPLDLKLGHNNWLRQVLFTPAT
	l		QAARQAACTIVEALATIPSRKQQVLDLLTSYLDELSIAGECAAE
1	l .		YLALYQKLITSAHWKYYLAARGVLPYVGNLITKEIARLLALEEA
	1		TLSTDLQQGYALKSLTGLLSSFVEVESIKRHFKSRLVGTVLNGY
1	1		LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
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I	ļ		BTAKRYNLDDYRTPVFIFERLCSIIYPKENEVTBFFVTLEKDPQ
1	İ	ļ	QEDFLQGRMPGNPYSSNEPGIGPLMRDIKNKICQDCDLVALLED
1	1		DSGMELLVNNKIISLDLPVAEVYKKVWCTTNEGEPMRIVYRMRG
i		•	LLGDATERFIESLDSTTDEEEDEEEVYKMAGVMAQCGGLECMLN
			RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRQQLVKLEMNTLN
1			VMLGTLNLALVAEQESKDSGGAAVAEQVLSIMEI\IQAEPNVEP
	[		LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIP
ŀ	1		YLSFGEVEKMQILVERFKPYCNFDKYDEDHSGDDKVFL\DCFCK
Ì			LAAGIK\NNSNGHQL\KDL\ILQKGITQNALD\YMKKHIP/SAA
			RIWDADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI
1			PNLHKLEGVS\SDEGIGTLA\ENL\LESLREHPDVNKKIDA\AR
}			RETRAEKKRMAMAMROKALGTLG\MTTNEKGQVVD/TRTALLEA
			DWEELIEEP\GLTCCICREGYKFQPTKVLGIYTFTKRVVLGGVW
1 .			ENKPRETSRATSTVSHFNIVHYDC\HLA\AVSLARGREBWESAA
1			LQNANTKCNGLLPVWGPHVPESAFATCLARHNTYLQECTGQREP
1			TYQLNIHDIKLLFLRFAMEQSFSADTGGGGRESNIHLIPYIIHT
			GLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFTV
1.	-		LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDRAV
1			
1			KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGWSCSLAEYIR
	ļ.		HNDNPIYEAADKALKTFQREFMPVETFSEFLDVAGILSEITDPB
			SFLKDLLNSVP
5789	1	2407	LPLHAVEKTGRPGQPALKMPGKLRSDAGLESDTAMKKGETLRKQ
1			TBEKRKKEKPKSDKTREIARERETVPPKAKQVKKKAEPSEVDMN
i			SPKSKKAKK\KERPSQNDISPKTKSLRKKKEPIEKKVVSSKTKK
			VTKNEEPSEBEIDAPKPKKMKKEKEMNGETREKSPKLKNGFPHP
1			EPDCNPSEAASRESNSEIEQEIPVEQKEG\AFSNFPISEETIKL
1			LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
1	Ì		1EKLHG\ELQDRKRGRAPQVLVLAPTRELANQVSKDFSDITKKL
1			SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT
1	ļ		KLNHVVLDBVDQMLDMGFADQVBEILSVAYKKDSBDNPQTLLFS
			ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH
1			WTORAAVIGDVIRVYSGHOGRTIIFCRTKKEAQELSONSAIKOD
1			AQSLHGDIPQKQRKITLKGFRNGSFGVLVATNVAARGLDIPEVD
			LVIOSSPPKDVESYIHRSGRTGRAGRTGVCICFYOHKEEYOLVO
			VEOKAGIKFKRIGVPSATRIIKASSKDAIRLLDSVPPTAISHFK
1			QSAEKLIEEKGAVBALAAALAHISGATSVDQRSLINSNVGFVTM
1			· · · · · · · · · · · · · · · · · · ·
			ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF
1			DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ
1 1			REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK
			GQKRSFSKAFGQ
5790	3786	1585	ARRORDPLOALRRRNOELKOOVDSLLSESQLKKALEPNKROHIY
3750			QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKBEEHTLLD
3,30	1		
3,50			KLTQQLQGLAVTISRENITEVGAPTEEEBESESEDSEDSGGEBB
3750			KLTQQLQGLAVTISRENITEVGAPTEEEEESESEDSEDSGGEEB DAEEEERKEENESHKWSTGEEYIAVGDFTAQQVGDLTPKKGEI
3,50			DAEBEERKEENESHKWSTGEEY I AVGDFTAQQVGDLTPKKGEI
3,30			DAEEBERKEENESHKWSTGEEYIAVGDFTAQQVGDLTPKKGRI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLBPYSEEREGQESSEE
3,50			DAEBEERKEENESHKWSTGEEY I AVGDFTAQQVGDLTPKKGEI

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location   corresponding				
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amino acid residue of amino acid sequence    Setting	Į.		to first	L=Leucine, M=Methionine, N=Asparagine,
remidue of maino acid sequence  maino acid sequence    Code,	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
antino acid pequence  Codent, /-ponesible nuclectide insertion  PUNGOINTUREATIONAL PROPERTY SOLLSEEROPERANY FLO PERMESOLAR PROMPENT PROPERTY SOLLSEEROPERANY FLO PERMESOLAR PROMPENT PROPERTY SOLLSEEROPERANY FLO GRESTORISH PROCESSOR FOR PROMPENT PROPERTY SOLUTIONS  GRESTORISH PROCESSOR FOR PROMPENT PROPERTY SOLUTIONS  REAGEN PROMPENT PROPERTY SOLUTIONS  REAGEN PROMPENT PROPERTY SOLUTIONS FOR PROMPENT PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROMPENT PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPER	ſ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
anino acid sequence  Codon, /-possible nucleotide deletion, 1-possible nucleotide insertion  PUNGOINTURINTHMAT PAGERESTISGLESENOPERNYSTIC  PENESSIOLA POINMONE TIREPRESTISGLESENOPERNYSTIC  PENESSIOLA POINMONE TIREPRESTISGLESENOPERNYSTIC  GENESIULICIPORINULSENITURINE TIREPRESTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNYSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGUESENOPERNSTISGU	1	residue of	amino acid	
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NVILIKAQTYELQESNYOLKITIVNTYGEOQDINKERSYQ1TUDY IDAQPEANLOBERKIT KELETYHIDSE HEVYETSPYCHSELKTI. DLIJMKENLDSKYYIIPYTAKADTYGKTELQKFKIKLMSELVSNG VQIYQFPTDDDTTAKWAAMNGQLPPAVUGSUBSWKYOKNAVAR RQYPHGVUQVENSINCDDYKLREMLICTIMBDLARGTHTRIYISI. YRACKLERMGFTDVOGPENKPUSVQGTYBAKREHGHERGKEESE MKQMFVQRUVKEKBALIKERBERELQARFEKHLGDERMKLEKK RKILBERITAPSKKKATSBIFHSQSFLATGSNIKRUKDOKNSOGP PVKQKVPEHRERSSGAANFIKKLEVCFDFAVICFISIFGEQPO LLIPMEKYPQVQGGYJSQSB  5792 2263 653 ARAFSFAWNGGFPVYVVTVHTCWVWGTVYTRPCSGDASCIQPY LARPKKLQL\RHSFTYTTSSHLGAENNILUVINVBDFDVBSKFER TVWVSVPKKTRNNGTLYAYTFIHHAGVLPHHDGKQVHLVSFLTT YMVPKPESHILATGSSDQJCFADKKPTSHHMODAVYSLQQ FGSSKADABVKGIRVDTNIYFILALTFEVAAPHLLFDIDLSN RVADIMVINSTTELPLIVSYDKVSLGELKHMODAVYSLQQ FGFSSKADABVKGIRVDTNIYFILALTFEVAAPHLLFDIDLSN RVADIMVINSTTELPLIVSYDKVSLGELKHMODAVYSLQQ FGFSSKADABVKGIRVDTNIYFILALTFEVAAPHLLFDDFAFKAD ISPHKKKKSMIGNSTKAVLMRCFSTVVIFLFLIBGGTSLIVLVUP AGVGAAILHKWKKALKGHTIFMGGMYFSGFTYSSSERKTEBY DTQMKKISTILYPLCVGGAVYSLLINIKYKSWYSMLINIKYNOV YAAGGI-HELGLPVNYKLKSVALLBUKKAPTYKAFNTFTDDVFAF ITINTTSIRLACFRDDVVPTVYLYQRWLYPVDKRRVNEFGESVE EKNTRAPHTD  5793 2263 653 ARABSPAWNGGVPVVYVTTCGVVNGTVVTRFCSGDASCIQDY YAAGGI-HOLGQLFVNYKLKSVALLBUKKAPTYKAFNTFTDDVFAF ITINTTSIRLACFRDDVVPTVYLYQRWLYPVDKRRVNEFGESVE EKNTRAPHTD  5794 1 S016 MGRISWGIRVGTVNYTYGLAFRHODAVYSLQQ FGFSSKADABVKGIRVGTVNYTHELLGAENNIDLULAVNSFDVNSV YAAGGI-HMLEQLFVNYKLKSVAHLLEWKAPTYKAFNTEIDUVFAF ITINTTSIRLACFRDDVVPTVYLYFLALTFPVNRFVHRPRIAL NVMANDVFVPGSSLFADVHRYMMGIQLGKTVTHLIPTLIPTLIPTLIPTLIPTLIPTLIPTLIPTLIPTLIPT	j	1	!	
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				PM-BTGK-LGTA-CANGEDKGTD-CANGEDCARA LGC-CANGEDCARC

SEQ	T Daniel and a	1 - 17 - 12 - 12 - 3	
ID	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
NO:	nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
"0;	location	1 '	Glutamic Acid, F=Phenylalanine, G=Glycine,
ı	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lyeine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P-Proline, Q-Glutamine, R-Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	sequence	Codon, /=possible nucleotide deletion,
ļ	acquence	<del> </del>	\=possible nucleotide insertion)
	ł ·	1	GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
1	į	I	PKGSPGSVGLKGBRGPPGGVGFPGSRGDTGPPGPPGYGPAGPIG
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1		l	DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
1			PGLPGIPGTPGBKGSIGVPGVPGKHGAIGPPGLQGIRGBPGPPG
Į			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
1	İ		FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
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1	ļ .	İ	PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
İ	1		EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
	1		GPKGSVGGMGLPGTPGRKGVPGIPGPQGSPGLPGDKGAKGEKGQ
1			AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
1	. 1	ĺ	PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
1	1	İ	TPGPTGPAGQKGEPGSDGIPGSAGRKGEPGLPGRGFPGPPGAKG
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ŀ	ì		PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFI.
i	,		VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
1			SCLRKFSTMPFLFCNINNVCNPASRNDYSYWLSTPEPMPMSMAP
l l			ITGENIRPFISRCAVCRAPAMVMAVHSQTIQIPPCPSGWSSLWI
i			GYSFVMHTSAGAEGSGQALASPGSCLBBFRSAPFIECHGRGTCN
ı			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR RT
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	2	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
1	2	1078	PGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE
	2	1078	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIK RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAMNLPLENP
	2	1078	FGEIGLLDPCMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
	2	1078	FGEIGLLDPGMDVYGGENTELGIKVWLCGGSMEVLPCSRVAHIR RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNPQWYLDHVYPEMRRYNNTVAYGR LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL
	2	1078	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIR RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGR LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
·	2	1078	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPGWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIWNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R
·	2	1078	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYMTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPOLARYTKEGFIHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRYTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGIAGIDLILRSCTGORWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETAKGRQVLDGPPRASPG QHRDPG
5797	2	891	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVABVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNPOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWPPOLARYTKEGPLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNPIQ NGALWKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVABVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNPOWYLDHVYPEMRRYMNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQBEQR
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLROP GIDIGDVSERRALRKSLKCKNPOWYLDHVYPEMRRYNNTVAYCE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFTQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQRANAEVMREMTKKLYSQYEEKLQBEQR KHSAEKRALLEETNSPLKAIEBANKKMQAABISLEEKDQRIGEL
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPGWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQREQR KHSARKRALLEETNSFLKALERANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQDLEHBTEMSGELTDSDKERYQQLEEAS
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYMNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPDLARYTKEGFIHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRYTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRKTLVDVTLENSNIKDQIRNLQQTYEASMBKLREKORQLE VAQVENQLLKMKVESSQEANABUMEMTKKLYSQYEEKLQEEQR RHSAEKEALLEETNSFLKAIERANKKMQAABISLEEKDQRIGEL DRLIERMEKERHOLQLQLLEHBTRMSGELTDSDKSRYQQLEEAS ASLRERIRHLNDMVHCQQKKVKOMVEEIESLKKKLQQKQLLILQ
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLDPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRCKTLVDVTLENSNIKDQIENLQQTYEASHDKLREKOROLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEGR KHSABKEALLEETNSPLKAIERANKKMQAABISLEEKDQRIGEL DRILERMEKERHOLQLQLLEHBTEMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKOMVEELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
	2	891	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLDPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASHDKLREKQRQLE VAQVENQLLKMKVESSQRANABVMREMTKKLYSQYEEKLQBEQR KHSAEKEALLEETNSFLKALEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHETRMSGELTDSDKERYQQLBEAS ASLRERIRHLMDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5797	-		FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLERP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNMKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFTQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSGRANAEVMREMTKKLYSQYEEKLQREGR KHSABKEALLEETNSFLKAIERANKKMQAABISLEEKDQRIGEL DRLIERMEKERHOLQLQLLEHBTEMSGENTDSDKERYQQLEEAS ASLREIRHLNDMVHCQQKKVKQMVEELESLKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVBTREIGVGCDLLP SQTGRTREIVMPSRNTPYTRVLELTMKKTIT
	2	891	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPQWYLDHVYPEMRRYNNTVAYCE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFTQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSGRANAEVMREMTKKLYSQYEEKLQBEQR KHSAEKRALLEETNSFLKALEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHBTEMSGELTDSDKERYQQLBEAS ASLRERIRHLMDMVHCQQKKVKQMVBELESLKKKLQQKQLLILQ LLEKISFLEGENNBLQSRLDYLTETQAKTEVBTREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT KTLGSRWKSNSNQEKQPYYEBQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQPFTVGQQPQIPITTGTG
	2	891	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPGWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQREQR RHSARKRALLEETNSFLKALERANKKMQAAEISLEEKDQRIGEL DRLIERMEKERHQLQLQLLEHBTEMSGELTDSDKERYQQLBEAS ASLERIRHLMDMVHCQQKKVKQMVEEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT KTIGSRWKSMSNQEKOPYYEBOARLSKIHLEKYNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGALTMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT
5798	644	891 115	FGEIGLLDPGMDVYGGENTELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLDPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLLLRSCTGGRYTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRKTLVDVTLENSNIKDQIRNLQQTYEASMOKLREKORQLE VAQVENQLLKMKVESSQBANABVMREMTKKLYSQYEEKLQBEOR RHSAEKEALLBETNSFLKAIEBANKKMQAABISLBEKDQRIGEL DRLIERMEKERHOLQLQLLEHETEMSGENTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVBEIESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTBVBTREIGVGCDLLP SQTGRTREIVMPSRRYTPYTRVLEHMKKTLT KILGSRWKSMSNQEKOPYYEGOARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKOLMRSRROEMRQFFTVGQQPQIPITTCTG VYYPGAITMATTTPSPQMTSDCSSTSASPEPSLEVVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
	2	891	FGEIGLLDPGMDVYGGENTELGIKVWLCGGSMEVLPCSRVAHIE RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKORQLE VAQVENQLLKMKVESSQEANABVMREMTKKLYSQYEEKLQEEQOR KHSAEKBALLEETNSFLKALERANKKMQAABISLEKKDQRIGEL DRLIERMEKERHOLQLQLLEHBTEMSGELTDSDKERYQQLEERS ASLRERIRHLNDMVHCQQKKVKOMVEELESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT KILGSRWKSNSNQEKOPYYEEQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNENINGBDEMEMYDDYEDDPKSDYSSENEAPPARYSAN LLSTYIKFINLPPETKATIQGVLRAGSQLRNADVELQQRAVEYL
5798	644	891 115	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNI.PLERP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNMKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQILDCDKVXSSLYKRWNFTQ MGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSGRANAEVMREMTKKLYSQYEEKLQBEGR KHSABKBALLEETNSFLKAIEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHOLQLQLLEHBTEMSGRITDSDKERYQQLEEAS ASLREIRHLNDMVHCQQKKVKQMVEEIESLKKLQQKQLLIIQ LLEKISFLEGENNELQSRLDYLTETQAKTEVBTREIGVGCDLLP SQTGRTREIVMPSRNTPYTRVLELTMKKTIT KIIGSRWKSNSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR TCTVDGKKLRIGSYKQLMSRRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLPPETRATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
5798	644	891 115	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRRP GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGPLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFTQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQRANAEVMREMTKKLYSQYEEKLQBEQR KHSAEKRALLEETNSFLKALERANKKMQAABISLEEKDQRIGEL DRLIERMEKERHOLQLQLDLEHBTRMSGELTDSDKERYQQLBEAS ASLRERIRHLNDMVHCQQKKVKQMVEBLESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNTYPYTRVLBLTMKKTLT KTLGSRWKSNSNQEKQPYYEBQARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTCTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNENINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN LLSTYIKFINLPPETKATIQGVLRAGSQLKNADVELQQRAVEYL TLSSVASTDVLATVLEEMPPPPERESSILAKKKKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
5798	644	891 115	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYCE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFTQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQBANABVMREMTKKLYSQYEEKLQBEQR KHSAEKRALLEETNSFLKALEBANKKMQAABISLEEKDQRIGEL DRLIERMEKERHOLQLQLGLEHBTEMSGELTDSDKERYQQLBEAS ASLRERIRHLMDMVHCQQKKVKQMVEBLESLKKKLQQKQLLILQ LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT KTIGSRWKSNSNQEKQPYYEROARLSKIHLEKYPNYKYKPRPKR TCIVDGKKLRIGSYKQLMRSRRQEMRQPFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPBPSLPVIQSTYGMKT DGGSLAGNENINGEDEMEMYDDYEDDPKSDYSSENEAPERAYSAN LLSTYIKFINLPPETKATIQGVLRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEBMPPFPERESSILAKLRKKGPGAGSAL DDGRRDPSSNDINGCMBPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFDGPAAQPSLGPTPEEAPLSPGPEDIGPPIP
5798	644	891 115	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPGWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLDPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQBEQR RHSARKRALLBETNSFLKAIERANKKMQAABISLEBKDQRIGEL DRLIERMERERHQLQLQLLEHBTEMSGELTDSDKERYQQLBEAS ASLRERIRHLMDMVHCQQKKVKQMVEBIESLKKKLQQKQLLILQ LLEKISFLEGENNBLQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT TCIVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNENINGEDEMEMYDDYEDDPKSDYSSENBAPEAVSAN LLSTYIKFTNLPPETKATIQGULRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEBMPPFPERESSILAKLRKKGPGAGSAL DDGRRDPSSNDINGGMBPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFKPAAPGSLGPTPEEAFLSFGPBDIGPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN
5798	644	891 115	FGEIGLLDPGMDVYGGENTELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNFOWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPOLARYTKEGFLHL GALGTTTLLDPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGQRWTIKNSIK*R EGAGALEPGPODMAAPPNIWTSCPGGETARGRQVLDGPPRASPG OHRDPG PRVROKTLVDVTLENSNIKDQIRNLQQTYEASMOKLREKORQLE VAQVENQLLKMKVESSQEANABWMEMTKKLYSQYEEKLQBEQR KHSARKEALLBETNSFLKALERANKKMQAABISLEKKDQRIGEL DRLIERMEKERHOLQLQLLEHETRMSGELTDSDKERYQQLEEAS ASLRERIRHLNDMVHCQQKKVKQMVEBIESLKKKLQQKQLLILQ LLEKISFLEGENNBLQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLEITMKKTLT TCTVDGKKLRIGSYKOLMRSRRQEMRQFFTVGQOPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNEMINGEDEMEMYDDYEDDFKSDYSSENEAPEAVSAN LLSTYIKFINLPPETKATIQGULRAGSQLKNADVELQQRAVEYL TLSSVASTDVLATVLERMPPFPERRSSILAKLKKKGPGAGSAL DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP PAASAGAGNLLVDVFDCPAAQPSLGPTPEEAPLSPSPDLIGPPIP EADBLLNKFVCKNNGVLFERQLLQIGVKSEFRQNLGRMXLFYGN KTSVQFQNPSPTVVHPGDLQTQLAVQTKRVAQQVDGGAQVQQVL
5798	644	891 115	FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE RKKRPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLRNP GIDIGDVSERRALRKSLKCKNPGWYLDHVYPEMRRYNNTVAYGE LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVXSSLYKRWNFIQ NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGGRWTIKNSIK*R EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG QHRDPG PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE VAQVENQLLKMKVESSQEANAEVMREMTKKLYSQYEEKLQBEQR RHSARKRALLBETNSFLKAIERANKKMQAABISLEBKDQRIGEL DRLIERMERERHQLQLQLLEHBTEMSGELTDSDKERYQQLBEAS ASLRERIRHLMDMVHCQQKKVKQMVEBIESLKKKLQQKQLLILQ LLEKISFLEGENNBLQSRLDYLTETQAKTEVETREIGVGCDLLP SQTGRTREIVMPSRNYTPYTRVLBLTMKKTLT TCTVDGKKLRIGSYKQLMRSRRQEMRQFFTVGQQPQIPITTGTG VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIQSTYGMKT DGGSLAGNENINGEDEMEMYDDYEDDPKSDYSSENBAPEAVSAN LLSTYIKFTNLPPETKATIQGULRAGSQLRNADVELQQRAVEYL TLSSVASTDVLATVLEBMPPFPERESSILAKLRKKGPGAGSAL DDGRRDPSSNDINGGMBPTPSTVSTPSPSADLLGLRAAPPPAAP PASAGAGNLLVDVFKPAAPSCLGPTPEEAPLSFGPBDIGPIP EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRQNLGRMYLFYGN

	T man 3/ - 1/ - 2	I need and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location corresponding	H-Histidine, I-Isoleucine, K-Lysine,
ļ	location	*	1
l	corresponding	to first	L-Leucinc, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
	T		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLBPNAQAQMYRLTL
ļ	1		RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQQRAVEYL
ł	1	i	TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
İ		1	DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
	ļ.	j	PASAGAGNLLVDVFDGPAAQPSLGPTPREAFLSPGPEDIGPPIP
l	Į	}	EADELLNKFVCKNNGVLFENOLLQIGVKSEFRONLGRMYLFYGN
ł		l	KTSVOFONFSPTVVHPGDLOTQLAVOTKRVAAQVDGGAQVQQVL
		ļ	NIECLROFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
		}	AAQDFFORWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
i		1	LLDNVDPNPENFVGAGIIOTKALQVGCLLRLRPNAQAQMYRLTL
ļ*			1
			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
1	1	1	QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQP
l	İ		CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPRE
l			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
1			DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
1		1	NGSNSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
1			GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
l			KVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
{	1	ļ	NMAPPSDWSPSWVMWLBLPRCLYNCKDIVLRRNTAGSLGFCIVG
i	İ		GYERYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
ļ	]		MIHACLARLLKELKGRITLTIVSWPGTFL
5802	3	290	CFSLYQIMBRIMDLPTLLRHAFREMPSVGGLFWMFRIRIILCLM
			GAFFYLISPLDFVPRALFGILGFLDDFFVIFLLIYISIMYREV
ł	1		ITORLTR
5803	2234	1299	RAOFGTTAEIYAYREEODFGIBIVKVKAIGRORFKVLBLRTOSD
3003	2234	1	GIOOAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
<i>'</i>	t		SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
Ĭ	į.		WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
l	1		LRCELDIMNKCTSLCCKQCQETBITTKNBIFSLSLCGPMAAYVN
	·		PHGYVHETLTVYKACNLNLIGRPSTEHSWPPGYAWTVAQCKICA
j			SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
Ì	i i		1
	<u> </u>		rcr .
5804	2	1707	EMEKOROEEORKRTERERKRRIEODMIEKRKIORELAKRAEQIE
ŀ			DINNTGTESASEEGDDSLLITVVPVKSYKT8GKMKKNFEDLEKE
ŀ		1	REBKERIKYBEDKRIRYEBQRPSLKEAKCLSLVMDDEIESBAKK
	1		BSLSPGKLKLTFERLERQRQENRKKQABERARKRLEBEKRAFEE
ł		-	ARROMVNEDEENDITAKI PKGYRPGKLKLSFEEMERQRREDEKR
	1 .	l	KABEEARRRIEBEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
1	1		GKLEINFEELLKQKMEEEKRRTBEERKHKLEMBKQBFEQLRQEM
Į.	1	1	GKKEERNETFGLSREYERLIKLKRSGSIQAKNLKSKFEKIGQLS
]	1		EKEIQKKIBEERARRRAIDLEIKEREAENFHKEDDVDVRPARKS
1			EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQFEQREI
			DAALQKKREBEEEEGSIMNGSTAEDEEQTRSGAPWPKKPLKNT
1			SVVDSEPVRFTVKVTGEPKPBITWWFEGEILQDGEDYQYIERGB
l		[	TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTIGOVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
3805	'	,,,	APKESOOOSEDREYEVKERLYPKSKERYDTYNIAGYQGEIEVGL
İ			YTIQILQLIPFPDNKNELSKRYMVNFVSGSSDIPGDPNNBYKLA
1	1 .	1	
1	1	1	LKNYIPYLTKLKFSLKKSFDFFDBYFVLLKPRMNIKQNEBAKTR
1	1	1	RKVAGYFKKYVDIFCLLEESQNNTGLGSKFSBPLQVERCRRNLV
		L	ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACQRFLGPAVFLLPW
1	•	1	ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
1	1		RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTBIYGBCGVC
	]		PRGORTNAOKYCOPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
1			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
ł	1		LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV
			THE PROPERTY OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, P-Phenylalanine, G-Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arqinine,
	amino acid	residue of	S-Serine, T-Threonine, V-Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
1		sequence	
	sequence		\=possible nucleotide insertion)
	i	ŀ	LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
I			GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
i			FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
L			EPSRILSEGANGH
5808	2	433	SLPDSGVVBYLSNGGVADNHKDFGELRYNEC_MNFSCNGKNGSS
į			EGRITHGFQLKSAYENNLMFYTNYTFDFKGVIDYIFYSKTHMNV
į.			LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
i	•		LVNGVHLPNRR
5809	464	2422	ILVPGPQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
j			RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
1	ľ	İ	EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
1	1		ESPKLHCQBINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
	1	l	SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWO
1		<b>[</b>	INSRRINPKISYVISIKGORLDPMESVREETVNLTTDSRTPEVC
1	1		LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
			SIFNETCLKLNRRSRKVGSEHMYQFTVLGORWYLANFSHATSFN
1	I	Ī	FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVOITIATPPA
)	}		VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGORWYOKEF
Į	1		AQENTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSBLPVVISL
l			TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
1 .	l .		LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
1	1		
1			RIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
5810			WAQVKDSSIMLLQMAGVGLGSLAVVIILTFLSFSAV
2810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIRAFVS
) .			BIESFFNTIBENCSKNEKRLBEQNBRMMKKVLAQYDRKAQSFER
			VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
i			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDOMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
J	•		BPQDDQKVNELVEEYRLTVKESYCIFEDLBPDRCYQVWVMAVNF
1	}		TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPRA
			TETYTLEYCROHSPEGEGLRSPSGIKGLQLKVNLQPNDNYFFYV
1	1		RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
1	1	·	SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
1			SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
ļ	1		VGLLLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAFALEKPG
1			KCTLHLGIRPPDSVRHK
5811	1918	851	AAALADPLPEDKWSARKRRPLKSSLGYEYTYSLLNPDPKSHDVY
1			wdiegavrryvopfinalgaagnfsvdsqilyyamlgvnprfds
			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNPLLYVPELA
	1		HSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
i i			RVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMT
1			weldrlinarsvenlatattiltslaqligkisnivikddvase
Į i			VYKAVAAVQKSAERLASGHLASAFVASQEAVTSSELAFFDPSLL
			HLLYPPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
			KTD
5812	5204	2744	GGRORGORGREGGAREHEVEPGTARPPPAASAMDASLEKIADPT
J			LAEMGKNLKEAVKMLEDSQRRTEBENGKKLISGDIPGPLOGSGO
			DMV91LQLVQNLMHGDEDEBPQ9PRIQNIGEQGHMALLGHSLGA
			YISTLDKEKLEKLITERILSDTTLWLCRIFRYENGCAYFHEERE
			GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGO
			YLCNOLGLPFPCLCRVPCNTVFGSOHOMDVAFLEKLIKDDIERG
	ļ		RLPLLLVANAGTAAVGHTÓKIGRLKELCEQYGIWLHVEGVNLAT
			LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
]			LTLVAGLTSNKPTDKLRALPLNLSLQYLGLDGFVERIKHACQLS
			QRLQRSLKKVNYIKILVEDBLSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
			EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
			erfkqevkatagllyvddpnwsgigvvryfhanddksslksypq
}			GENIHAGLLKKLNELESDLTFKIGPBYKSMKSCLYVGMASDNVH
	1		AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS
1			BERLLBEGVLRQIPVVGSVLNNFSPVQALQKGRTFNLTAGSLES

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GOFFIGHESOKI * EVFLDREPLLRVSYMETYNETITDLLCGTYKM RPLIIREDVNRNYVADLTBEVYYTSEMALKMITKGESRHYGE TKMMQRSSRHTIFRMILESREKGESNCGSGVKVSHLMIVDLA GSERAAQTGAAGVELKEGCNINSLETICGVIKKLSDCGVEGFI NYRDSKLITRILQNSLGENPKTRIICTITPVSPDETLTALQFAST AKYKKNTPYVNEVSTDEALLKRYKKSIMDLKKQLEEVSLETTAQ AMEKODLAGILEKKDLIGKVONEKIENLITMMUTSSSITLQGSL KAKRKRVTWCLGKINKMKNSNYADQPNIPTNITTKTHKLSINL LREIDSSVCSESDVFSNTLDTJESIEMPATALLAGENIESEKIN SLRADYNNLVLDVEQLETBEEMELKIKRNNLDEFHALERTK KOQEMQLIHEISNLKNLVKHREVYNDDLERHELSPKVELLREKED QIKKLGSYIDSGKLENIKMIDLSYSLESIEDDKOMKOTLFIDATV ALDAKRSSAFLRSENLELKKKMKELATTYKOMENDIGLYGSGLE AKKROWDLEKKELGSAFNEITKLTSLIDGKVPKDLLCNLELEGK AKKROWDLEKKELGSAFNEITKLTSLIDGKVPKDLLCNLELEGK AKKROWDLEKKELGSAFNEITKLTSLIDGKVPKDLLCNLELEGK SUSTDOPPONSTLHMDEGDKYKMVLEENERMIGEIVNLSKE NYRSTOOPPONSTLHMDEGDKYKMVLEENERMIGEIVNLSKE AQKFDSSLGALKTELSYKTGELGEKTREVQERLNEMEGLKRGLE NROSPLOTVEREEKTLITEELQQTLEEVERTLTGEKDLAGTGL KEISEVSRULHMEENTGETKDEFQQKMVGIDKKQDLEARAKTYTL TADVKNNEITEQQRKIFSLIGGBLKAQGETUNGKEGLES KISEEVSRULHMEENTGETKDEFQQKMVGIDKKQDLEARAKTYTL TADVKNNEITEQQRKIFSLIGGBLKAQGETVAREKHAIKKEGLESISR KENIEMTISMGELRILGBULKAQGLVADEKHAIKKEGLESISR TCDRLAEVEEKLKBKSQQLQEKQQCLLNVQEEMSEMQKKTNEIE NLKNELKNKELTLEHNETERLAGKLMENYEEVESTTKERKVL KELGKSPTREDBLRGYIRSTEKQDKTVAGEKTHAITKERGELL OESGESIKSLTKERRUNLTTIKARLEYKTELAGUKEETLAHIELKEHQE SGSKGEGSIKMELTHERVATRUSERGYTKERKUTHERTLARIGE GESGESIKSLTKERRUNLTTIKARALEYKHOLKKEHTETLARIGE SGSKGEGSIKMEKNNETTKIVSENEOPKPROSALLRIETEMLEG LSKRLQSSBENMEKNNETTKIVSENEOPKPROSALLRIETEMLG LSKRLQSSBENMEKNNETTKIVSENEOPKPROSALLRIETEMLEG LSKRLGSSBENMEKNNETTKIRSREVILBRENTEKTEV AKHLETBEBLRVANCCLKSGESTIGHTKREKVENGEKERSTEGTIGKG LARINKLONKTGEITSEKEGDINIKGISKEKTBILTRUCHEKMEKVORGE KARDSALGSIESEKMELTURNELGESEGTIMTKERESTENERVY LERAINKLONKTGEITSEKEGDINIKGIKSKERBMKRVORGA LGIERDOLKENTKEIVANGKESGERGYOFLOMTKERDEKKEVERGE	1			
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TKMMORSSESHTI FRMILESREKGEPSNCEGGVKVSHINIJVDLA GSERAAGNGAAGVRIKEGCNINRSIJFILGOVIKKIJCAGVEGFFI NYRDSKUTRILQNSIGGMPKUTRI LCTITPVSFDETLTALQAFST AKYMKNTPYVWEVSTDEALLKRYRKE IMDLKKQLEEVSLETRAQ AMEKOQDAQLLERKOLLQKVQNBKI ERUTRHLVTSSSLTIJQGSL KARKRRUTWGLGKINKMKNSNYADQPNI PYNITTKTKIKLSINL LRBIDESVCSESDVFSNYLDYLGSI BMMPATKLLNQENIBSELN SLRADYDNIJVLDYEQIKTEKEEMELIKLKERKODLBEFRALBEKTIK KOQRMQI.HBISNLKNIJVRIKEVYNQOLLENBISSKVEILIRKED QIKKLQBYIDSQKLENIKMDLSYSIASI EDPKOMKOTI-FDAETV ALDAKRESAFLRSENLELKEKKKELATTYKÇMERDIQLYGSQLEE AKKRMOYDLEKBIQSAFNETTKLTSI.LIGEVYRDILCHLEEK YTOLQKEINKSVESNERALRERVILLSELKSLSPSEVERLRKEIQD KSERLHI ITSEKDKLFSEVYHKESVQGLLERIGKTKDDLATTO SNYKSTDQPPONFKTLHMDEGQKYKMVLERHERNOGEIVNISKE AQKFDSSLGALKTELSVKTQBLQEKTREVQERLMEMQLEBEL NRDSPLQTVEREKTLITEKLQQTLERKTLTDLKQCLGESL CIERDQLKSDIHDTVANNIDTQBQLKRALBSLKQHGETINTLKS KISEBVSRNLHMEENTGETKDEFQQRWGIDKKQDLEAKNTOTL TADVKDNEI IEQQRK FSLLQEKRELQOMLESV LAEKEQKKTDL. KENIEMTIENGGEIRLIGGBLKKQOKLOMLESVIAREKQKKTDL KENIEMTIENGGEIRLIGGBLKKQOKLOMESVIAREKQKKTDL KENIEMTIENGGEIRLIGGBLKKQOKLOMESVIAREKQKKTDL KENIEMTIENGGEIRLIGGBLKKQOKLOMESVIAREKGELSF TCDRLASVERKLKBKSQOLQBKQQLLNVQEEMSEMQKKINBIE NLKNELKNKSLITLEHMETERLBLAQKLNENYBEVKSITKERKVJ KELQSFETERDHLRGVIRR HATGLGTKEBLKTAHTHLREHGE TIDBLRRSVSSKTAQI INTQDLEKSHTKLQEEIPVLHEBGELLP NVKKVSSFTQETMMELBLLITEQSTTKDSTTLAR IEMBELRINBEKF QESGEIKSLTKRENDILKTKREDVHOLGKHIRETIARIQE SQSKQBSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSRRLGSBIDEMKSVAKEKDDLQRLGBVLQSEDDLKENIKEIT AKHLETBEBLKVAHCCLKEGETTHRLRVNISKRETEISTIQKQ LEAINDKLQNKIQEIYEKEBQLNIKQISEVQEKVNBLKQFKEBE KAKDSALQSIESMLBLNINELGSGEBIQIMIKEKBEMKSTYKERD LGIBLKGOFTQKLNLBNIETGENIRLTVILLENBERSVYTKERD				
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KARRRRYTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL LRRIDESVCSSBOYFSNTLDTLSEIBMAPATKLLNGENIBSELN SLRADYDNIALDYBGLGHTBKEEMBLKLKERNDLDBFFALBRKTK KDQBMQLJHEISNLKNLVKHREVYNQDLENBLSSKVELLREKED QIKKLQBYIDSQKLENIKHDLSYSLBSIEDPKOMKQYLFDAETV ALDAKRESAFLRSENIELKEKMKKELATTYKQMENDIQLYQSQLE AKKEMOVDLEKKELQSAFNBITKLTSLIDGKVPKDLLCYLFLEGK ITDLQKELNKRVBENBALRREVILLSBLKSLPSBVERLRKBIQD KSBELHIITSEKDKLPSEVVHKESTVQGLLBEIGKTKDDLATTQ SNYKSTDQEPOMFKTLJHMDFGQKYKMVLEENERMOGIVNISKE AQKFDSSLGALKTBLSYKTQBLQBKTREVQERLNEMEQLKEQLE NROSPLQYTVEREKTLITEKLQQTLEBVKTLTQEKDDLKQLGESL QIERDQLKSDIHDTVVNNIDTQDEQLRNALBSLKQHQETINTLKS KISEBVSRNLHMERBTGETKDEFQQKMYGIDKKQDLEARNYQTL TADVKDNEIIBQQRKIFSLLGBBLKCQGKIVAQEKNHAIKKBCELSR KISEBVSRNLHMERBTGETKDEFQCKMYGIDKKDDLEARNYQTL KRNIEMTIENGBELKLLGBBLKCQGLLWQEEWSEMQKKTNBIB NLKNELKNKELTLEHMETERLAQKLNEMYEBVKSITKERKVL KELQKSPETBRDHLRGYIRRIBATGLOYKEBLKAHGHLKEHQE TIDELRRSVSBKTAQIINTQDLEKSHTKLQBEIFVLHEBQBLLP NYKKVSSTQETMNBLELLTEQSTTKDSTTLARIBMERLRILNEKF QESQEGIKSLTKERDNLKTIKBALBVKHDQLKKHIRETLAKIQE SQSKQGSLMNKKENDETTKIVSEMEQFKPNDSALIRIBIEMLG LSRILGESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBERLKVAHCCLKSQBETIDELRVNJSSKEPTEISTIQKQ LRAINDKLQNKIQEIYEKEBQLNIKQISRVQEKVMBLKQFKER KAKDSALQSIESKMLBLTHRLQSSQEELQIMIKEREMKRVQEA LQIERDDLKENTKETVANKESQBEETQIMIKEREMRRVQEA				
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KDQRMQLIHBISNIKNIVKHREVYNQDLENBLSSKVELIREKED QIKKIQBYIDSQKLENIKHDLSYSIJBSIEDPKOMKQTIFIDAETV ALDAKRESAFIRSENELKEKMKELATTYKOMENDIQLYQSQLE AKKKMQVOLEKBIQSAFWBITKLTSILIDGKVPKDILICNLELEGK KREMINITTSEKDKLIFSEVVHKESRVQGLLEBIGKTKDDLATTQ SNYKSTDQFFQNFKTILMDVEQKYKMVLEBERNNQEIVNLSKE AQKFDSSLGALKTBLSYKTQBLQBKTREVQERLNEMEQILKBL NRDSPLQTVEREKTLITEKLQQTLEEVRTLTQEKDDLRQLQESL QIBRDQLKSDIHDTVNMNIDTQCLRNALESLKQHQETINTLKS KISEBVSRNLHMERNTGTKDEFQOKMVGIDKKQDLEKNTQTL TADVKDNBIIBQQRKIFSLJGEKNELQQMLESVIAEKEQLKTDL. KENIEMTIENQBELKLLGDBLKKQQBIVAQEKNHAIKKBGELSR TCDRLABVERKLKBKSQQLQBCLANVQERMSEMQKKINBIE NLKNELKNKELTLEHMETERLELAGKLMENYBEVKSITKERVL KELQKSFFTREDHLRGYTREIBATGLQTKBELKIAHIBLKEHQBE TIDBLRRSVSBKTAQIINTQDLEKSHTKLQBEIPVLHEBOBLLP NVKKVSETQBTMNELELLTEQSTTKDSTTLARIBMERLRINEKF QESQBEIKSLTKRRDNLKTIKRALBVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQRSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIT AKHLETEBELKVAHCCLKEQBBTINELRVNLSBKETBISTIQKQ LBRAINDKLQNKJQEIYBERBQLNIKQISBVQEKVNBLKQFKEER KAKDSALQSIESKMLBLTNRLQESQEBIQIMIKEKEBMKKVQBA LQIERDQLKENTKRIVAKMKESQBKBYQFLKMTAVNBTQEKMER IEHLKEQFETQKLNLENIETENIRLTQLILHENLEBMRSVTKERD			' 	
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QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS KISEBVSRNLHMERNTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEI IEQQRKIPSLIQEKNELQQMLESVIAEKEQLKTDI. KENIEMTIENQEELRLIGDELKKQQKIVAQEKNHAIKKEGELSR TCDRLABVEEKILKEKSQOLQERQQQLLNVQEEMSEMQKKINEIE NLKNELKNKELTLEHMETERLELAQKLNENYEEVKSITKERKVL KELQKSPETERDHLRGYIRBIBATGLQTKEELKIAHIHLKEHQE TIDBLRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMBELELLTEQSTTKDSTTLARIEMERLRLNEKH QESQEEIKSLTKERDNLKTIKBALBVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIELGLG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKBIV AKHLETEBELKVAHCCLKEQBETINELRUNLSBKETBISTIQKQ LBAINDKLQNKIQEIYEKEBQLIKQISBVQEKVBLKQPKEER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKEBMKRVQEA LQIESDQLKENTKETVAKMKESQEKEYQFLKMTAVMETQEKMCE IEHLKEQFETQKUNLENIETENIRLTQILHENLEEMSVTKERD		·		
KISEBVSRNLHMERNTGETKDEFQQKMVGIDKKQDLEAKNTQTL TADVKDNEIIEQQRKIFSLIQBKNEIQQMLESVIAEKEQLKTDL KENIEMTIENQEELRLLGDBLKKQQKIVAQEKNHAIKKEGELSR TCDRLAEVEBKLKBKSQQLQBKQQQLLNVQBEMSEMQKKINBIE NLKNELKNKSLITLEHNBTERLEILAQKINENYEBVRSITKERKVL KELQKSFETERDHLRGYIRBIBATGLQTKBELKIAHIHLKEHQE TIDBLRRSVSBKTAQIINTQDLEKSHTKLQBEIPVLHEBQBLLP NVKKVSFQETMNBELBLITEQSTTKDSTTLARIEMERERLNEKKP QESQESIKSLTKERDNLKTIKBALBVKHDQLKEHIRETLAKIQE SQSKQBSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIENLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBBBLKVAHCCLKEQBBTINELRVDLSBKEFBISTIQKQ LBAINDKLQNKIQEIYEKEBQINIKQISBVQEKVBELKQFKEER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKBKEBMKRVQEA LQIESDQLKENTKEIVAKMKSSQEKBYQFLKMTAVNETQEKMCE IEHLKEQFFTQKLNLENIETENIRLTQILHENLEEMSSVTKERD				
TADVKDNEI IEQQRKI FSLIQEKNELQQMLESVI AEKEQLKTDI. KENIEMTI ENQEELRILGDELKKQQ BIVAQEKNHAI KKEGELSR TCDRIABVERKI.KBKSQQIQBEQQQQILNVQBEMSEMQKKINE IE NIKNELKNKELTI ENIMETERLELAQKI NENYEEVKSI TKERRVI. KELQKSPETERDHLRGYIRRI BATGLQTKEELKI AHIHLKEHQE TIDBLARSVSEKTAQI I INTQDLEKSHTKLQEE IPVLHEEQBILLP NVKKVSETQETMNBLELLITEQSTTKDSTTI.AR IEMERLERINEKP QESQEE I KSLTKERDNIKTI KBALEVKHDQI KEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKI VSEMEQFKPKDSALLRIE I EMLG LSKRLQESHDEMKSVAKEKDDI QRIQBVI QSESDQI KENIKBI V AKHLETBEBLKVAHCCI KEQESTINELRVHLSEKETE I STIQKQ LEBAINDKLQNRI QE I YEKEEQINIKQI SEVQEKVNBLKQFKEHR KAKDSALQSI ESKMLBLITNILQESQEE I QIMIKBKBEMKRVQBA LQI ERDQLKENTKBI VAKMKSSQBKBYQFI KMTAVNBT QEKMCE I EHLKEQFETQKINLENIETENIRI TQI LHENLEEMS SVTKERD				
KENIEMTIENQEELRILGDELKKQQEIVAQEKNHAIKKEGELSR TCDRIABVERKIKBKSQQIQBKQQQLINVQEEMSEMQKKINEIE NIKNELKNKELITLERIMETERLEIJAQKINERVEUKS ITKERKVI. KELQKSFETERDHLRGYIREIBATGLQTKEELKIAHIHIKEHQE TIDEIRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP NVKKVSETQETMNELEILITEQSTTKOSTTIAR IEMERLRINEKF QESQEEIKSLTKERDNIKTIKBALEVKHDQIKEHIRETLAKIQE SQSKQEQSINMKEKDNETTKIVSEMEQFKPKDSAILRIEIEMIG LSKRIQESHDEMKSVAKEKDDIQRIQBVIQSESDQIKENIKEIV AKHLETBEBLKVAHCCIKEQEETINELRVHLSEKETEISTIQKQ LBAINDKLQNKIQEIYEKEBQINIKQISEVQEKVNELKQFKEHE KAKDSALQSIESKMIBLITNRLQESQEEIQIMIKEKEBEMKRVQEA LQIERDQIKENTKBIVAKMKSSQEKEYQFIKMTAVNETQEKMCE IEHLKEQFETQKINLENIETENIRITQIILHENLEEMSSVTKERD				
TCDRLAEVEBKLKBKSQQLQBKQQQLLNVQBEMSEMQKKINBIE NLKNELKNKELTLEHMBTERLBLAQKINENYBEVKSITKERKVL KELQKSFBTERDHLRGYIRBIBATGLQTKEBLKIAHIHLKEHQB TIDBLRRSVSBKTAQIINTQDLEKSHTKLQBEIFVLHEEQBLIP NVKKVSBTQBTMNBLELLTEQSTTKDSTTLARIEMBERLRLNEKF QESQBEIKSLTKERDNLKTIKBALBVKHOQLKEHIRETLAKTQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQBSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBEBLKVAHCCLKEQBBTINBLRVHLSBKEFBISTIQKQ LBAINDKLQNKIQEIYEKBBQLNIKQISBVQEKVBLKQFKEFB KAKDSALQSIESKMLBLTNRLQBSQEBIQIMIKEKBEMKRVQBA LQIESDQLKENTKBIVAXMKBSQBKBYQFLKMTAVNBTQEKMCB IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMSSVTKERD				
NLKNELKNKELTLEHMETERLEJQKLNENYEEVKSITKERKVL KELQKSPETERDHLRGYIREIBATGLQTKEELKIAHIHLKEHQE TIDBLRRSVSEKTAQIINTQDLEKSHTKLQKEIPVLHEBQBLLP NVKKVSETQETMBELELLTEQSTTKDSTTLARIEMERLERLNEKP QESQEEIKSLTKERDNLKTIKBALBUKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIENLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETEBELKVAHCCLKEQBETINELRVHLSBKETBISTIQKQ LBAINDKLQNKIQEIYEKEBQLIKQISBVQEKVBLKQFKEER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKEBMKRVQEA LQIESDQLKENTKEIVAKKESQEKEYQFLKMTAVMETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMSSVTKERD	. ]			
KELQKSFBTERDHLRGYIRBIBATGLQTKEELKIAHIHLKEHQE TIDBLRRSVSBKTAQI INTQDLEKSHTKLQBEIPVLHBEQBLLP NVKKVSBTQBTMNBELBLLTEQSTTKDSTTLARIBMERERLINEKF QESQESIKSLTKERDNLKTIKBALBVKHDQLKEHIRETLAKIQE SQSKQBQSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQBSHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETBBBLKVAHCCLKEQBBTINELRVHLSBKEFBISTIQKQ LBAINDKLQNKIQEIYEKBEQIMIKQISBVQEKVBELKQFKEFER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKBKEBMKRVQEA LQIESDQLKENTKBIVAKKESQEKBYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMSSVTKERD		i		
TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIFVLHEEQELLP NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRINEKF QESQEEIRSLTKERDNIKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKEIU AKHLETEEBLRVAHCCLKEQEBTINELRVNLSEKETEISTIQKQ LEAINDKLQNKIQEIYEKBEQLNIKQISBVQEKVNBLKQFKEER KAKDSALQSIESKMEBLTNRLQESQEEIQIMIKEKEBMKRVQBA LQIESDQLKENTKBIVAKMKESQBKBYQFLKMTAVNBTQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				
NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLMMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQEVIQSESDQLKENIKEIV AKHLETBEBLKVAHCCLKEQEBTINELRVNLSEKETBISTIQK LRAINDKLQNKIQEIYEKEEQLNIKQISEVQEKVNBLKQFKEER KAKDSALQSIESKMLBLINRLQESQEEIQIMIKEKBEMKRVQBA LQIERDQLKENTKBIVAKMKSSQBKBYQFLKMTAVNBIQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMSSVTKERD				
QESQEEIKSLTKERDNLKTIKBALEVKHDQLKEHIRETLAKIQE SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG LSKRLQESHDEMKSVAKEKDDLQRLQBVLQSESDQLKENIKBIV AKHLETEBELKVAHCCLKEQEBTINELRVNLSEKETBISTIQKQ LBAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVNBLKQFKEHR KAKDSALQSIESKMLBLINRLQBSQEBIQIMIKBKBEMKRYQEA LQIERDQLKENTKBIVAKMKSSQBKBYQFLKMTAVNBIQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMSSVTKERD				- · · · · · · · · · · · · · · ·
SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIENIG LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV AKHLETBEBLKVAHCCLKEQBETINELRVNLSEKETEISTIQKQ LBAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVBLKQFKEER KAKDSALQSIESKMLBLTNRLQESQEEIQIMIKEKEBMKRVQES LQIESDQLKENTKBIVAKKESQEKBYQFLKMTAVNETQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD				· · · · · · · · · · · · · · · · · · ·
Lekriqeshdemksvakekddiqriqesesdqikenikeiv akhigetebeijkvahccikeqebetineirvihiseketeistiqkq lerindkiqnkiqeiyekebqinikqisevqekvdelkqpfkeer kakdsalqsieskmibitnriqesqebiqimikekebmkrvqba lqiesdqikbitnkrivakkesqekbyqfikmtavnetqekmce iehlkeqfetqkinibnieteniritqiihenleemsvykerd	1			· · · · · · · · · · · · · · · · · ·
AKHLETEBBLKVAHCCLKEQEBTINELRVNLSBKETBISTIQKQ LBAINDKLQNKIQEIYEKEBQLNIKQISBVQEKVNBLKQFKEER KAKDSALQSIESKMLBLTNRLQESQEBIQIMIKBKBEMKRVQBA LQIERDQLKENTKBIVAKMKBSQEKBYQFLKMTAVNBTQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEBMRSVTKERD	l		Į.	
Leaindklonkigeiyekbeglnikgisbvoekvnblkofkeer Kakdsalgsieskmlblynlobsgebigimikekbemkrvoba Loierdolkentkbivakmkesobkbyoflkmtavnbtobkmce Iehlkeofetoklnlenietenirlyoilhenlebmrsvykerd	Į.	ļ		
KAKDSALQSIESKMLBLTNRLQESQEBIQIMIKEKEBMKRVQBA LQIERDQLKENTKBIVAKMKBSQEKBYQFLKMTAVNBTQEKMCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEBMRSVTKERD	j	ľ	Ţ	
LQIERDQLKENTKBIVAKMKBSQBKBYQFLKMTAVNBTQBKMCB IBHLKBQFBTQKLNLBNIETENIRLTQILHENLBBMRSVTKERD		1	1	
IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD			,	
			į	- · · · · · · · · · · · · · · · · · · ·
DLRSVEBTLKVERDQLKENLRBT1TRDLEKQEBLKIVHMHLKEH			[	LQIERDQLKENTKBIVAKMKESQEKBYQFLKMTAVNBTQEKMCE
				LQIERDQLKENTKBIVAKMKESQEKEYQFLKMTAVNETQEKNCE IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	Bedreice	
<u> </u>	Bedgence		\=possible nucleotide insertion)
ı	<u> </u>		QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR IAHMHLKEQQETIDKLRGIVSEKTDKLSNMOKDLENSNAKLOEK
	ĺ	-	
1	1	į	NSTTLSQCXIQXXAQEMSVXXQTSUVCXXATTLQHSUAXALSQI
1			LEIENLNLAQKLHENL3EMKSVMKERDNLRRVEETLKLERDQLK
į	}		ESLQETKARDLBIQQELKTARMLSKEEKETVDKLREKISEKTIQ
l	1	j	1\$DIQKDLDKSKDBLQKKIQBLQKKELQLLRVKEDVMMSHKKIN
i			EMEQLKKQFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDK
[		ł	LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
}			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
1			RIMKKLKYVLSYVTKIKEEQHBCINKFEMDFIDEVBKQKELLIK
		}	IQHLQQDCDVPSRBLRDLKLNQNMDLHIBBILKDFSESBFPSIK
1	l	ł	TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
1	1	Ì	NNFFNNRI LAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
1	1		KNYQTLKTSLASGAQVNPTTQDNKNPHVTSRATQLTTEKIRELE
1			NSLHEAKESAMHKESKIIKMQKELEVTNDIIAKLQAKVHESNKC
l	l	· .	LEKTKETIQVLQDKVALGAKPYKEBIEDLKMKLGKIDLEKMKNA
1	[	· ·	KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
1	]		DPQPSNKPLTCGGGSGIVQNTKALILKSEHIRLEKEISKLKQQN
Į.	1		RQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
1	ŀ		SPKVTGTASKKKQITPSQCKKRNLQDPVPKESPKSCFFDSRSKS
l	<u> </u>		LPSPHPVRYFDNSSLGLCPBVQNAGAESVDSQP\GFWARLFQGK
	}		DVP\ECKTQ
5815	23	1460	SELVMWTVQNRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
1	1		TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
i .	}		SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
1			QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQPSIVDY
]			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
ĺ			SWYSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
			AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
			NEKNKLEMNKVQVDAHGNILLSTLBIRNETSGSEVLTSVSDPKA
1			TMYSYDSASIQYRKPLSSRB\A+GRAPORHGVPSKGRIRRRAS\
i l	•		QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
J			TVYHERORLELCAVHALNNVLQQQLFSQEAADBICKRLAPDSRL
ì			NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
·			VIGLILNLPSPVSLGLLSLPLRRRHLRNPCARL/VTVSYYNLDS
			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
	İ		SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
[			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
			KKRVDRLRHHLLPMYSYDPARELHEAEQELLSDMGDPKVV\QAG
	i		RVATSTSGCHCWMSRRDLTPLPHPSBPGVLDCLGPCHLLPLLSP
			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
			HPQALMGRGPPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
			DRRLGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKBKDGTKIASKI
			TXBLKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
			TAAAAATGQKNLLNGKGVRNQBGQISGARPKVLTGNLNVQAKAK
		,	PLKKATGKDSPCLSIAGPSSRSTDSSMBFSISTECLDEPKENGS
			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
			NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
			AKLDHNTTTEKQAPKRKMVKOVHTALPKVNAKIVAMPKNLNOSK
	ļ		KGETINNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
			DVRDNNNKDSVSEQKPHKPLINLASEISDAKALQSSCRP\DPQK
			- · · · · · · · · · · · · · · · · · · ·
1			PLNDQBKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
1			
j	ŀ		
	ļ		NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCV3DVS LCRPERTNGTLNSAGRDKKSKVPVEGLTIPSKLSDESAMDEDKH

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Cluberia Brid E Phone I I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I aliant I alia
MO:			Glutamic Acid, F⇒Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ı	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotice deletion,
	sequence	<b>1</b>	\=possible nucleotide insertion)
<b> </b>			ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
1			
1	i		WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
j			GSNDRGISKCGTMLCHDPLGRSSSDTSTPEELKIYDSNLRIBVK
	1		MKKQSSNDLFQVNSTSDDBIPRKRPEIWSRSAIVHSRERENIPR
	1		GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEBLGSDEGE
{			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
1	J		CKONKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1	i l		SSRSRQLLREDKKVNNGSNVENDIQQRSKPLDSDVKSQERPCHL
1			DLHQRBPNSDIPKNSSTKSLDSFRSQVLPQEGPVKBSHSTTTEK
1			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIRAFEQ
1	i :		KVESETHVTDMDF+DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV
1	ļ		PEDLSLAQYLINGTLLLARDSSKPQGITHIDTLNRWSELTSPLD
1	i l		SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLIGALHIVMTLVVAAARAEKEAFVQSESIIBVLRFDDGGL
			LQTETTLGLSSYQQKSISLYRGNCR?IRPEPPMLDFHEQPVGMP
1			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFONRKILPGGNT
1			SPDVS/VPLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
1			RLRPFLGARVTVNSSFSPI INIHNPHSEPLOVVEMYSSGGDI.HL
1			
f			RLPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
			TNASDSTEFIILPVEVBVTTAPGIYSSTEMLDFGTLRTQDLPKV
}			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
1			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
			LPEEAKTMPKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN
			NILLITNASKFHLPVRVYTGFLDYFVLPPKIBERFIDFGVLSAT
!			EASNILFAIINSNPIBLAIKSWHIIGDG\LSIELVAVDRGNRTT
1			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1			DGAIQITTDYELLTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
1 :			VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
			KKSKIANIYPDPGLQCGDHCYVGLPPLSKSBPKVQPGVAMQEDM
1 1			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
1			TABLSWPSILSSPRHLKFPLTNTNCSS\BEBITLENP/SQDVPV
1	·		YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
1 1			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
	*		RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR
			FKITEALLKDCTDSLKLRBPNFTLKRTFKVENTGQLQIHIETIE
1			ISGYSCEGYGFKVVNCQBFTLSANASRDIIILFTPDFTASRVIR
1 1	l		BLKFITTSGSBFVFILNASLPYHMLATCARALPRPNWKLALYII
) !	1		ISGIMSALFLLVIGTA\YLEAQGIWBP\FRRRLS\FEASNPPFD
]		ĺ	VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
, ,	' i	ì	GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAQAA
1 1	1		SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
1 i			PLECHPOPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
] [	j		SSEDSDITSLIRAMDKDFDHHDSPALHVFTEQPPSPLPKSKGKG
	l		KPLCRKVKPPKKQBEKEKKGKGKPQEDBLKDSLADDDSSSTTTB
1	1		TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI
1 .	1		KKBIPTDVKPSSLELPYTPPLESKORRNLPSKIPLPTAMTSGSK
; I	i		SRNAQKTKGTSKLVDNRPPALAKFLPNSQBLGNTSSSBGBKDSP
1 1	}		PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
, I	ļ		PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
1 [	}		SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
] <b>!</b>		į	HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
]		į	VFSKLGLSRSCNQASQRSWNKFNSGPSYLWESPATDPSPSWPAS
<b> </b>	l	]	
] ]	•	Ī	SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
j l			TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
5820	210	1055	RSSDPWSNSHFPHRN
5020	310	1270	RVSLSGPVSLGVLLCARSSTMGKRUNRVAYMNPIAMARSRGPIQ
j Ì	İ	İ	SSGPTIQ\VI*IDQGLPGKK*KSN*KRKK/DSKALAEFEEKMN
j j		ļ	ENNKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\
<u> </u>	<u>_</u>	1	SSSSSSSSSSSSSEDEDKKQGKRRKKKKNRSHKSSESSMSETES

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	E=Histidine, I=Isoleucine, K=Lysine.
İ	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,   -possible nucleotide insertion)
	ocquence	<del> </del>	DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
			ESEYIBEVRAKKKSSEEREKATEKTKKKKKHKKHSKKKKKKAA
1	i		SSSPDSP+H+EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF
Ì			GLIPGLESSHSDATV
5821	179	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
1	ĺ		PT/IKDCSIAATGKRPSARFPHQRRKKRRENDDGLAEGGPQRSN
İ			TYVIKLFDRSVDLAQFSENTPLYPICRAWMRNSPSVRERECSPS
1			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
			SRIPSPLAALRMQGTP*RWSPFBPEPSPSTLIYRNMQRWKRIRO RWKEASHRNQLRYSBSMKILREMYERQ
5822	454	4379	QTLKEMPIVMARDLEETASSSEDEEVISQEDHPCIMWTGGCRRI
1			PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSBAQKVNHFPRSYB
}			LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYABFCNSYS
			KDRGPWIVKPVASSRGRG\VYLINNPNQISLEENILVSRYINNP
1			LLIDDFXPDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
1			NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY LKQBGRDTTALMAHVEDLIIKTIISABLAIATACKTFVPHRSSC
			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
			MFTVVGFVCQDPAQRASTRPIYPTFBSSRRNPFQKPQRCRPLSA
		•	SDABNKNLVGSAREKGPGKLGGSVLGLSMBBIKVLRRVKBENDR
			RGGPIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
			APELKI *SINSKAKLHAALYERKILSLEVRKRRRRSSRIRAMRP
			KYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE
1 .			LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
1		*	QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
			LERTRILAHQLGDFIIVYNKETEQMARKKSKKKVERREEDGVNM
			ENFORFIRQASEAELEEVLTFYTOKNKSASVFLGTHSKISKNNN
			NYSDSGAKGDHPRTIMEEVKIKPPKQQQTTBIHSDKLSRFTTSA
			EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
			RCRSGSHTIGPFSSFQSAAHIYSQKLSRPSSAKAGSCYINKHHS
			GIAKTOKEGEDASLYSKRYNQSMVTAKLQRLAEKQAARQYSPSS
			HINLLTQQVINLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
			SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
	į		KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQA1FGSQT
j			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
[			VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1 .			DLSISSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
			DSPLLGPPVGBPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
]	1		RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAARKPKK
			EIPASPSRTKIPABKESHRDVLPDKPAPGAVNVPAAGSHLGQGK RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
			CTPQPVAKAKSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSWQAKRVDVSRLAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
	I		QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1 1	!		PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1 1	1		GSPPSRVPQALNFSPEESDSTFSKSTATEVARBEAKPGGDAAPS BALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSB
	1	ļ	SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPRADK
	1	!	ENVDSPLLKF
5824	42	2293	LLTALSMEGGGGRDEPSACRAGDVNMDDPKKEDILLLADEKPDF
			DLSLSSSANEDDEVPFGPFGHKERCIAASLELNNPVPEQPPLP
			T8KSPFAWSPLAGEKFVEVYKRAHLLALHIESSSRNQAAQAAKP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Clutaria Acid B Bland 3
1.0,	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
			H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	]	\=possible nucleotide insertion)
			EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
1		} ·	DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP
1	ł		RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGIPGAAEKPKK
1	ļ		ELPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGQGK
ŀ		<u> </u>	RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
1	Ì		CTPOTES CARREST CARREST CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTRO
ŀ	ļ	,	CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
1			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
1	İ		GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
İ	l		QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
ſ	ļ		RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
1			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
1			BALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
1			SRPLIDIMINTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
1			ENVDSPLLKF
5825	2	4210	FLQIESASPAPPSSGFLAAHPHSPGGSLATKGRSRLSAPGMLHL
1	_		SAAPPAPPPEVTATARPCLCSVGRRGDGGKMAAAGALERSFVEL
1			SGAERERPRHFREFTVCSIGTANAVAGAVKYSESAGGFYYVESG
1			
			KLFSVTRNRFIHWKTSGDTLELMEESLDINLLNNAIRLKFONCS
1			VLPGGVYVSETQNRVIILMLTNQTVHRLLLPHPSRMYRSELVVD
1			SQMQSIFTDIGXVDFTDPCNYQLIPAVPGISPNSTASTAWLSSD
			GRALFALPCASGGIFVLKLPPYDIPGMVSVVELKQSSVMQRLLT
l I			GWMPTAIRGDQSPSDRPLSLAVHCVEHDAFIFALCQDHKLRMWS
1			YKBQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLYL
			GIF\MHAPKRGQFCIFQLVSTESNRYSLDHISSLFTSQETLIDF
			ALTSTDIWALWHDAENQTVVKYINFEHNVAGQWNPVFMQPLPER
1			BIVIRDDQDPREMYLQSLFTPGQFTNEALCKALQIFCRGTERNL
			DLSWSELKKEVTLAVENELQGSVTEYEFSQEEFRNLQQEFWCKF
ł i			YACCLQYQEALSHPLALHLNPHINMVCLLKKGYLSFLIPSSLVD
			HLYLLPYENLLTEDETTISDDVDIARDVICLIKCLRLIEESVTV
			DMSVIMEMSCYNLQSPEKAAEQILEDMITIDVENVMEDICSKLQ
)			BIRNPIHAIGLLIREMDYETEVEMEKGFNPAQPLNIRMNLTQLY
1			
			GSNTAGYIVCRGVHKIASTRFLICRDLLILQQLLMRLGDAVIWG
1		•	TGQLFQAQQDLLHRTAPLLLSYYLIKWGSECLATDVPLDTLESN
			LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
			PSQPKAPLSQTGLNWPEMITAITSYLLQLLWPSNPGCLFLECLM
·		•	GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
			BCFCQAASKVGKBEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLD
j j	j		VIGLPELVIQLATSAITRASDDW\KSQATL\RTCIFKHHL\DLG
1 [			\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS
[ ]	ļ		YVNLHNEVVGI IESRARAVDLMTHNYYELLYAFHIYRHNYRKAG
j l	j		TVMFBYGMRLGRBVRTLRGLBKQGNCYLAALNCLRLIRPBYAWI
ļ l			VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE
; I			CSLARIRLTLAOHD?SAVAVAGSSSAEEMVTLLVOAGLEDTATS
1 1			LCQTFKLPLTPVFEGLAFKCIKLQFGGRAAQARAWAWLAANOLS
1 1			SVITTKESSATDRAWRLLSTYLERYKVQNNLYHHCVINKLLSHG
1			VPLPNWLINSYKKVDAARLLRLYLNYDLLDLTPYQVIRICGC
5826	<del></del>	023	
2020	3	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
! I	į		AAAQRSRQKHTDKADALHQQHESLBKDNLALRKEIQSLQAELAW
[	ŀ		WSRTLHVHERLCPNDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
j l	}		CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
Į	i		AVVAEPPVQLSPSPLLYASHTGSSLQGSSSKLSALQPSLTAQTA
; l	ļ		PPOPLELEHPTRGKLGSSPDNPSSALGLARLOSREHKPALSAAT
, l			WQGLVVDPSPHPLLAFPLLSSAQVHF
5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
Į ⁻ !		~~~	RENEDKVNKAAKVP*+HLKTLRHPCLLRFLSCTVRADGIHLVTE
; 1	į		
) [	i		RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
; l	l		SSVFVSRDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
	İ		EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
, ,	l		SPOOTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
LI			TLKSEERTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

motleckide location corresponding to first anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid anino acid a	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
molectide location corresponding to first amino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid antino acid a			•	
Location   Corresponding   Lo first   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amino acid   amin				(A=Alanine, Cacysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequence  sequ	NO:			Guttamic Acid, F=Phenylalanine, G=Glycine,
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amino acid	1 .	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid	1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine.
residue of amino acid sequence (Codon, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide insertion)  WWW.SERVERMINGSTERS.PLOFERVIPULICLE AND A-possible nucleotide deletion, A-possible nucleotide insertion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide nucleotide deletion, A-possible nucleotide nucleotide deletion, A-possible nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleotide nucleoti	1			
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ASGCADTQULIMRITHPDELHCKGLTKRNLKRIHPDSPPHLLDITY PRTPHPHERKVETVEDFFLHLIRLIGSLR*SICRSLLDLLMISE LLILLQQQRPVUGLQCTWKRPUIS*TLF*CHQNVCQQPRKKK QKT*VTSPVKVK/VSIPLAVTDALBHIMBQLAVLTQTVSILEQR LTTTERKLKDCLENGQKLFSAVQGKS  5830  4496  3139  GGRMAAFEERDLTQEQTEKLLQFQDLTGIESMDQCRHTLEQHW NIBAAVQDRLMSQEGUVESVFNPPPSRFLQVNTADHRIYSYVVSR PQPGGLGGGYYLLMLPFRFTYTVIDIFRFALMRIFREPPSRKV TDPVGDIVSFMISPEEKYGRAHPVPYQCTYSQALMDAKRERPL LVYLHHODHQDSDEFCRNTLCAFEVISLINTMEDWAGSTINKPE GTNEVGALRENTYPFLAMIMIKINGRRS*PVVVGRLEGGLI\QPDDL INQLTFIMDANQTYLVSERLERBERRQTQVLRQQQDBAYLASIR AQQEKRKKRBRERRKRKKEVQQQXLABERRQNIQEEKERK LECLPPEPSDDPBSVKIIFKLENDSRVERRPHSQSLITVIHDP LPSIKESP\ERKQLEA\MPPRRVVLPCLIPSE\MPNPPTLQE\A GLSHTSVLFVQDLIDB  5831  71  2897  FCSEDKCCLYLPDSINRSKSCTAKPGAHSQDEHAVMDSERQVKD TDDIRSPRHSILDSGYIDCMDSRRSDSLSPPHGRDDSFDSLDS FGSESRGTPSDPVVLRSSSDGGSDSESDLPHRKIDDSFDSLDS FGSESRGTPSDPVVLRSSSDGGSDSESDLPHRKIDPTKLOW ARHTSHGEPKSAVPPNQYLPNKSNQTAYVPAPLIRKKARREE'R KSMSTATSPAGLGKKALQDYGPRT\PVS\DDABSTSMFDMRCSE AAVQPHBRARQCGLQLINNGLAREDDKMQDLARMSRRRSVS QDLIKKBERKKMEKLLAGBOGTSERRKSIKTYRRIVQRERRRR RELHEAYKNARSQBEARGILQQYIERFTISBAVLERILEMPKILE RESISTEPBLSSFLNDPRPMKYLRQQSLPPPKTATVETTILARS VLIDTSMSAGSSGPSKTVTPRAVPMLTPRFYSQRNSQDVLKTPK VOGKVSVMSTVHRBEREKRECTVAPAHSILTKSQMFRGVARVH GSPLELKQDNGSIEINIKKPNSVPQELAATTRKTEPNSQEDKND GGRSRRGHIELASSEPQHFTTTVTRGSFTVAPABFSPSPQLKND VSEKDQNKPPENHBSKGKURLUSQDLSTSSSMTEGSGTMKIDL KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPBEKRR QKMQQCGSRLLGRRYQ\KKODK\LKES\WERGAKVERERRRY YSEBP\$IT\DEDVEPTVSSSSADDLSTSSSMTEGSGTMKIDL GNQDEKQDRRWKSPGGDDSDLLLKTRRSDDLEEKGSITEGAL ANGGMPVEKGYMEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSEGBVKPTTI-LDKSIMHQTESPSFRRKSIGKKICSSCCL PILKGAMMIETINLYFHIQCRCG\ICKGLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL  FGREGGAMATIENTINLYFHIQCRCG\ICKGLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL  PGREGGAMATIENTINLYFHIQCRCG\ICKGLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL		i	ĺ	
PRTPHPHERKVETVED PILHLIRLIQGIR*SICRSLLDPLLWISE LILIPQQQKPVGLCQTRVKRPVDIS*TLP*CHQNVCQPRKKK QKT*VTSPVKVK,VSIPLAVTDALSHIMEQLNVLTQTVSILEQR QKT*VTSPVKVK,VSIPLAVTDALSHIMEQLNVLTQTVSILEQR LTITEDKLKDCLENQQKLPSAVQQKS GGMAAPEREDLTQGTREILQFQDLTGIESHDQCRRTLEQHNW NIEAAVQDRLNEQEVPSVFNPPPSRPLQVNTADHRIYSTVVSR PQPRGLLGGGYYLINLPFRFTYTTLDIFRFALSFIRPDRSKV TDPVGDIVSFMBSPBEKYGRAPHVPYQCTYSQALDAKRELRFI LVYLHGDDHQDSDEFCRWTLCAPEVUSLINTRMLPWACSTNKDB GYRVSQALRENTYPPIAMINLKDRE*PVVVGRLBGLI\QPDDL HQLTFIMDANQTYLVSSRLERBENQTQVLRQQQDEAYLASLR ADQEKRRKRBERREKRRKKEVQQXLABBERRQNIQBEKERK LECLPPEPSGPDDPSESVKITFKLABBERRQNIQBEKERK ADQEKRRKRBERREKRRKKEVQQXLABBERRQNIQBEKERK LECLPPEPSGPDDPSESVKITFKLABBERRQNIQBEKERK ADQEKRRKNBERREKRRKKEVQQXLABBERRQNIGBEKERK GSHTTSVLFVQDLTDB FGSRCCCTYLPPSESVKITFKLABBERRQNIADBERGVKD GLISHTEVLFVQDLTDB FGSRSQCTPSPDVVLRGSSDGRGSDSSDLPRHGNDSFDSLDS FGSRSRQTPSPDVVLRGSSDGRGSDSSDLPRHGNDSFDSLDS FGSRSRQTPSPDVVLRGSSDGRGSDSSDLPRHKKDDWKKDDMS ARRTSRGBPKRAVPFNQYLDWKSNQTAYVPAPLEKKKARREBEVR KSMSTATSPAGLGKKALQDYGBRT\PVS\DDABSTSMFDDRCSE BAAVQPHSRARQGDQLQLINDLARMKSRRRSUS QDLIKKBERKKMEKLLAGEDGTSERRKSIKTYRRIVQEKERRE RELHEAYKNARSQEBRGLIQQYLEFRTISEAVLERLEMPKILB RESHSTEPNLSSPLINDPNMKYLDLAPPSQPFNSQDVLKTFK VDGKVSVNGETVPKAVPMLTPRPYSQPFNSQDVLKTFK VDGKVSVNGETVPKAVPMLTPRPYSQPFNSQDVLKTFK VDGKVSVNGETVPKAVPMLTPRPYSQPFNSQDVLKTFK VDGKVSVNGETVPKAVPMLTPRPYSQPFNSQDVLKTFF VDGKVSVNGETVPKRESEKEREPTVTAPAVEFPSSPQLKND GGSRGNILLASSEPQHFTTVVRCSFTVAFVEFPSSPDLKND GGKRGNGLELASSEPQHFTTVVRCSFTVAFVEFPSSPDLKND GGKRGNGLELASSEPQHTTTVTRCSFTVAFVEFPSSPDLKND GGKRGNGLELAGREVGKVELVLSQKVVAFKSPSPEPFATLTFPFLD KMPBANQLHLPRILNSQVDSPSSEKSSPVTTFPKWAMDPBEKKRR QKMQQGGRLLQRRYQ\KEQDK\LKEE\MERGSGTNKKIDL GNQDBKQDRRWKKSPQGDDSDLLLKTRESDRLBEKGSITTEGAL AHSGMPVSKGVPBEDQLDTEAGARHCSTNDLAQDPSQKQCTSM PTHSGEDVAPKTLPLKS HILDLESPSERRKSISKKLCSSCGL PILGKGAAN I ETILNIYPHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLINCMCYMRSRSAGQPTTL  5832  5832  2454  829  PGREFEHGSCAFPQGCCTMLHICQYFLQGKCKKFGTSCKRSHDFSN	1	1		
LLILPOQQRPVUK_/VSIPLANTDALEHIMEQLINVLTQTVSILEQR QRT+VTSPVKVK/VSIPLANTDALEHIMEQLINVLTQTVSILEQR LTTTERKLROCLEMQQKLFSAVQQKS  5830  4496  3139  GGRMAAPERERDLTQEQTEKLLQFQDLTGIESHDQCRHTLEQHW NIEAAVQDRLINEQEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR PQPRGLLGMGYYLINLPFRFTYTILDIFRFALRFIRPDPSSRV TDPVGDIVSFMBSPRBKYGRAHPVFYQGTTSQALNDAKRELRFL LVYLHGDBHQDSDEFCRPTLCAPUS_ISLNTYMENPMACSTNKDS CYRVSQALRENTYPPIAMIMLKDRRE+PV\VGRLEGLI\QPDDL INQLTFIMDANQTYLVSRRLERBERNQTQVLRQQQDEAYLASLER ADQBKRKKRERBERKRRKRKEVSUGNLAPHAGASTNKDS LECLPPPSPDDPDSVKIIFKLPDDSRVERRPHFSQSLTVIHDP LPSIKRSP\BKRQIEA\MPPRR\VLPCIPSBE\WPNPPTLQR\A GLSHTTBVLFVQDLTDB  5831  71  2897  FCSEDKCCLYLPPSINRSKSCTAKPGAHSQDBHAVMDSRQVKD GLSHTTBVLFVQDLTDB  FGSRSQTDSPDVVLRGSSDGRGSDSSSDLPHRKLPDVKKDDMS ARRTSGBFKGAVPFNQYLPKNSNQTAYVPAPLRKKKARREEYR KSWSTATSPAGLGKKALQDVGPRT\PVS\DDABSTSMPDMRCSE BAAVQPHBRARQEQLQLINNQLBREDDKMQDDLARMSSRRRESVS QDLIKKBERKREMEKLLAGEDGTSERRSIKTYRETUGRERDRE REHHRAYNGASGBERGGLQUFTERFTISEAVLRRLEMBVKILB RSHSTEPNLSSPLNDPNPMKYLRQQSLPPPRFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTERPYSQPKNSQDVLKTFK VDGKVSVNGETVHREBEKEREFLYRTPAHSLIKTSQMFEGVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTERTPEPSQLKND GGKSRGNIELASSEPQHFTTTVTRCS-TTAFVEFPSSPLKND VSEKDQKKPCHEMBGKVELVLSQWVKPRSBFFSFATLTFPFLD KMPBARQLILPNLNSQVDSPSSERSPVTTPFKPMAWDPBBKRRR QEKWQCGGRELLQERYQ\KEQDK\LLEEK-MERGGSTNKKIDL GGKSRGNELLASSEPQHFTTTVTRCS-TTAFVEFPSSPLKND VSEKDQKKPCHEMBGKVELVLSQWVKPKSBFFSFATLTFFFLD KMPBARQLILPNLNSQVDSPSSERSPVTTPFKPMAWDPBBKRRR QEKWQCGGRELLQERYQ\KEQDK\LLEKTSSMTEGGSTNKKIDL GGCGRRGNIELASSEPQHFTTTVTRCS-TTAFVEFPSSPLKND VSEKDQKKPCHEMGSVLPLUSIESPSERRSSIGKKLCSSCGL PILGKGAMI IETIANLYFHIQCFRCS\LCKGGLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL  FGREPFHGSCAPQGCCTMLHLCQYFLQGBCKRGTSCKRSHDFSN	I	<b>l</b> .		
GKT*VTSPUKVK/VSIPLAVTDALEHIMBQLNVLTQTVSILEQR  LTLTERKLKCLENQQKLPSAVQQKS  5830  4496  3139  GGKMAAPERRIDLTQEGTEKLLQFQDLTGIESMDQCRHTLEQHWW NIEAAVQDRINTSQEGVEKLLQFQDLTGIESMDQCRHTLEQHWW NIEAAVQDRINTSQEGVESVFNEPSBRPLQWTADHRIYSYVVSR PQPRGLIGMGYYLINLPFRFTYYTILDIFRPALRFIRPDPRSKV TDEVGDIVSFMISPERKYGRAHPVEYQGTSSQALNDAKRELRPL LVYLHGDDHQDSDEFCRWTLCAPEVISLITYRMLPWACSTNKQB GYRVSQALRENTYPPIAMINLKDRRE*PVVVGRLEGLI\QPDDL INQLTFIMDANQTYLVSERLERBERQTQVLRQQQDEAYLASLE ADQBKRRKKRERREKRRKKEVQQQKLABERRQNLQBEKERK LECLPPPSPDDPESVKIIFKLPNDSRVERRPHFSQSLTVIHDP LPSLKESP\BKVQIEA\WFPRFYLYLPCLPSEE\WFNPPTIQE\A GLSHTSVLFVQDLTDS  FCSKBKCTLYLPDSINRSKSCTAKPGAHSQDEHAVMDSRRQVKD TDDIPSPKRSIEDSGYIDCMDSERSDSLSUPHRKLPDVKKDDMS ARRTSHEBPKGAVPFNQYLPNSNGYTAYVPAPLEKKKARREEYR KSMSTATSPAGLGKKALQDVGBRT\PVS\DDASSTSMPDMRCSE BAAVQPHSRARQGQQLQLINNQLREEDDKWQDLARMSGRRESVS QDLIKKBERKKREKLLAGBGTSERKSIKTYREIVQBKERRE RELHRAYKRARSQBERAGILQQYIERFTISEAVIERLEMPKILB RESISTEPNLSSFINDPNPMKYIRQQSLPPPFFTATVETTIARAS VLDTSMSAGSGSPSTVTYPKAVPMLTPPRYSQPKNSQDVLKTFK GSPLEIKQDNGSIEINIKRPMSVPQBLAATTRKTEPNSQBUKND GGRSRKGNIELASSPQHFTTTVTRCS-TVAPVEFPSSPQLKND VSEKKOKVSWGETVHRBEEKERECTYVAPAHSLITKSQMFECVARVH GSPLEIKKQDNGSIEINIKRPMSVPQBLAATTRKTEPNSQBUKND VSEKKOKKPENBGKVELVISQKVVKPRSPBFBATLTIFPFID KMPBANQLHLPNINSQVDSPSSERSPVTTPKWAPVEFPSSPQLKND VSEKKQKRPERBMGKVELVISQKVVKPRSPBFBATLTIFPFID KMPBANQLHLPNINSQVDSPSSERSPVTTPKWARDPERBKRRR QEKKQQQGSRILQBRYQ\KEQDK\LKEE\MRKAKERRR QEKKQQBQRRILDRINGCTDSPSSERSPTTTPKWARDPERBKRRR QEKKQCBQRRRKKSPCCDDSDLLIKTRRSDRIEBERGTNIKIDL GNCODBKQDRRNKKSPCCDDSDLLIKTRRSDRIEBERGTNIKIDL GNCODBKQDRRNKKSPCCDDSDLLIKTRTSDRIABERGSITMCAL AHSCNPVSKGVPEDHQLDTERAGPHCCTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINIGIESPSERRKSISGKKLCSSCGL PILGKGAMI IBTIANLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL  5832  2454  829  PGRFFFHGSCAPPQCCTMLHICCYFLQGRCKFGTSCKRSHDFSN	ł	<b>i</b> .		<del></del>
5830  4496  3139  GGRMAAPERDLTGEGTEKTLGPODLTGIESMDCCRHTLEQHNW NIEAAVQDRINEGEGVPSVWPPPSRPLGVNTADHRIYSTVVSR PQFRGLLGWGYYLIMLDFRFTYYTILDIFRPALRFTRPDPSRKV TDPVGDIVSFMHSFERKYGRAHPVFYQGTYSQALNDAKRELRFL LVYLHGDDHQOSDEFCRNTLCAPEVISLINTRNLFWACSTNKDE GYRVGQALRENTYPFLAMINIKDRRE-PV\VGGLEGLI\QPDDL INQLTPIMDANQTYLVSERLERBERNQTQVLRQQDDBAYLASLR ADQEKERKKRERVGQCKLAEERRGONLGEKERK LECLPPEPSDDDESVKIIFKLPNDSRVERRPHPSGSLTVHHDP LYSLKESP\RKPQIEA\NPPRR\VLPCIPSES WPNPPPTLQE\A GLSHTRVLFVQDLTDB  5831  71  2897  FCSEDKCTYLPPSINRSKSCTAKPGAHSQDEHAVMDSRQVKD TDDIFSPKRS ISDEGYIDCMDSRRSDSLSP PRHGRDSFDSLDS FGSRSRQTPSPDVVLRGSSDGRGSDSSDLPHRKLPDVKKDDMS ARRTSHGSPKGAVPFNQYLDNISNGYAVPAPLRKKARREEYR KSMSTATSPAGLKKALQOVEPRT\PVS\DABSTSMFDNRCSE EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWSRRKESVS QDLIKKBERKKMEKLLAGEDGTISERRSIKTIRKTVQEKKERRE RELHAYKNARSGERAGILQOYIERFTISEAVLRELEMPKILB RESHERPRINGSPLINDDFPMKYLRQQSLPPKFTATVSTTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQUVLKTFK VOCKVSVNGETVHREEEKERCCTVAPAHSLTKSQMFECVARVH GSPLELKQDNGSIENIKKPNSVPOBLAATTRKTEPNSQBDKND GGKSRKGNIELASSEPQHPTTTVTRCSPTVAPVBFPSSPQLKND VSEEKDQKKQLOGSESLILVSQKVVKPKSPEPRATLTFPFLD KMPRANGLHLPRINSQVDSPSSEKSPVTTPFKFWAMDPBKKRR QEKWQQEGSRLLQERYQVKEQDKLKEE\WEKAQKEVEBEERRY YEERP 1I \LEDPVVPFTVSSSADQLISTSSSMTEGSGTMNKTDL GNCQBKGQRGRLLDGRYQVKCOMPQLERRY YEERP 1I \LEDPVVPFTVSSSADQLISTSSMTEGSGTMNKTDL GNCQBKGVFENDHQLERKGSLTEGAL AHSGNFVSKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSGNGTSN PTHSSERVKGVFEDHQLDTEAGAPHCGTNPQLAQDPSGNGTDVRIR PGREEGERGAPGCCUMHICQYFLQGEKCKFGTSCKRSHDFSN	1	j		LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
S830  4496  3139  GGRMAAPERROLTQEQTEKLLQPQDLTGIESMDQCRHTLEQHNW NIERAVQDRLMRQEGVPSVPNPPPSRPLQVNTADHR1YSTVUS PQPERGLLGWGVYLIMIPFFRTYYTILDIFRPADRFTRPPRSRV TDPVGDIVSFMHSPREKYGRAHPVPYQGTYSQALNDAKRELRFL LVYLHGJDHQDSDEPCENTLCAPEVISLINTRMLFWAGSTNKYB GYRWSQALRENTYPFIAMINIKDRRE*PVVGRLEGLI\QPDDL INQLTPIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLASLR ADQEKRRKREBERRRRKKEWQQQXLAEBERRENGIQBEKERK LECLPPPSSEDDPESWKI IFKLDNDSRVERRFPHSQSLTVHDP LPSLKESP\EKPQIEA\NPPRR\VLPCIPSBE\WPNPPTLQE\A GLSHTEVLFVQDLTDB  5831  71  2897  FCSEDKCCTYLPPDSINRSKSCTAKPGAHSQDBHAVMDSRRQVKD GLSHTEVLFVQDLTDB FGSERRQTPSDPVVLRGSSDGRGSDSESDLPHRKLEDVKKDDMS ARRTSRBPKGAVPFNQYLDNKSNGTAVVPAPLRKKKARREWS NETATSRBPKGAVPFNQYLDNKSNGTAVVPAPLRKKKARREWS QDLIKKBEKRKMRKHLLAGGBOTSERRKSIKTYRE IVQRERRE RELHEAYKNARSQEARGILQQYIERFTISRAVLERLEMPKILB RSHSTBPNLSSTLNDDFMKYLRQQSLPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTKAVPMLTPRFVSQPKNSODLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMFEGVARVH GSPLEILKQDNGSIENIKKPNSVPGRIAATTRKTEPNSQBDKND GGKSRGNIELASSBPQHFTTTVTRCSPTVAPWEPPSSPLKND VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPBATLTFPPLD KMPENNGLHLPRINSQVDSPSSEKSPVTTPFKFMAMDERBKRRR QKKWQGQGRELLGBRYOLKEGNKLKEW KREQKEVEREERRY YEERP*II\EDPVVPFTVSSSSADQLSTSSSNTEGSGTMKIDL GNCQDBKQDRRRKSPGGDDSDLLLKTRRSDRLBEKRGSLTRGAL AHSGNPGKGVPERDHQLADPSQNQQTSN PTHSSEDVKPKTLPLDKSINHGIESPSERRKSISKKKICSSCGL PLGKGAMIIIETINLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLINCNDCYMRSRSAGQPTTL PGRRPHGSCAPPGCCTMLHICQYFLQGKCKFGTSCKRSHDFSN	1	<b>[</b>	• •	QKT+VTSPVKVK/VSIPLAVTDALEHIMKQLNVLTQTVSILEQR
S830  4496  3139  GGRMAAPERROLTQEQTEKLLQPQDLTGIESMDQCRHTLEQHNW NIERAVQDRLMRQEGVPSVPNPPPSRPLQVNTADHR1YSTVUS PQPERGLLGWGVYLIMIPFFRTYYTILDIFRPADRFTRPPRSRV TDPVGDIVSFMHSPREKYGRAHPVPYQGTYSQALNDAKRELRFL LVYLHGJDHQDSDEPCENTLCAPEVISLINTRMLFWAGSTNKYB GYRWSQALRENTYPFIAMINIKDRRE*PVVGRLEGLI\QPDDL INQLTPIMDANQTYLVSERLERBERNQTQVLRQQQDEAYLASLR ADQEKRRKREBERRRRKKEWQQQXLAEBERRENGIQBEKERK LECLPPPSSEDDPESWKI IFKLDNDSRVERRFPHSQSLTVHDP LPSLKESP\EKPQIEA\NPPRR\VLPCIPSBE\WPNPPTLQE\A GLSHTEVLFVQDLTDB  5831  71  2897  FCSEDKCCTYLPPDSINRSKSCTAKPGAHSQDBHAVMDSRRQVKD GLSHTEVLFVQDLTDB FGSERRQTPSDPVVLRGSSDGRGSDSESDLPHRKLEDVKKDDMS ARRTSRBPKGAVPFNQYLDNKSNGTAVVPAPLRKKKARREWS NETATSRBPKGAVPFNQYLDNKSNGTAVVPAPLRKKKARREWS QDLIKKBEKRKMRKHLLAGGBOTSERRKSIKTYRE IVQRERRE RELHEAYKNARSQEARGILQQYIERFTISRAVLERLEMPKILB RSHSTBPNLSSTLNDDFMKYLRQQSLPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTKAVPMLTPRFVSQPKNSODLKTFK VDGKVSVNGETVHREEEKERECPTVAPAHSLITKSQMFEGVARVH GSPLEILKQDNGSIENIKKPNSVPGRIAATTRKTEPNSQBDKND GGKSRGNIELASSBPQHFTTTVTRCSPTVAPWEPPSSPLKND VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPBATLTFPPLD KMPENNGLHLPRINSQVDSPSSEKSPVTTPFKFMAMDERBKRRR QKKWQGQGRELLGBRYOLKEGNKLKEW KREQKEVEREERRY YEERP*II\EDPVVPFTVSSSSADQLSTSSSNTEGSGTMKIDL GNCQDBKQDRRRKSPGGDDSDLLLKTRRSDRLBEKRGSLTRGAL AHSGNPGKGVPERDHQLADPSQNQQTSN PTHSSEDVKPKTLPLDKSINHGIESPSERRKSISKKKICSSCGL PLGKGAMIIIETINLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLINCNDCYMRSRSAGQPTTL PGRRPHGSCAPPGCCTMLHICQYFLQGKCKFGTSCKRSHDFSN	ł		•	LTLTEDKLKDCLENQQKLFSAVQQKS
NIEANQDRINEQEGUPSVFNPPPSRPLQVNTADHRIYSYVVSR PQPRGLIGWGYYLIMLPFRFTYTYTLDTFRFADRFTRPDPRSRV TDPVGGUTVSIMHSFREKYKGRAHPVFYQGTYSQALIDNARELRPL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPFLAMIMLKDRRE*PV\UGRLEGLI\QPDDL INQLFPIMDANQTYLUSERLERBERNQTQVLRQQQDEAYLASIR ADQEKERKREBERERKRKKEEVQQQKLABEERRONLQEEKERK LECLPPPSPSDDPSSVKIIFKLPNDSRVERRFHFSQSLTVIHDP LFSLKESP\BRFQIEA\NPPRR\UDCTPSB\WPNPPTLQE\A GLSHTKVLFVQDLTDE  5831 71 2897 FCSGMCCLYLPDSINRSKSCTAKPGAHSQDEHAVMDSRQVKD TDDIESPKRSIEDSGYIDCWDSRSDLSPPHGRDDSFDSLDS FGSRSQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS ARRTSHGSPKRAVPFNQYLDNKSNQTAVVPAPLRKKKAEREEYR KSWSTATSPAGLGKKALQDYGBTY-VPS\DDASTSMFDMRCSE BAAVQHBRRARQEQLQLINNQLRERDDKMQDDLARWKSRRSVS QDLIKKBERKKMEKLLAGBGGTSERKSIKTYRRIVQEKERRE REHHRYKNARSOBKARGILQGYIERFTISRAVLERLEMPKILB RSHSTBPNLSSFLNDUPPMKYLRQQSLPPPKFTATUETLIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQDKNSQDVLKTFK VOGKVSVNGETVHREBEKERECPTVAPAHSLIKSQMPPSVARVH GSPLELKQDNGSIEINIKKPNSVPQKLAATTEKTEPNSQBKND GGKSRGNIELASSERQEPTTTVTRCSSTVAFVBEBPSSPQLKND VSEKBQKKPENBWSGKVELVLSQKVVKPKSPEPFATLTPPPLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPKFWAMDPERKRR QKKWQQGGBELLGRYQYKBQDK\LKETKRSDRLEKGSLTBGAL AHSGNPVSKSUVEDHQLDKTRGSRLEKGSLTBGAL AHSGNPVSKSUVEDHQLDTRAGAPHCTTNPQLAQDPSQNQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAMI IETLILVFHIQCFRCG\LKTGSQLGDAVSGTDVRIR NGLLINCNDCYMRSRSAGQPTTL NGLLINCNDCYMRSRSAGQPTTL	5830	4496	3139	
PQPRGLIGWGYYLIMLPFRFTYYTILDIFRPALRFIRPDPRSKV TDPVGDIVSFMHSFREKYGRAHPYYQGTISQAIMDAKRELRFL LVYTHGDDHQDSDEFCRINTLCAPEVISLINTRMLEWAGSTNKPE GYRVSQALRENTYPFLAMIMIKDRRE*PV\VGRLEGLI\QPDDL INQLTFIMDANQTYLVSERLERBERNQTQVLRQQODEAYLASLR ADQBKRRKKREBERRKREKVQQOKLABERRGNLQODEAYLASLR LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHPSQSLTVIHDP LPSIKESP\RKFQIEA\NPPRR\VLPCIPSRE\WPNPPTLQE\A GLSFTRVLFVQDLTDB  5831 71 2897 FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDEHAVMDSERQVKO TDDIFSPKRSIEDSGYIDCWSDERSDSLSPPRHGRDDSFDSLDS FGSRSRQTPSPDVVLRGSSDGRSDSSEDLPHRKLPDVKKDDMS ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAKREEYR KSMSTATSPAGLGKKALQDVGPRT\PVS\DDABSTSMFDMRCSE EAAVQPHSRARQEQLQLINNQLREBDDWRODLARWKSRKRSVS QDLIKKBERKKMEKLLAGBDGTSERRKSIKTYRBIVQEKKREEYR REHHRAYKNARSOBEAGGILQQYIERFTISRAVLERLEMPKILB RSHSTBPNLSSPLNDDRPMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTREPYSQPKNSQDVLKTFK VOGKVSVNGETVIRREBEKERCPTVAPAHSLTKSQMFESVARVH GSPLELKQDNGSIEINIKKPNSVPQBLAATTRKTEPNSQBKND GGRSRKINIELASSEPQHFTTTVTRCSSTVAFVBBSDFQLKND VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPPFLD KMPEANQLHLPNINSQVDSPSSERSVTTPFKFWAWDPERKRRR QKKWQGGGBLLGBRTQ\KEQMK\LLKTRESDFLEEKGSLTRGAL AHSGNPVSKSUVFBDHQLDTRAGAPHCTTNPQLAQDPSGNQQTSM VSEKDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAMIIETLNIFHIQCFRCS\ICKGQLGDAVSGTDVRIR RGLINCNDCYMRSRSAGQPTTL NGLLINCNDCYMRSRSAGQPTLUR UGLINCNDCYMRSRSAGQPTLR PGRRFRHGSCAFQKQCIMLHILQYFLQGSCKFGTSCKRSHDFSN	3330	1150	3133	
TDPVGDIVSFMHSPREKYGRAHPVPYQGTYSQALNDAKRELRFL LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWAGSTINCPE GYRVSQALRENTYPPILAMIMIKDRRP PV VVGRIEGLI VQDDDL INQLTPIMDANQTYLVSERLERBERNQTQVLRQQODBAYLASLR ADQEKRRKREBERKRRKKEEVQQQKLABERRRQNLQBEKERK LECLPPEPSPDDPSSVKI I FKLPNDSRVERRFHPSQSI-TVIHDP LFSLKSSP\EKRQIEA\MPFRR\VLPCIPSEE\MPNPPTLQE\A GLSHTBVLFVQDLTDB  71 2897 FCKDKCCLYLPDSINRSKSCTAKPGAHSQDBHAVMDSERQVKD TDDIESPKRSIEDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS FGSRSQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS ARRISHSPPSGAVPFNQYLPMSNQTAYVPAPLEKKKABREEYR KSMSTATSPAGLGKKADVOPGERT\PVS\DDASSTSMEDMRCSE EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRESYS QDLIKKBEBRKRWEKLLAGEDGTSERKSIKTYRKIVGBERRRE REILHEAYKNARSQEBARGILQQYIERFTISRAVLERLEMPKILB RSHSTBPNLSSFLNDPNMKYLRQQSLPPPKFTATVETTIARAS VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTPK VDGKVSVNGETVHREBEKERCPTVAPAHSLIKSQMPEGVARVH GSPLELKQDNGSIEINIKRPNSVPQBLAATTRKTPEPNSQBDKND GGKSRKGNIBLASSEPQHFTTTVTRCSPTVAFVBFSSPQLKND VSEKNQKVENERMSGKVELVLSQKVVKPKSPBFEATLITPFILD KMPBANQLHLPNLNSQVDPSSEKSPTTTPFKFWAMDPBEKRRR QKKWQOGGBELLLGRRYQ\KEQDK\LKEB\WEKAQKBVEREERRY YBBEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDBKQDRRWKKSPCGDDSDLLLKTRRSDRLEBKGSLTEGAL AHSGNPVGKGVHEDHQLDTBAGAPHGGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAMIIETIMLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLINCNDCYMRSRSAGQPTTL NGLINCNDCYMRSRSAGQPTTL S632 2454 829 PGRFFHIGSCAFPGCCIMLHLCQYFLQGKCKFGTSCKRSHDFSN				
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VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK VDGKVSVNGETVHREBEKERECPTVAPAHSLITKSQMFEGVARVH GSPLELKQDNGSIEINIKRPNSVPQBLAATTRKTEPPNSQBDKND GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND VSEKDQKKPENEMSGKVELVLSQKVVKPKSPEFEATLITFPFLD KMPBANQLHLPNLNSQVDSPSSEKSPVTTPFKKWAWDPBEKRRR QEKWQQEQERLLQBRYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YEBEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSFQGDDSDLLLATTRESDRLBEKGSLTEGAL AHSGNPVSKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMIELTLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCMDCYMRSRSAGQPTTL  5832 2454 829 PGRFFRIGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN	]			RSHSTEPNLSSFLNDPNPMKYLROOSLPPPKFTATVETTIARAS
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GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTPPFLD KMPEANQLHLPNLNSQUSPSSEKSPVTTPFKFWAWDPERKRRR QEKWQGEQBRLLQBRYQ\KEQDK\LKEE\WEKAQKEVEREERRY YEBEP*II\EDPVVPFTVSSSSADQLSTSSSNTEGSGTMNKIDL GNCQDBKQDRRWKKSPQGDDSDLLLKTRESDRLEEKGSLTEGAL AHSGNPVSKGVFEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLGSSCGL PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCMCYMRSRSAGQPTTL  5832 2454 829 PGRFFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN				=
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QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEKEERRY YEEEP*11\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL GNCQDEKQDRRWKKSFQGDDSDLLLATTRESDRLEEKGSLTEGAL AHSCNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL PLGKGAAMI LETLINLYFHIQCPRCG\ICKGQLGDAVSGTDVRIR NGLLNCMDCYMRSRSAGQPTTL  5832 2454 829 PGRFFRGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN	[			KMPRANOLHLPNLNSQVDSPSSEKSPVTTPPKFWAWDPRRKRRR
YEBEP*II\EDPVVPFTVSSSADQLSTSSSMTEGSGTMNKIDL GNCQDBKQDRRWKKSFQGDDSDLLLKTRESDRLBEKGSLTEGAL AHSGNPVEKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN PTHSSEDVKPKTLPLDKSINHQIBSPSERRKSISGKKLCSSCGL PLGKGAAMIIETLINLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL  5832 2454 829 PGRFFRHGSCAFQKQCIMLHICQYFLQGBCKFGTSCKRSHDFSN	1 1			
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PLGKGAAMI LETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL 5832 2454 829 PGRFFRHGSCAFQKQCIMLHICQYFLQGBCKFGTGCKRSHDFSN	j ;	,		
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5832 2454 829 PGRRFRHGSCAFQKQCIMLHICQYFLQGBCKFGTSCKRSHDFSN				
				PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
SKNLKKLISKLIGMSSULVSKLIPTI YKNAHDI KNKSSAPSKVPPLF	5872	2454	829	PLGKGAAMIIETLINLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLINCNDCYMRSRSAGQPTTL
	5832	2454	829	PLGKGAAMI IETLINLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR NGLLNCNDCYMRSRSAGQPTTL PGRRFRHGSCAFQKQCIMLHICQYFLQGBCKFGTSCKRSHDFSN

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
1	1	nucleotide	
ID	beginning nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
No:	location		H=Histidine, I=Isoleucine, K=Lysine,
1	1	corresponding	
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
<del></del>		f	VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
1	}		RVHFHLPYRWOFLDRGKWEDLDNMELIKEAYCNPKIERILCSES
i .			ASTPHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
			<u>-</u>
1			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
l .	}		PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN+KGLPQTQIR\AP
1	}		QDVTTMQTCNTXFFGPKSIPDYWDSSALPDPGFQKITLSSSSEB
	ł		YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
1	·		GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
i			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
I .	İ		GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
1			TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVOFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
-555	-/-	7203	ROGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
1			GRDWNVKWBEN: LHAVAKNYTLLOTIPPFERPFKDHCVCLEWNM
1			
ŀ			GYIWNLRANRIPQCPLENDVVALLGFPYASSGRNTGIVKKFPRF
		}	RNRELEATRORMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN
1			EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKENFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDPHYNDTAGYFII
1			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
1			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
			PSMCRAPPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
į.			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
İ	l	•	FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
}			YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDBIL
1	[ ·		KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
			EAAIENYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
'	1		KKAASKGLEQAVNGLGWYYHKFKKNYA\KAAKYWLKA\BB\MGN
j	l .		PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHRAAQGGHMEGTL
			WCSLYYITGNLETFPRDPEKAVVWAKHVABKNGYLGHVIRKGLN
			AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
ŀ	'		GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLE_S
			VQMYAQAALDGDSQGPFNLALLIRRGTIIPHHILDFLBIDSTLH
1	· ·		SNNISILQELYERCWSHSNEBSFSPCSLAWLYLHLRLLWGAILH
			SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
L			STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
			SAAPGPIPGQSSS+VPLRLEQIQQKADCPLSLELALKPRMAAQV
1			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
			NAFVTGIARYIEQATVHSSMNEMLREGQEYAVMLYTWRSCSRAI
Į l			POVKCNEOPNRVEIYEKTVEVLEPEVTKLMNFMYFORNAIERFC
			GEVRRLCHAERRKDFVSRAYLITLGKFINMFAVLDELKNMKCSV
			KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
			QQLEVISGYBELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF
1			GLYLMDGSVSNTYKLDAKKRINLSKIDKYFKOLOVVPLFGDMOI
			RLARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
			RPISELARYSNSEVVTGSGRQEAQKTDABYRKLFDLALQGLQLL.
1			SONSAHVMEVYSUKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
[			EEKPALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDPSQ
1			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
1			RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLBSLIADKSGSK
1			KILRSSLEGPTILDIBKPHRESFFYTHLINFSETLQQCCDLSQL
			WFREFFLELTMGRRIOFPIEMSMPWILTDHILETKEASMMEYVL
1			YSLDLYNDSAHYALTRFNKQFLYDBIEABVNLCFDQFVYKLADQ
1			IPAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
			HVOLLGRSIDLNRLITORVSAAMYKSLELAICRFESEDLTSIVE
]			LOGLLEINRMTHKLLSRYLTLDGFDAMFRRANHNVSAPYGRITL
			HVFWBLNYDFLPNYCYNGSTNRFVRTVLPPSQEFQRDKQPNAQP
1			QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
1			MERLLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
]			EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
			EVCDLLHAAPFONILPRVHVKEGKRLDAKMKRLESKYAPLHLVP
			<del></del>

SRQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= :)
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ľ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ			
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	j.	\=possible nucleotide insertion)
<del>                                     </del>	<del></del>		LIBRIGTPOOIATAREGOLLTKERLCCGLSMFEVILTRIRSFLD
)			DPIWRGPLPSNGVMHVDECVEFHRLWSAMOFVYCIPVGTHEFTV
		j .	
		1	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
ł .	ļ	i	EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGBGTPVE
ŀ	İ	l	HVRCFQPPIHQSLASS .
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
1	•		DACCAVLSQBSTRYLYGBGDLNFSDDSGISGLRNHMTSLNLDLQ
l	i	ĺ	SONTYHHEREGSRMNGSRTLTHSISDGQLQGCQSNSKLFQQEPQ
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í	1	}	TAPAQVPQGPNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSQQT
,	1	ļ	PRPNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
1	1	İ	RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
	I	1	PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
l	1	1	SOSSAHSOYNIONISTGPRKNOIBIKLEPPORNNSSKLRSSGPR
l			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDRIMSRSQPKVYISA
i	1	I	NAATODEQVMRNOPTLFISTNSGASAASRNMSGQVSMGPAFIHH
I			
l	I		HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP
i .	1	l	GVVSPTFELTNILINHPDHYVETENIHHLTDPTLAHVDRISETRK
ļ	i	1	LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A
1	1	ł	QEFETSWGNIWRLRLYRRF*NYAGNVAHTCSPSYSVD*ALLVHQ
ł	ì	1	KARMERLORELBIOKKKLDKLKSEVNEMENNLTRRRLKRSNSIS
i	1	į	QIPSLBEMQQLRSCNRQLQIDIDCLTKBIDLFQARGPHFNPSAI
	1	ł	HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTBDDBGAQWNCTA
			CTFLNHPALIRCEQCEMPRHF
5836	361	2303	FAITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
1			SDVNYQCLFSAHVLHLRGVLTTQFVEDERGNVFLWNGBIFSGIK
ſ	1	,	VZAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
		· ·	HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
1	l	1	VPAS\DFSBLILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
l			VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
1			
	Į.		FPMCHLQERYFKSFLLMYT*KEVIQQFIDVLSVAVKKRVLCLPR
Į.	1		DENLTANEVLKTCDRKANVAILPSGGIDSMVIATLADRHIPLDE
i	i	(	PIDLLNVAPIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
	† .	İ	AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSMB
ł	1	ł	BLQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
ŀ	1	1	VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKKIM
l		l	MELGRISSRNIGRODRVIGDHGKEARFPFLDENVVSFLNSLPIW
	1	]	RKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
l	1	į	KMEKINEKASDKCGRLOIMSLENLSIBKETKL
L		<u></u>	
5837	4792	903	NGNAVAQAPVINCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
<b>!</b>	1	1	KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
l	1	[	QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
ŀ	1		RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
l	1	ì	MIRVWNTLSIKNNYDVKNFWOGVKSKVTALCNHPTKEGCLAFGT
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]	l	}	HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
		1	P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
1	[	1	VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
i	Ī		DPDCTYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIBLEKKRLSQ
ł	I	1	PKAKPKKKKPTLRTPVKLESIDGNEEBSMKENSGPVENGVSDQ
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I	I	'	EGREQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
}	1	]	ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
l	1		VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
ł	I	[	HLENGHPELPHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
1	i		GYHVWLWAVBAPAKQLCFQDQYVKAASHLLSIHKVYBAVE:LKS
1	l .	Į	NHFYREA IA I AKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
l	1	İ	
1	1	Ī	CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
l	i	1	LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLB
1	1		RKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
ŀ	I		QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW
			1 B B C C C C C C C C C C C C C C C C C

ano l	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	acquence:	ļ	DEAVOALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
	i		HOSPATPAPKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
			T = .
	ł		TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
	l	1	LSTFKELFSEKHASLQNSQRTVAEVQETLAEMIRQHQKSQLCKS
	1	Ì	TANGPDKNEPEVEAEQPLCSSQSQCKEEKNEPLSLPELTKRLTE
i	ľ	<b>!</b>	ANGRMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAGEMQQ
}	1	<b>!</b>	QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
3636	1 ***	1	ISLDLESSCYTKKLSPEKBIYEMES\PSGRIWGNVSTITFQYNG
	į.	}	LGDNMECKGNLEGOVSKSEGLYMCVKITCBEKATESHSTSSTFH
}		ì	RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
l		i	
l	I	1	RNTFSKKPSYI*HQ\KFRLGBKPYECMECGKAFGRTSDLIQHQK
l	1	1	IHTNEKPYQCNACGKAFIRGSQLTBHQRVHTGEKPYDCKKCGKA
1	I	1	FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
	1	1	EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
1	1		SQLNEHQRIHTGEKPYECKECGKTFFRGSQLTYHLRVHSGERPY
i	l	i ·	KCKECGKAFISNSNLIQHQRIHTGEKPYKCKECGKAFICGKQLS
	· ·	1	EHORIHTGEKPFECKECGKAFIRVAYLTOHEKIHGEKHYECKEC
		•	GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
ł		Į.	RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
İ	1	i	GRAFSRGSEHTLHORIHIGEKPYTCVQCGKDFRCPSQLTQHTRL
		1	HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
		7455	GRPFPRPPRALPRLPLRGRRODGRWTVDFEECLKD\SPRFRAAL
5839	1	2425	
1	•		EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
1	ŀ		RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
1	1	l	EIN*GHSFQNFVKBDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
	i .		PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSBLGPYMKDLGAQLDRLVGDA
1			AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
	1	Į	RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
	i	Ł	HCKDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
l	1	1	AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
			CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
i			VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG
	ł	i	OROEKBAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
		1	EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
1	į	ì	TVSANSLYEPEGERQDSSMFLDSKHLNPGLQLYRASYEKNLPKM
1		[	AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFILQNGAN
			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
1	1	1	LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
	1	1	
L	<u> </u>	<u> </u>	RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPRQHLTTLNQISSPRWRSPQRAFMSALSKTQTQSAPALQ
l	1	1	GLSSLLQSVTGNPVPASHAASQSTSASPANTTVYTIKGRNLPSS
1		I	AQPFIPKSFNYSPNSSTSEVSSTSASKASIGQSPGLPSTAFKLP
	1	1	SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1		1	\ZMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHFSDFQ
1	1	1	RGPTSTSIDNIDGTPVRDBRSGTPTQDBMMDKPTSSSVDTMSLL
1		1	SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
1	i	1	SPYKOPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
1			PPSAMMNLOKKPAKSILKSSKLSDTTEYQPILSSYSHRAQEFGV
	1	1	KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
	1	}	SPSKNDSFFTPDSNHNSLSQSTTGHLSLPQKQYPDSPHPVPHRS
1	1	1	
1		i	LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
1	1	1	RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQBEHY
1		I	RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT
1		1	VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
		1	SLGGGGGGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
1			LPPSPLEHGTPFQRBPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
1		1	VDLSNPFTKRAALAHAAPPPPPGRHSGIPFPTPPPPPPPGRHSS
1			SGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
1		I	KDHSSLLQGTLAEHPGVLPGPRDHGGPTQRDLNGPGLSRVRESL
l		_l	

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
•	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	B.	aequence	
	sequence	<u></u>	\=possible nucleotide insertion)
ŀ		1	TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII
İ	Ì		LRSPRPDFRPREPPLSRDPFHSLKRPRPPFARGPPFFAPKRPFF
Į	1	ì	PPRY
5841	1908	762	GLRLFLVLTVWPMMKPSWLSRTEPSKRLLCRTLWCQSGWSSRSY
]	ł	t ·	TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
l .	i	i	RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
ł		l .	GDGLDSGLARRGSAVSALASGLVREPMLGPPFHPTPRFKAVSAK
1	ì	1	SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
1	ł	J	QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
	1	į	
1	1	1	\VEPMCKESDHIHIIALAQGLQRVHPGWBYMGPRPRAATTNPHI
	İ		FP+GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
			IGHCYRGFSVVVKWSYFTPPPLSHDPPPMFY
5842	307	1918	QBPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
1	1	1	WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
i	I,	Į.	HRSRDTAEPSFPKIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
ļ	]	Ĭ	RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPQBA\EG
1	į.	1	KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLQPSS
ŀ	ŧ	ì	RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
ì			RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
İ	1	j	NRTLPSVSRKARFIQDGRPCPIIIWDASLSSASNDTHSSVKLTW
1	}		GTYQQLLKQKCNQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
i			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
ì	i		DPRHLVFIDNKGPFDRSEDNLNFKLLEGIKEFPASAVYVLKSOH
[	ĺ	Į.	LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
		ì	AHGVKVLPMNR
5843	500	1453	GTARLVTCWVLHGQ+VKKPAWEPGVVWL+Q+RCRPKGWGLGAGM
}			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
ì			DALVTFHQQKPIEPRRBLLTQPCRQKDPANVDYBDLFLYSNAVA
1			REAACPVSAPREASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
1	ł	}	LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCBLVVT
1			LGCPRIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
į			LTAPGTKRQKGPHQEGREVGQLH*GDPRGQBLAPNGSESPJLPG
į	1 .	ł	VOARAPGIGRA
5844	202	2471	PDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
3544	1 202	23/2	KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHI.
1			QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEOG
	i .	Í	PRGKPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPCM PGKPGAMCMPGAKGRIGOKGRIGPMGIP+POGPPGPHGLPGIGK
į.		<b>,</b>	
1	ł	Į	PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV
1	1		KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\QGPLGK\PGAPGEP
l	}	ļ	GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGKQGL
	l	ļ	PGLPGPPGLPGIGKPGPPGPKGDRGMGGVPGALGPRGEKGPIGA
1		ļ	PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
	l	1	PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP
Į.		l	GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
1		i	PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL
1		}	PGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDGVKPPHAYG
			AKKGKNGGPAYEMPAFTAKLTAPFPPVGAPVKFNKLLYNGRQNY
}	1		NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
1	[		BYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
		}	SFSGYLLYPM
5845	215	2061	HASNKSASLODKMANPKEKTAMCLVNKLARFNRVOPOYKLLNER
	]		GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
1			KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
!		1	PPPNNRANYNFOVMYNORYHCPIPKIFYVOLTVGNNBFFGEGKT
ſ .			1 1
			RQAARHNAAMKALQALQNEPIPERSPQNGESGKDMDDDKDANKS
			BISLVFEIALKRNMPVSFEVIKESGPPHMKSPVTRVSVGEFSAE
			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
			IVKAGPBYGQGMNPISRLAQIQQAKKEKBPDYVLLSERGMPRRR
j			BPVMQVKVGNEVATGTGPNKKIAKKNAABAMLLQLGYKASTNLQ
L			DQLEKTGENKGWSGPKPGFPEPTNMTPKGILHLSPDVYQEMEAS

	1 50 - 51 - 5-2	To Maked and	I hmino poid
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł .	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			1
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l .	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
<del> </del>	<del> </del>		RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
		1	NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC
ļ.	Į.	İ	DROSGKECVTCLTLAPVOMTFHAIGSSIEASHDOV*YATAILLC
i	ł		
l	1		YGPARKWKAIKMBAMCAHAALLSLIHYLLAPSARLEKSKLFALG
l .	1		M.
5846	1126	456	FSKLIMKTFIIGI8GVTNSGKTTLAKNLOKHLPNCSVISODDFF
1	1	1	KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMBSARHSVVS
!	ŀ		TDQESABBIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
Ì	1	ł	
	J		RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
į.	ł	i	RSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
I	i	(	IQGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQRSVTFKDVIVDFTQEB
1	1	I	WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
ĺ	1	1	PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEKLSPEVIVEK
1		Ì	
1	1	1	HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKKIKVTEKTIPS
Ì	Į.	Í	wekgpvnnefgksvnvssnlvtqepspeetstkrsikqnsnpvk
1	1	1	KEKSCKCNECGKAFSYCSALTRHQRTHTGEKPYKCN*/CVEKAF
I		j .	SRSENLINHQRIHTGDKPYKCDQCGKGFIBGPSLTQHQRIHTGE
1	1	I	KPYKCDECGKAFSQRTHLVQHQRIHTGEKPYTCNECGKAFSQRG
į.	į.	<u> </u>	HFMEHQKIHTGEKPFKCDECDKTPTRSTHLTQHQKIHTGEKTYK
I	I	l	
i	i	1	CNECGKAFNGPSTFIRHMIHTGEKPYECNECGKAFSQHSNLTQ
i		}	HQKTHTGEKPYDCAECGKSFSYWSSLAQHLKIHTGEKPYKCNEC
!	ŀ	ł	GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNLNQHQKT
1	1	ł	HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYQCHECGKTF
ł	ł	-	SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHLTQHKRIHTGA
ĺ	l .	l	KPYECAECGKAPRHCSSLAQHQKTHTEEKPYQCNKC8KTFSQSS
1		ł.	HLTOHORIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK
1	1	1	
1 .	1		CNRCGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
		L	KHQRLHPGI
5848	22	2961	AAPRRILRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
1	1	1	GDGMRGLAVFISDIRNCKSKEAEIKRINKRLANIRSKFKGDKAL
i .	]	1	DGYSKKKYVCKLLFIFLLGHDIDFGHMBAVNLLSSNRYTEKQIG
1	i ·	1.	YLFISVLVNSNSBLIRLINNAIKNDLASRNPTFMGLALHCIASV
j	1		GSREMARAPAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
l	1	1	· ·
		ł ·	VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEBFKTSV
l	I	Ī	SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
i		1	PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
1	Į.	I	ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALKSMCTLA
1			SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
1	1	}	APQIVAEMLSYLETADYSIREBIVLKVAILABKYAVDYTW\YVD
I	1 .	l .	TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
I	1.	1	
	1	i	APACHENLVKVGGYILGEFGNLTAGDPRSSPLTQFHLLHSKFHL
1	I	i	CSVPTRALLLSTYIKFVNLPPEVKPTIQDVLRSDSQLRNADVBL
1	1	1	QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
1	1	1	GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
	i	1	LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNFA
ł	1	ŀ	RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
j .	1	1	· ·
Ì	1	i .	NFTPTLICSDDLQPNLNIQTKPVDPTVEGGAQVQQVVNIBCVSD
	1		
1	1		FTEAPVLNIQFRYGGTFQNVSVQLPITLNKPFQPTEMASQDPFQ
			FTEAPVLNIQFRYGGTFQNVSVQLPITLNKPFQPTEMASQDFFQ RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP
			RWKQLSNPQQRVQNIPKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV
5849	35A5	1805	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF
5849	3545	1895	RWKQLSNPQQEVQNIPKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQP KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
5849	3545	1895	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES
5849	3545	1895	RWKQLSNPQQEVQNIPKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQP KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
5849	3545	1895	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES
5849	3545	1895	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
5849	3545	1895	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHRBDKHITIBDLWKRWKTSEVHNW TLEDTLQWLIBFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNMMKDFILTVSI
5849	3545	1895	RWKQLSNPQQRUQNIPKAKHPMDTEVTKAKIIGFGSALLEZVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSXEAV SQRLCELLSAQF KRRIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHRRDKHITIEDLWKRWKTSEVHNW TLEDTLQWLIEPVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKIQLKALDVVLFGPLTRPHNMKDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
5849	3545	1895	RWKQLSNPQQEVQNIPKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDRHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKIQLKALDVVLFQPLTRPHNMKDFILTVSI VIGVGGCWFATTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE
5849	3545	1895	RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANEVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLITLRTSKEAV SQRLCELLSAQF KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDRHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKIQLKALDVVLFGPLTRPPHNMKMDFILTVSI VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQBENRNVAVEKQNL*RKMHDEINYAKEEACRLRELREGAE CRLSRQYAEQRLEQVRMALKKABKEFELRSSWSVPDALQKWLQ
5849	3545	1895	RWKQLSNPQQEVQNIPKAKHPMDTEVTKAKIIGFGSALLEEVDP NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV SQRLCELLSAQF KRREIKETVPHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ P*DPCMSLSPPCFTREDRFSLEALQTIHKQMDDDKDGGIEVEES DEFIREDMKYKDATNKHSHLHREDRHITIEDLWKRWKTSEVHNW TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI SQLKISDRSHRQKIQLKALDVVLFQPLTRPHNMKDFILTVSI VIGVGGCWFATTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE

		· · · · · · · · · · · · · · · · · · ·	Children and There are a market for the same a market of
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
i	location	corresponding	L-Leucine, M-Methionine, N-Asparagine,
l	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	S=Serine, T=Threonine, V=Valine,
ŀ	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	residue of	amino acid	
I	amino acid	sequence	Codon, /~possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
	1		AHSSSLDEVDHKILEAKKALSELTTCLRERL/RWQQIEKICGFQ
}			IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
1	1	}	PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
		ł	PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNREE
	]	]	ERAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
			IIS/DERYQEMRCP*RIPSGGIL
5850	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
ł			LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
	1	ļ	SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
1	1		EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
}			QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
1			QFILELPHGPTGSPKDLSLQLMPHIPAQCIPPSCNYMILVATSG
1	1		DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
1	1		RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
ļ			KSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
i	Ì		KILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKB
l		ţ	R*AQTFFTVQ*IFLPNLSNLKRHLHLMANKDGQLMTKLFNRLES
1		į.	QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
ľ		1	PHTAVAKVVADRVQDKTCPVIISSTAHYSKFAPAIMQALKIKEI
i	J	ļ	NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
ł			VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAAIAAAEKPAGSPSVMTRAGDHNRQ
	Į.		RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVRLY
Į.	l	]	GNSLLLTAVYGLVVAGSVLVLGAI IGDWVDKNARLKVAQTSLVV
į.		1	QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
		ĺ	ANLASTATAITIQRDWIVVVAGRDRSKLANMNATIRRIDQLTNI
	· ·		LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVBYVLLWKVYQKT
i	i	i	PALAVKAGLKEBETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
1			BLEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
1			LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
ŀ			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTPPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
1		ł	SSSYPSLPALLRARSAPGHCTHRSCGPBWRIDSISRLEMQGARR
ŀ		İ	SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGFPITSGPG/WFRQ
1			YYPPISGRH*VLPTBSDPYYVAMDFGGHGL9SHYSPGVPYYLQT
i		İ	FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
			ESGAWALAPGLPAIHGRSWES
5853	223	1346	RILGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
1		}	PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIPRP
l		Į.	LILHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
ſ		1	GGVETPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
1			HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
1			SRWVRGNPRTGTAATLIGFSRNPTINGSENWGSLVSIQEEGPDT
1		Į.	GWEREKRNPAEMGNPORWASPIHTPPLGPBILRAMPEALRAMPE
1		1	ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLCMGPVP
I			LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
1		1	LXHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
		Į.	RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
1	1	1	GAETIKDLLE/ENFPELKNBLDLQMEKAHRIPLKFNEKKAASRH
1		!	IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
		1	RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
		}	LGKYINQELSLKILLKDLLQLTENIN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
]			PISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS
1			nvslhisylaipflad9flkpv/l*pcnsakhlsfklsslsmvs
		i	GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
	1		LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
1	1		KIISTSAWQKVLCFSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
	1		NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
	1	1	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R-Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence	1 1	\=possible nucleotide insertion)
	10040000		FFLSPKPNSLHOLPSO\TPYOALTGAALAGSYPIWENENTLSWL
i		1	
1		1	PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
1	1		ILPPNOTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
	ł	1	GLAGITTSITSYQTLFTTLSNTVBDMHTSITSLQRQLDFLVGVI
	ì		LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
l		1	RAAEL+HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
1	Í	i	CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV+YQSLRGNH
i	1		SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
	1		PODVLLYFPROPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
1	ì	l	IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
F	Į	1	VDYRGYGKSEGEASERGLYLDSEAVLDYVMTSPDLDKTKIYLSG
		1	
1	i	İ	RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
	1	ł	MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
ì		ł .	LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALBQFIKEVVKSH
			SPEEMAKTSSNVTII
5857	1597	563	KLIGKVLVLSVVADAMAAFAVBPQGPALGSEPMMLGSPTSPKPG
1	Į.	1	VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
ł	1		PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
i	l i		VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
i .		ĺ	GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
1	1		NMWMSNTGNWMHIRYOSKLOARKALSKDGRIFGESIMIGVKPCI
ı	1		DKSVMKSSDRCALSSPSLAFTPPIKTLGTPTOPGSTPRISTMRP
1			LATAYKASTSDYQVISDRQTPKKDBSLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP
1 3335	333		PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
ļ	1	· ·	
	1		PSSGVPTTPPQAGGPPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP
	ļ	*	GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
Ĭ.	'		GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
İ			LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
İ	· ·	1	ALA*NCPKPRLG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
į	4	Í	MFPQ+NCWGRKPFRPNLGPHLKGAVCNRWDDPWBGPTGKGHCLN
	<u> </u>	•	FAS
5859	307	1503	GSSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
			NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
	Į.		RTPIORTPHEIMRRESNRLSAPSYLARSLADVPREYGSSOSFVT
l			EVSPAVENGDSGSRYYYSDNFFDGQRERPLGDRAHEDYRYYEYN
	1		HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
	1		VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWBRVESSEFGT
1			YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQOTERNO
İ	[		SLLVPANPYHTABIPDWLOVYARAPVKYDHILKWBLFOLADLDT
1	[		
1	1		YQGMLKLLFMKBLBQIVKMYBAYRQALLTKLENRKQRQQWYAQQ
L-50.55	<u> </u>		HGKNP
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
1	Į į		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
	]		SWEKIHGKSSQTVAVHHPQYGFSVQGBYQGRVLFKNYSLNDATI
1	1		TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
			PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
	<b>!</b>		NETATIISOYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
}	1		OYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
	[		OWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTOK
1	]		, , , , , , , , , , , , , , , , , , , ,
1			VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
	]		PSPLSTL\ATIKGWTQLPTIIA*CSGVGALFIV\LVKCFGLGIF
]			CYRRRTPRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV
[			KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
	L		KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFNLVASSGDDSQGGDKCGCBVGSWVGSMRVVMARLL
i l			SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC
]	]		TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
1	[	1	LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
	L		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
, vo:	location	corresponding	H-Histidine, I-Isoleucine, K-Lysine,
<b>i</b> :			
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 :	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			Α .
5862	1556	483	PPFQLIMGEIKVSPDYNWFRGTVPLKKIIVDDDDSKIWSLYDAG
1			PRSIRCPLIFLPPVSGTADVFFRQILALTGWGYRVIALQYPVYW
1			DHLEFCDGFRKLLDHLOLDKVHLFGASLGGFLAOKFAEYTHKSP
1	,		RVHSLILCNSFSDTSIPNOTWTANSFWLMPAFMLKKIVLGNFSS
l 1			GPVDPMMADAIDFMVDRLESLGOSELASRLTLNCONSYVEPHKI
1			· · · · · · · · · · · · · · · · · ·
1			RDIPVTIMDVFDQSALSTEAKEEMYKLYPNARRAHLKTGGNFPY
<u> </u>			LCRSAEVNLYVQIHL/R/RNSMEPNTRPLTHQWSVPRSLRCRKA
1			ALASARRSSSVSLAVNDELTRCVLV+SVASAPVSRPFPSGSSGS
l i			PVLTVSGK
5863	2714	249	PFPSRGSLPLAAPREDTMGPLMVLFCLLFLYPGLADSAPSCPON
] 1			VNISGGTFTLSHGWAPGSLLTYSCPQGLYPSPASRLCKSSGQWQ
1			TPGATRSLSKAVCKPVRCPAPVSFENGIYTPRLGSYPVGGNVSF
			BCRDGFI\LRGSPVRQCRPNGMWDGETAVCDNGAGHCPNPGISL
			GP\VRTGFRFGHGDKVRYRCSSNLVLTGSSERECQGNGVWSGTE
1			PICROPYSYDFFEDVAPALGTSFSHMLGATNFTQKTKESLGRKI
1			QIQRSGHLNLYLLLDCSQSVSENDFLIFKESASLMVDRIFSF3I
			NVSVAIITFASEPKVIMSVINDNSRDMTEVISSLENANYKDHEN
			GTGTNTYAALNSVYLMMNNQMRLLGMBTMAW\QBIRHAIILL\T
1			
1			DGK\SHMGGSPKTAVDHIREILNINQKRNDYLDIYAIGVGKLDV
1	,		DWRELNZLGSKKDGERHAFILQDTKALHQVFEHMLDVSKLTDTI
Į į			CGVGNMSANASDQERTPWHVTIKPKSQET\C\RGALISDQWVLT
1			AAHCFRDGNDHSLWRVNVGDPKSQWGKEFLIEKAVISPGFDVFA
1			KKNQGIL\EFYGD\DIALL\KLAQKVKM\STHCQGPSCLP\CTM
1		•	\RANLGFLRETPKGSTCR\DHENEL/VWNKQSV\PAHF\VAL\N
1	·	-	GSKLEHLTLRMGVEWTSCCRGLSPKKKTM\PPNLT\DVRB\VVT
J	J .		D\QFL\CS\GPQEDESP\CK*E\SGGA\VFLERRFRLSAGGVWC
1			SWGL\YNP\CIGSA\DKNSPKKGPSVAKVPPPTR/DFHIN\LPP
	·		Q*SPWLROHPGGMS*IFLPLLANGHLSPFACPARICRPLEFLPS
j i			EWATLETL
5864	173	1013	PLISVPQSLISLPQPLLCFPGGQEPSAPSPCLYSFLWACSFTMG
3001		1025	KLPPSIPPSSPLACVLKNLKPLOLTPDLKPKCLIFFCNTAWPQY
I	· '		KLDNDSK*PRNGTFEFSILQVLDNSCHKMGKWSEVPDVQAFF\S
1	i		HWSLPSLCSQC/GLIPNLSSFSPFCSPG/PPPQVPSP/TESFFS
i			·
1			MDSSDLPPSPQAAPRQARPGPNSHLASAPPPYNPFITSPPHTWS
			SLQFHSVTSPPPPAQQFTLKKVAGAKGIVKVSAPFSLSQIR*RL
			GSFSSNIKIQPSSWLIWQQP
5865	568	1684	CLPGPRWGBGWRAGHTIVGCIFFKTAIISHFKGGMYLCVCMCTC
[			LSVCVCVQVGSWICV/CVSMCACVSLCTC\ICRCISMYTREHAC
			ACTRV+VYMCMS/VCTCVSTCIDVRVCAHVCVYMCLCLGYA+AC
			TCV*MCVCMHEHVCMC/VCACSCVLL/CRGHICM/MCMSAYICI
			/CVYVCVLCVWACMRMSTCVWLVYG*ACTCVWMHM/CSCTCR/C
1	!		VHVCCMSMHACECLCVYLHICGCAGTRRWWAGSARGSRSCSRLP
	l		CWAPGPGLSLPGPSCPSVEQGLGGGPGQLQGRSGEAREGEHRGW
!			GSPAAVCSRNCTVSPRRGADCFEAPDVPKQPPGWGRASFEERGC
1 .		1	GGRGWVCAPPLNGPQCCCFSIKPELKAKKKK
5866	98	3197	ARPEVPAPPAWLSRRGAAKMGDKKDDKDSPKKNKGKERRDLDDL
2000	²⁰	3171	
1			KKEVAMTEHKMSVEEVCRKYNTDCVQGLTHSKAQEILARDGPNA
1	]		LTPPPTTPEWVKFCRQLFGGFSILLNIGAILCFLAYGIQAGTED
] 1		•	DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ
!			QALVIREGEKMQVNAREVVVGDLVEIKGGDRVPADLRIISAHGC
			KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA
i I			RGVVVATGDRTVMGRIATLASGLEVGKTPIAIBIBHFIQLITGV
			AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV
			CLTLTAKRMARKNCLVKNLKAVETLGSTSTICSDKTGTLTQNRM
			TVAHMNFDNQIHRADTTEDQSGTSFDKSSHTWVALF*H/LLGFC
ł i	]		NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
i			RNKKVARIPFNSTNKYOLSIHETEDPNDNRYLLVMKGAPERILD
i I		}	RCSTILLQGKEQPLDEEMKEAPQNAYLELGGLGERVLGPCHYYL
			PREOFPRGFAPDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
<u> </u>	<u>L</u>		KCRSAGIKVIMVTGDHPITAKAIAKGVGIIFEGNETVEDIAARL

CEO	Predicted	Predicted end	Invino soid gramont control
SEQ			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ŀ	residue of	I.	
l l	<b>■</b> *	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Į.	amino acid	sequence	Codon, /≈possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILONHTRIVPAR
1	ļ		TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
1	Į.	Í	
ł		ľ	AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL
1	ļ		TSNIPEITPFLLPIMANIPLPLGTITILCIDLGTDMVPAISLAY
1	i .		EAAESDIMKROPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
[		1	YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYBQRK
l .	[		VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
1	1		GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
l.			YDEIRKLILRRNPGGWVEKETYY
			l
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
1			GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRP2KAPE
1	]		DP\$QNWKALQEWILLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
			BTSPQVKGERMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
1			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GOPOPHPPR/IDI
1	Į.		WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
i			1
ł	1	1	GLTRALALDCEMVGVGPKGERSMAARVSIVNQYGKCVYDKYVKP
1			TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
1			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
1			ILGLQVQQAKHCSIQDAQAAMRLYVMVKKBWESMARDRRPLLTA
Į.			PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
	1		ESWORGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
3000	2122	833	
	1		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
i .	1		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1			LESRV+T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1	Į į		IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
Į	1		CCLPVCAVNFKCLHELVKHEENGLVFEDSRELAAQLQMLFSNFP
i	i		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	<u> </u>
3003	2122	633	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
l .	l		TERSAFTERDAGSGLVTRLRERPALLVESTSWTEDEDFSILLAA
1			LESRV+T\MTLDGHNLPSLVCVITGKGPLRKYYSRLIHQKHFQH
I	i		IQVCTPWLEARDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
ł	1		CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
	!		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
FORG			
5870	2122	833	LTAGASHTODASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
I			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
1	}		TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
1	1		LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
1	]		IQVCTPWLBABDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
1			CCLPVCAVNFKCLHELVKHEENGLVFEDSERLAAOLOMLFSNFP
1	<u> </u>		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	. 3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
l	<u> </u>		VLKLL*LSLRRL*LKPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
I			LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLPPTKT
1	1		CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
I			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
1	]		YERYCHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
J	j i		
i	]		CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTKLHSSSVGLGKRQ
I	]		L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
1	}		SHNIDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
F :	1		FLRDGYRTSLEDPNRCYYKPARIKLFDGIRCEFPIFFLYMMIDG
1			VFRGNPKQVQBYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
l			KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
1	1		DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
1	l i	•	FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
1		*	PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
]	ļ		DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPTLDMLAA
į l		:	LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTEBLPEFKS
			PRELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHRIL
L			QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

Predicted   Predicted   Predicted   No.   Despiration   Predicted   Docation   Docation   Corresponding   Control   Control   Control   Corresponding   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Control   Co		Decede about	Predicted end	Amino agid coment containing signal portido
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to first minio acid residue of anio acid sequence  ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide deletion, _\possible nucleotide insertion)  ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide insertion)  ##SOKEMSWERASALISKWUSLAPSITIWIVQKGVTLGAFG EREWISNPLSPWIQNITYEKSTHERERAVIQQELVINIGNI		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first minio acid residue of anio acid sequence  ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide deletion, _\possible nucleotide insertion)  ##Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide insertion)  ##SOKEMSWERASALISKWUSLAPSITIWIVQKGVTLGAFG EREWISNPLSPWIQNITYEKSTHERERAVIQQELVINIGNI			-	
maino acid residue of amino acid sequence  8-Serime, T-STRTeonine, V-Valine, W-T-Type(poban, Y-Tyrosine, N-Unknown, *-stop Codon, /-possible nucleotide deletion, /-possible nucleotide disection)  ASSOKIMSVERRASSILISKVDSLAPSITIVE/CKSCVDTLARGE EEREVISRUS-LSPHUJORI ITYKE/STRDERESHVJOGELVIRIAGE EEREVISRUS-LSPHUJORI ITYKE/STRDERESHVJOGELVIRIAGE EEREVISRUS-LSPHUJORI ITYKE/STRDERESHVJOGELVIRIAGE EEREVISRUS-LSPHUJORI ITYKE/STRDERESHVJOGELVIRIAGE EEREVISRUS-LSPHUJORI ITYKE/STRDERESHVJOGELVIRIAGE SEVENDIDIOLI IQOQOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLSKIRIPTONIPULOS SEVENDILIDIOLOGOMORGIMINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDOLOGOMORI/CKRINGIDIOLOGOMORI/CKRINGIDIOLOGOMORI/CKRINGIDIOLOGOMORI/CKRINGIDIOLOGOMORI/CKRINGIDIOLOGOMOR			L	
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KGGYKGNGLACSAIPENSYKEVLRAPGTINDRIKKLÄHKKISHK KKAKIKNVTPEPTRYPTPKVNIQPFNYBELVSRGGNSHGG\KKG NERMKRSCLADBERRERKALKD*HERREPFRS\DVPFPKVKEAGE FGIIL\VORKALTSKLEHKADLANISVDCSPRIBG\CDW\KQDR\ BODFDW\MPPADR\DNAIG\CPYMAVEDGSRIBG\CDW\KQDR\ BODFDW\MPPADR\DNAIG\CPYMAVEDGSRIBG\CDW\KQDR\ BODFDW\MPPADR\DNAIG\CPYMAVEDGSRIBG\CDW\KQDR\ BODFDW\MPPADR\DNAIG\CPYMAVEDLAGGKK\GDIEKLLL\ PDLQPOSMFCLLEDYRLAGDKVGKLRVFVKNSNNALAWEKTTEE DEKKKTGKIQLYQGTDATKSIIFEAERGKHRANARRITOETFD GCCPDSLLSVDD ACPRIARRERVESLERSWHIRARWSRGONNMAARRITOETFD VISDORYSLGSSWASHROAGKSILGSLAVPSKGSRAWYDD VISDORYSLGSSWASHROAGKSSILGSLAVPSKGSRAWYDD SYPKRECGRDLEPSHSNSRQVIGHRKLGHFSQDMKFALRGSW EQDMCHPVSQSSSWSGBYSFGPSAVLGDRGSSRLIEKSCLERE\ SENDYDVDHSG\BA\DSVLRGS\SQVQA\RGRAINIVDQEGSLIG KGGTGGLITARGGYGKLVTLRWSTRIFTVNRITPKTQGTNQI QKNTBSPDVTLGTNPGTEDIQPPTQKIPLGRIGNUTPROTINGTTNQI GKTSPDVTLGTNPGTEDIQPPTQKIPLGRIGNUTPRILBET ETCARMLASKKCSILREBHDPCFFTIIFLKEGALETPKVINNELL MMLLDKGAVKTKNCFFEIIRPFDKYIMRLQGHLESVTPLIMAG SPRQRKIL*AUGLQDILAPSPAAPINFRDSILGAKAPSILSDAVP QRADHRVGTILQLVKRVIEGSLEPKRETLLEGDPAVMPLSDEN SILSYKYYKILKIARMQRMERIRRGADQKPTSADCARMANISRAV RNIKKKLDP\QRRGILARAGG\LSG\KARRA\TTGTTLIFLE APGLHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGEPSPKRAVDIISRAPGTS-PC-RADIMKUNGRTAR KLARFVAQVQ\PBIEQP\SILRNSTNDDLMFL\HDODRS\AFK FY\RKVVPELCPSICFTSSPHN\HTGGGDTT\GSGBEPVDLMB GRARFBDB PPPRRBLESPFVMPEEDENGGGRBAPA\CRG GPSLEGSTPADGLPGRA\AEDDL\ALGAPALFTGILQVTCFPPG RGFSKSLKVGMIPARKVCLIQBPKWHEPVILADRPRGSPMS KKKKPKOLDPAQQK\LTVX\KIGGD\AKDRACHTARDRPRGSPMS KKKRPKOLDPAQQK\LTVX\KIGGD\AKDRACHTARDRPRGSPMS KKKRPKOLDPAQQK\LTVX\KIGGD\AKDRACHTARDRPRGSPMS KKKRPKOLDPAQQK\LTVX\KIGGD\AKGRSGHGLSSLK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPIGSFTAKMAYSWQL IFVF  S875 296 1848 LAALEGLPLWISGRGFREYLLIGLSAPSALGAMRSVSYVQNA LEPSGSLPHAICLGDVONDTILRILVVGDTSKKVYVKNDGGRP WILTCSCQGMITCGVGVONOVTIKIGKULVARRGWHHEDILTPK VLDASGHHETLIGEBQRPVPKQHIPANTKVNLISDIDGGGCREL VUGYTDRVVRAFRWELGEGPBHLTGQLVSIKKMLBGQVDISS VLDASGHHETLIGEBQCAYALLCTKKNDTSSPPASEGFTDISS		)	Į	
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MAYELSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNPEDSTLFGREYIDHLKAML VESGCPLQVKKAPEPEMREEKKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTILQLVKRVIEGSLSPKERTLLKEDPAYMPLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLERASGPSPKRAGVDISEAPQTSSPCPSADIDMKDMGRTAE KLARFVAQVG\PSILEQF\SI\ENSTDNPDLWFL\HDQNSS\APK FY\RKVPELCPSICFTSSPHNL\HTGGGDTT\GSQBEFVDLMB GRAEFEDEPPPRHAELESPEVMPEBEDEDDEDGGBEAPA\PGRG GPSLEGSTPADGLPGEA\ABDDL\ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLPPHAICLCDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCGGUDCNKGKNLLVAVSARGWPHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGGCREL VVGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRFGIBIIKWAGFHTIKDDIKFSQLFQTLFBLBT
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VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYMPLSDEN SLBYKYYKLKLAEMQRMSERNLRGADQKPTSADCAVRANLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGSPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWPL\HDQMSS\APK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB GRAEFEDBPPPRBBELESPEWMPEBEDEDDEDGEBRAPA\PGRG GPSLEGSTPADGLPGEA\ABDDL/ALGAPALFTGLLQVTCFFPG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKOLDFAQQKL\TDK\NLGFQ\MLQKMGKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGGGCREL VVGYTDRVVRAFRWBELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLFQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPILMAC
QRADHRVVGTIDQLVKRVIEGSL9PKERTLLKEDPAYWPLSDEN SLEYKYYKLKLÆMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\WQRRGLLRAGG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB GRÆFFEDPPPREAELESPEVMPEBEDEDDEDGGBRAPA\PGRG GPSLEGSTPADGLPGEA\ARDDL\ALGAPALFTGLLQVTCFPPG RGPSSKSLKVGMIPPAPKRVCLIQBPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAMGGSCWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDLDGGGCREL VVGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKNAGFHTIKDDIKFSQLFQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNBFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
SLEYKYYKLKLAPMQRM9ENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LrG\WKARR\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLBASGP3PKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PBIEQF\SI\ENSTINPDLWFI\HDQMSS\APK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB GRAEFEDEPPPRBAELESPEVMPEBEDEDDEGGBRAPA\PGRG GPSLEGSTPADGLPGEA\ABDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQBFKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLPPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGGGCREL VVGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLBGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEPL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTINSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFKDSTLFGRBYIDHLKANL
RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLERAGPSPRKPAGVDISEAPQTSSPCPSADIDMKDDGRTAE KLARFVAQVG\PSILEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQBEFVDLMB GRAEFEDEPPPRHAELESPEVMPEBEDEDDEDGGBEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCGGUDCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGGCREL VVGYTDRVVRAFRWBELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP
APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFF FY\RKKVFBLCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB GBAEFEDEPPPRBAELESPEVMPEBEDEDDEDGEBRAPA\PGRG GPSLEGSTPADGLPGEA\ABDDL/ALGAPALFTGLLQVTCFFFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NIGFQ\MIQKMGMKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGGCREL VWGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRPGIBIIKWAGFHTIKDDIKFSQLVQTLFBLET BTCAKMLASFKCSLKPEHRDPCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCPFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALTTNSLCRKSLALLGQTFSLAS SFROBKIL*AVGLQDIAPSPAAFPNPEDSTLFGRBYIDHLKAVL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLBASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFF FY\RKKVFBLCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB GBAEFEDEPPPRBAELESPEVMPEBEDEDDEDGEBRAPA\PGRG GPSLEGSTPADGLPGEA\ABDDL/ALGAPALFTGLLQVTCFFFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NIGFQ\MIQKMGMKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGGCREL VWGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRPGIBIIKWAGFHTIKDDIKFSQLVQTLFBLET BTCAKMLASFKCSLKPEHRDPCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCPFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALTTNSLCRKSLALLGQTFSLAS SFROBKIL*AVGLQDIAPSPAAFPNPEDSTLFGRBYIDHLKAVL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
QDPSLEASGP9PKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVPELCPSICFTSSPHNI\HTGGGDTT\GSQB6FVDLMB GRAEFEDBPPPRHAELESPEVMPEEDEDDEGGEBAPA\PGRG GPSLEGSTPADGI-PGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKOLDFAQQKL\TDK\NLGFQ\MLQKMGNKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGGCREL VVGYTDRVVRAFRWEELGGGPEHLTGGLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET BTCAKMLASFKCSLKPEHRDPCFFTIKFLKHSALKTPRVDNBFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALETINSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWPLSDEN SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMLYSRAV
KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWPL\HDQNSS\AFK  FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB  GRAFFEDBPPPRRAELESPEVMPEBEDDEDGEGBRAPA\PGRG  GPSLEGSTPADGLPGBA\ABDDL/ALGAPALFTGLLQVTCFPFG  RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS  KKKKPKOLDFAQQKL\TDK\NIGFQ\MLQKMGWKBGHGLGSLGK  GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL  IFVP  5875  296  1848  LAALGGLPLWRLSRRGFRBYLLGLSAPSALGGAMRSVSYVQRVA  LEPSGSLPPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP  WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK  VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGGGCREL  VVGYTDRVVRAFRWBELGGGPBHLTGGLVSLKKWMLEGQVDSLS  VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRFGIBIIKWAGFHTIKDDIKFSQLFQTLFBLET BTCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNBFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRILLKSVTPILMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFKDSTLFGRBYIDHLKAWIL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTLQLVKRVLBGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILFLR
FY\RKKVPELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLME GRAEFEDEPPPREAELESPEVMPEBEDEDDEGGBRAPA\PGRG GPSLEGSTPADGLPGEA\ARDDL\ALGAPALFIGILQVTCFPPG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEGPEHLTGGLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEPL ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEPL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQORLLKSVTPLLMAC NAYBLSVKMXTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\WQRRGLLKAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
GRAEFEDEPPREAELESPEVMPEBEDEDDEDGEBEAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGILQVTCFPPG RGFSSKSLKVGMTPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLPPHAICLGDVONDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSABGWPHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDLDGGGCREL VVGYTDRVVRAFRWBELGGGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRPGIBIIKWAGFHTIKDDIKFSQLYQTLFBLBT ETCAKMLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPILMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNPEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBBKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFIR APGLKHHGRQAPGLS\QARPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR
GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMTPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDLDGDGCREL VWGYTDRVVRAFRWEELGGEPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKANL VSSGCPLQVKKAEPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVGTIDQLVKRVIEGSLSPKERTLKEDPAYWFLSDEN SLEXKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAHLYSRAV RNLKKKLLP\WQRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDFSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PBIEQP\SI\ENSTDNPDLWPL\HDQNSS\AFK
GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMTPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDLDGDGCREL VWGYTDRVVRAFRWEELGGEPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKANL VSSGCPLQVKKAEPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVGTIDQLVKRVIEGSLSPKERTLKEDPAYWFLSDEN SLEXKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAHLYSRAV RNLKKKLLP\WQRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDFSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PBIEQP\SI\ENSTDNPDLWPL\HDQNSS\AFK
RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGVRBYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPBLMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHESALETPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKANL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSKNLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDFSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGTT\GSQBSPVDLMB
KKKKPKOLDPAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSIGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGGEPEHLTGGLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVPSRPGIBIIKWAGFHTIKDDIKPSQLYQTLFBLET BTCAKMLASFKCSLKPEHRDPCFFTIKFLKHESALETPRVDNEFL NMLLDKGAVKTKNCPFBIIKPFDKYIMRLQDRLLKSVTPLLMAC MAYBLSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNPEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\MQRRGLLKAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFI\HDQMSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGTT\GSQBSPVDLMB GRAEFEDEPPPRBAELESPEVMPEBEDEDDEGGBBAPA\PGRG
GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF  5875 296 1848 LAALGGLPLWRLSRRGFRBYLLGLSAPSALGGAMRSVSYVQRVA LBPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHBTLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWBELGGEPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNEPL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYKLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\QQRRGLLRAQG\LRG WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLME GRAFFEDEPPPRAELESFEVMPEEEDEDDEDGGEBAPA\FGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLQVTCFFFG
1FVF  5875 296 1848 LAALGGLPLWRLSRRGYREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLPPHAICLGDVDNDTLINELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEQQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKMLASFKCSLKPEHRDPCFFTIKFLKESALKTPRVDNBFL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPILMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLABMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\WQRRGLLRAQG\LRGAVKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFI\HDQMSS\AFK FY\RKKVFELCPSICFTSSPHNL\TTGGGDTT\GSQBSPVDLMB GRAEFEDEPPPRBAELESPEVMPEBEDEDDEGGBERAPA\PGRG GPSLEGSTPADGLPGBA\ARDDL/ALGAPALFTGILQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQBPKVHEPVRIAYDRPRGRPMS
1FVF  5875 296 1848 LAALGGLPLWRLSRRGYREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLPPHAICLGDVDNDTLINELVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEQQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVFSRPGIBIIKWAGFHTIKDDIKFSQLVQTLFBLBT ETCAKNLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QARPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GRAFFEDEPPPRBAELESPEVMPEBEDEDDEGGBBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSKSLKVGMIPAPKRVCLIQBERVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
5875 296 1848 LAALGGLPLWRLSRRGYRBYLLGLSAPSALGGAMRSVSYVQRVA LBPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQCMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHBTLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPBLMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVFSRPGIBIIKWAGFHTIKDDIKFSQLVQTLFBLBT ETCAKNLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QARPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GRAFFEDEPPPRBAELESPEVMPEBEDEDDEGGBBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSKSLKVGMIPAPKRVCLIQBERVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASCHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLFELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRPGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNEFL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTILQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHGRQAPGLS\QARPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMB GRAFFEDEPPRHAELESPEVMPEBEDEDDEGGERAPA\PGRG GPSLEGSTPADGLPGRA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKGLKVGMIPAPKRVCLIQBPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL
WITCSCQCMLTCVGVGDVCNKGKNLLVAVSAKGWFHLFDLTPAK VIDASCHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPBLMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS				QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIBIIKWAGFHTIKDDIKFSQLYQTLFBLET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHESALKTPRVDNEFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFRDSTLFGRBYIDHLKANL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLEXKYYKLKLABMQRMSENIRGADQKPTSADCAVRAHLYSRAV RNLKKKLLP\WQRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDFSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSPVDLMB GRAFFEDEPPPRRELESFEVMPEBEDEDBEDGGBRAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF
VLDASCHHETTLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKPSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRFL ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRFL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMXTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFKDSTLFGREYIDHLKAML VSSGCPLQVKKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWPLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GRAEFEDEPPPRBALLESPEVMPEEEDEDDEDGEGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGSPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLGMGMKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP LAALGGLPLWRLSRRGYREYLLGLSAPSALGGAMRSVSYVQRVA
VLDASCHHETTLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKPSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRFL ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRFL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMXTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFKDSTLFGREYIDHLKAML VSSGCPLQVKKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWPLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMIYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTILFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLME GRAEFEDEPPPRBALLESPEVMPEEEDEDDEDGEGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGSPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLGMGMKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP LAALGGLPLWRLSRRGYREYLLGLSAPSALGGAMRSVSYVQRVA
VVGYTDRVVRAFRWEELGEGPEHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLPELMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYKLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLKEDPAYWFLSDEN ELBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\MQRRGLLRAQG\LRG WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB GRABFEDEPPPRBAELESPEVMPEBEDEDDEDGEBEAPA\PGRG GPSLESSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGPSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NILGFQ\MLQKMGNKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP
VTLGPLGLPBLMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKMLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNBFL MMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRILLKSVTPILMAC NAYKLSVKMXTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYMFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNIKKKLLP\WQRRGLLRAQG\LRAQG\LRAV\TGTQTTLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDMGRTAR KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFI\HDQMSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGDTT\GSQBSPVDLMB GRAEFEDEPPRBAELESPEVMPEBEDEDDEDGGBERAPA\PGRG GPSLEGSTPADCLPGEA\ARDDL/ALGAPALFTGILQVTCFFFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKRPKOLDFAQQKL\TDK\NIGFQ\MLQKMGMKBGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL LFFGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKFSQLYQTLFBLBT ETCAKMLASFKCSIKPEHRDFCFFTIKFLKESALKTPRVDNBFL NMLLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNPEDSTLFGRBYIDHLKAML VSSGCPLQVKKABPEPMREBBKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAB KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGDTT\GSQBSFVDLMS GRAFFEDEPPPRBAELESPEVMPEBEDEDDEGGBBAPA\PGRG GPSLEGSTPADGLPGBA\ARDDL/ALGAPALFTGILQVTCPFPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVP LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LRFSGSLFPHATCLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSABGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
/SGDPSCPRRGAAPDIWPYPQQBCLHSPNWQHQT\SHGTESSGS	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRPGIBIIKWAGFHTIKDDIKFSQLVQTLFBLET ETCAKNLASFKCSIKPEHRDPCFFTIKFLKHESALKTPRVDNBFL MILLDKGAVKTKNCFFBIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYBLSVKMKTLSNPLDLALALETTNSLCRSLALLGQTFSLAS SFRQBKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAML VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLBYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QARPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFBLCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMB GRAFFEDEPPPRHAELESPEVMPEBEDEDDEGGBRAPA\PGRG GPSLEGSTPADGLPGRA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNBLVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHBTLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS
	5875	296	1848	QKNTPSPDVTLGTNPGTEDIQPPIQKIPLGLDLKNLRLPRRKMS PDIIDKSDVPSRPGIBIIKMAGFHTIKDDIKPSQLYQTLFBLBT ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPI ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPI ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPI ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPI ETCAKNLASFKCSLKPEHRDFCFFTIKFLKESALKTPRVDNRPI MAYBLSVKMKTLSNPLDLALALSTTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFRDSTLFGREYIDHLKAML VSSGCPLQVKKKABPEPMREBEKMIPFTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKBRTLKKEDPAYWPLSDEN SLBYKYYKLKLABMQRMSRNLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\MQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAR KLARFVAQVG\PBIEQF\SI\ENSTDNPDLWPL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQBSFVDLMB GRAFFEDEPPPRRAKLESFEVMPEEEDEDDEDGEGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFFFG RGPSSKGLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGMKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEPSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSARGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGGCREL VUGTTDRVVRAFRWBELGEGPBHLTGQLVSLKKWMLEGQVDSLS VTLGPLGLEBLMVSQPGCAYAILLCTWKKDTGSPPASEGPTDGS

			No.
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
XD	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /-possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			GLFALCTLDGTLKLMERMERADKLLWSVQVDHQLFALEKLDVTG
		,	NGHEEVVACAWDGQTYIIDHNRTVVRFQVDENIRAFCAGLYACK
l	}	1	EGRNSPCLVYVTFNQKIYVYWEVQLERMESTNLVKLLETKP\ST
			TACCRSWAWILTTSL*LVPCFTKRSTIQTSHHSVLPQASRIPPS
l		į	wtcliagegff*tptlppkgvfgshcaaagsitkQ
5876	1122	224	HLPLGVPSKVAGAAAMEPQEKRETQVAAWLKKIFGDHPI?QYBV
			KPRTTRILHHLSERNRVRDRDVYLVIEDLKQKASEYESEAKYLQ
	1	1	DLLMESVNFSPANLSSTGSRYLNALVDSAVALETKDTSLASFIP
[	ł		AVNOLTSDLFRTKSKSBEIKIRLRKLEKNLTATLVLEKCLQEDV
{	1	{	KKAELHLSTER\AKVDNRRQNM\DFLKAKSREFRFGIQAAGEQL
l	i	l	SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLRSYLD
		1	LMP\NPSHCSK+RIBBAK\RELA\SIBABLTRRVS\MMEL
5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLLSALEDLEV
] -30//	2030	1	LSRELIEMLAISRNOKLLQAGBENQVLELLIHRDGEFQELMKLA
1	i	i	LNOGKIHHEMOVLEKEVEKROSDIQQLQKQLKEAEQILATAVYQ
l			AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVPGD
Į.	1		PRRPYPTDLEMRSGLLGOMNNPSTNGVNGHLPGDALA/RRKIAR
			CPCSTVS/NGSQMTCR+INIILILQKSVCEL
5878	950	2113	GLWKCMOLQGPHTHRVQP*PTPRQQGPQ\VPVAVIAGNRPNYLY
50/0	950	2113	RMLRSLLSAQGVSPQMITVFIDGYYEBPMDVVALFGLRGIQHTP
i	ł	ľ	ISIKNARVSQHYKASLTATFNLFPEAKFAVVLEEDLDIAVDFYS
<b>!</b>	ł	<b>,</b>	PLSQSIHLLEEDDSLYCISAWNDQGYEHTAEDPALLYRVETMPG
I .	ļ		LGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECII
	1	į.	PDVSRSYHFGIVGLNMNGYFHEAYFKKHKFMTVPGVQLRNVDSL
			KKKAYEVEVHRLLSEAKVLDHSKNPCEDSFLPDTEGHTYVAFIR
ĺ			MEKDDDFTTWTQLAKCLHIWDLDVRGNHRGLWRLFRKKNHFLVV
}	1		GVPASPYSVKKPPSVTPIFLEPPPKREGAPGAPEQT
F000	3	981	RITEAAAAGSGSRAAGWAGSPPTLLPLSPTSPRCAATMASSDED
5879	(	701	GTNGGASEAGEDREAPGKRRRLGFLATAWLTFYDIAMTAGWLVL
1	<b>j</b>		AIAMVRFYMEKGTHRGLYKSIQKTLKFFQTPALLEIVHCLIGIV
ŀ			PTSVIVTGVQVSSRIFMVWLITHSIKPIQNEBSVVLFLVAWTVT
]	ì		BITRYSPYTFSLLDHLPYFIKWARYNFFIILYPVGVAGELLTIY
ł			AALPHYKKTGMFSIRLPNKYNVSPDYYYFLLITMASYIPLFPQL
f	ł	1	YFHMLRQRRKVLHG\G*L*KRMIK*SLQTRCFFQNNQDYLSPSF
	1	1	NNKNKOLCEISWIVWPLKI
5880	1138	1324	SLWCLVAGGLGLGPSSONPLORAGILARPREARGTFSALTACSA
5880	1130	1324	SVTSKGKSSSGNWPSAASDRDSPVPLRPPGPVQLPSGTGWVLSD
ĺ	1	1	*KKKRGRCSS/WLSQPQHEREKEVVLLRRSMAEGERARAASDVL
1	1	1	CRSLANETHOLERTLTATAHMCQHLAKCLDERQHAQRNVGBRSP
i	1	I	DOSEHTDGHTSVQSVIEKLQBENRLLKQKVTHVEDLNAKNQRYN
1	1	1	ASRDRYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLERKINDC
1			ASVKQBLAASRTARDAALERVQMLBQQILAYKDDYMSERADRER
l	l	Į.	AOSRIQBLEBKVASLIHQVSWRQDSREPDAGRIHAGSKTAKYLA
1	1	l	ADALELMVPGGWRPGTGSQQPEPPAEGGHPGAAQRGQGDLQCPH
1	ĺ	I	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	<u> </u>		CLQCFSDEQGEBLLRHVABCCQ CGTHPSPTEAPRAOHLTMDCTWRILFLVAAATGTHAQVQLLQSG
5881	26	441	
Į	1	Į.	SEVKKPGASVMVSCYVSGYTLTKLSMHWVRQAPGKGLE*MGPFD
1	1		LQDVBTIYPQKFQGRVSMTEBTSTETTQ/AYLELSSLRSEDTAV
	ļ		HHCATOTV
5882	2407	2216	SGCVEMLYSHSLEYNPBWISVQSAVAPAQLALNSDGDL*LHSGB
ſ	I	1	RTRRD*QLPEAGGPGLQEPLQLGELDITSDEFILDEVDG\VDLR
	1	1	HYSKQVELELQQIEQKSIRDYIQESENTASLHNQITACDAVLER
ļ		I	MEQMLGAFQSDLSSISSEIRTLQEQSGAMNIRLRNRQAVRGKLG
<u> </u>		l	BLVDGLVVPSALVTAILEAPVTEPRFLEQLQELDAKAAAVREQE
			ARGTAACADVRGVLDRLRVKAVTKIRBFILQKIYSFRKPMTNYQ
! !			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ IPQTALLKYRFFYQFLLGNBRATAKEIRDEYVETLSKIYLSYYR
			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNBRATAKEIRDRYVETLSKIYLSYYR SYLGRLMKVQYBBVARKDDLMGVEDTAKKGFFSKPSLRSRNTIF
			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNBRATAKEIRDRYVETLSKIYLSYYR SYLGRLMKVQYEBVAEKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTRLEAPILVPHTAQRGEQRYPFFALFRSQHYAL
			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMTNYQ IPQTALLKYRFFYQFLLGNERATAKEIRDRYVETLSKIYLSYYR SYLGRLMKVQYEBVARKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTRLEAPILVPHTAQRGEQRYPFEALFRSQHYAL LDNSCRBYLFICRFFVVSGPAAHDLFHAVMGRTLSMTLKHLDSY
			ARGTAACADVRGVLDRLRVKAVTKIREFILQKIYSFRKPMINYQ IPQTALLKYRFFYQFILGNERATAKEIRDRYVETLSKIYLSYYR SYLGRLMKVQYEBVARKDDLMGVEDTAKKGFFSKPSLRSRNTIF TLGTRGSVISPTRLEAPILVPHTAQRGEQRYPFRALFRSQHYAL

SEO	Predicted	Predicted end	The same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the same of the sa
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
!	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence	Coduction	\=possible nucleotide insertion)
<del></del>	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		PRPELILEMNVQSVRSTDPQRLGGLDTRPHYITRRYAEFSSALV
1			SINQTI PNERTMQLLGQLQVEVENFVLRVAABFSSRKEQLVPLI
i	1		NNYDMMLGVLM\E*ERAADDSKEVESFQQLLNARTQEFIEELLS
			PPFGGLVAFVKEAEALIERGQAERLRGEEARVTOLIRGFGSSWK
			SSVESLSQDVMRSFTNFRNGTSIIQGALTQLIQ\LYHRFHRV\L
i		}	SOPOLRALPARAELINIHHLMVELKKHKPNF
5883	2	1374	BFPGRRFRAVMEAGAGAGAGAGWSCPGPGPTVTTLGSYRASEG
1	-	23/1	CERKKGQRWGSLERRCMQAMEGEVLLPALYEEREEREREKERVE
			BEEEQVQKGGSVGSLSVNKHRGLSLTETELEBLRAQVLQLVABL
l		•	BETRELAGQHEDDSLELQGLLEDERLASAQQAEVFTKQIQQLQG
1.			ELRSLREEISLLEHEKESELKEIEGELHLAQAEIGSLRQAAKDS
j			ATEHESDIASLQEDLCRMQNELEDMERIRGDYEMEIASLRARME
'	]		MKSSEPSGSLGLSDYSGLQEELQELRERYHFLNEKYRALQESNS
1	ł i		SLTGQLADLESERTQRATERWLQSQTLSMTSARSQTSEMDFLRP
1			DPEMQLLRQQLRDAREQMHGMKNKCQELCCRLRRLQHHRQVSEE
1			EQRRLQRELKCAQNEVLRFQTSHS\SPSHPLPPIPPSSPCLL+A
1			LVVISALLWCWWAETSS
5884	4261	2522	GVLARASARLRVPLTGVRACAEPEVGABPAKVAGAABPDEDGGR
1		•	SRLRDCGDYTPSERLGPKGAMLWFQGAIPAAIATAKRSGAVPVV
1			FVAGDDEQSTQMAASWEDDKYTEASSNSFVAIKIDTKSEACLOF
			SQIYPVVCVPSSFFIGDSGIPLEVIAGSVSADELVTRIHKVROM
			HLLXSETSVANGSQSESSVSTPSASFEPNNTCENSQSRNAKLCE
1 1			IPSTSDTKSDTATGGESAGHATSSQEPSGCSDORPARDLNIRVE
			RLTKKJ.BERREEKRKBEBQRBIKKEIERRKTGKEMLDYKRKOEB
1 1			BLTKRMLBERNREKAEDRAARERIKQQIALDRAERAARFAKTKE
1 ' 1			BVEAAKAAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSP
	·	•	TNOFPSDAPLEEARQFAAQTVGNTYGNFSLATMFPRREFTKEDY
1 1			KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSSGDIW
1 1			TLLGTVLYPFLAIWRLISNFLFSNPPPTQTSVRVTSSEPPNPAS
			SSKSEKREPVRKRVLEKRGDDFKKEGKIYRLRTQDDGEDENNTW
			NGNSTQQM
5885	900	467	AAGGGRRSRLSRSWPTGPSKSPSGVRCCG\RR\AWEDKDBFLDV
1 1			IYWPRQIIAVVLGVIWGVLPLRGFLGIAGFCLINAGVLYLYFSN
1 {			YLQIDEEEYGGTWKLTKEGFMTSFA/IVHGHLDHLLHCHPL*LM
			VYSSQVLPIQSKGPS
5886	86	1341	PYRGRALITLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
] [	i	i	GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFRLKTSELPPLKNG
[	· ·		BVLLEALFLTVDPYMRVAAKRLKBGDTMMGQQVAKVVBSKNVAL
	!		PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
	1		MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
	i		KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLRETLKKASPDGY
	ì		DCYFDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGFLPPGP
			PPBIGIYQELRMRAFVVYRWQGDARQKALKDLLKWVLELPYFVI
	į	i	D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE
5887	1937	104	NMPAAFMGMLKGDNLGKTIVKA
3007	1227	104	APGCRGCRATRCPCRGPRWDSLGDBAARSPAAPGGAPGLLGLRE
	ł	[	RPDRCHPGGDDRGPQLHRGSPG/SPSBLSRRPGPPGLPGLQGPP
	ŧ		PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS
l f	į	i	ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI
	ļ		FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNARSY
	ł	j	VSFTTKLDIPTAAKYRYGVPLQTSDSPLRFPSSLTSSLCTDNNP
, I		1	AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK
			KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV
, l			LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ
		[	ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI
	J	ì	LHSTTEQDCLALEGVRTPVLFGYTMQSGCKI.RLTGALPCQLVAQ
- 1		ļ	KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
. 1	ľ	ļ	DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSPPEAN
. i	1	1	SGNERTILISTAVTFVDVSAPARAGFRAPPAINARLPFNFFFPPF V

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110:	location		
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	-	\=possible nucleotide insertion)
5888	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
"""	1	2242	LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENBITGALLP
ŀ	ŧ		CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
ł			
İ	ŧ		GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
1	<u>l</u>		SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
ľ	1		PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
i			QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
ŀ	i		IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
l			DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
j .	ļ.		DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
1			YSTDPKLKDAREILKQIKYRNLFKYVGETQPTGQIKIKREDYES
E			LPKEVASAKPKVLLDVKLKARDFIVDVINMDYGMOKKNPIDHVS
1	[		FYCKTAPNRAIRITKNOVSQLLP\BKFAEQ\LIRVYCKKVDRKS
1	1		LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
1			NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
F000	7.033		
5889	1831	731	LPAACGRPVTARPRQAPEGRSGRPRDL>PYPPQVPPPRPDRVAI
1			VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
1	<b>,</b>		LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
į.			FGIPIL\DLASMTSIRQFVQKFKMKKIPIHVLINNAGVMMVPQR
]	1		KTRDGFBEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
1	į.		SATHYVABLNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
1	İ	Į	AAEGSHVTANVVDPGVVNTDLYKHVPWATRLAKKLLGWLLFKTP
ſ	1		DEGANTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
Ì			LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLOSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
<u> </u>			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
İ			ILBKEGPRSLPRGLGPNLVGVAPSRATYFAAYSNCKEKLNDVFD
1	1	•	PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1	j		RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1			
i .	1		KQKLLEYKTASTMENDEESVKRASDFVGMMLAAATSK\LVATTI
	i		AYPHEVVRTRLREGTKYRSPFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
i	`		GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1			LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1			ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1	1	1	PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
Į	1		KOKILEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
ì	<b>j</b>		AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
]	<b>!</b>		LVROIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMORLOVVLGHLRGPA
1 2022	1 2,03	3,5	DSGWMPOAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
	]		·
i	l		TPDKLLSAVMTAVLKDVNLRPBQLGDICVGNVLQPGAGAIMARI
i	[		AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
1	[		CGVESMSLADRONPONITSRIMEKEKARDCLIPMGITSENVAKR
1	i .		PGISREKQDTFALASQQKAARAQSKGCFQABIVPVTTTVHDDKG
i	1		TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
1			DGAAATLLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
	]		AIPVALQKAGLTVSDVDIFBINE\AFASQAAYCVEKLRLPP*EG
Į.	[	•	*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
f			PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEPT
5555		1033	CFERTEDIGGVWRPKENVEDGRASIYOSVVTNTSKEMSCFSDPP
1		. •	, - · · · · · · · · · · · · · · · · · ·
]	]		MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQF(YTTVLSVRKCP
1	]		DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
	}		GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
1	]		NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
	<b>{</b>		TAVKMMIEQQMNRWPNHENYGLEPQNKYIMKEPVLNDDVPSRLL
ı	(		CGAIKVKSTVKELTETSAIPEDGTVEKNIDVIIFATGYSFSFPF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	
ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1		\$ ·	
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	aedneuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
			F 1
1	ì		ABLQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
1	l		QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
	Ì		SY*YRLVGPGQWEGARNAIPTQKQRILKPLKTRALKDSSNFSVS
	ł	Î	FLLKILGLLAVVVAFF\CQLQWS
		1673	RYSPKKVLONKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
5894	174	15/3	
	i		DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
į.	<b>j</b>		RLRELCOOWLOPETHTKEHILELLVLEOFLIILPKELOARVOEH
1	1	1	HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVERMAPL
			KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
1	}	•	,
]	1	f	SGKISEPMEAHNEGSNLERHQAKPKEKIEYKCSEREQRFIQHLD
1			LIEHASTHTGKKLCBSDVCQSSSLTGHKKVLS*ERKVIQC\HGV
1	İ	]	LGKAFORSSHLVRHOKIHLGEKPYQCNECGKVFSQNAGLLEHLR
1			IHTGEKPYLCIHCGKNFRRSSHLNRHORIHSQEEPCBCKECGKT
1			FSOALLTHHORIHSHSKSHOCNECGKAFSLTSDLIRHHRIHTG
I		[	
1	i	Ì	BKPFKCNICQKAFRLNSHLAQHVRIHNEBKPYQCSECGEAFRQR
1		Į.	SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLPWNSHRKSRHFINQRGIHGE
1	·	ł	MRLFVSDGVPGCLFVLAAAGRARGRAEVLISTVGPEDCVVPFLT
	i .	ł	RPKVPVLQLDSGNYLPSTSAICRYFF\LLSGWEQDDLTNQWLEW
		İ	
1	j	i ·	EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
	l .	l	RQ\NCPFLAGETESLADIVLMGALYPLLQDPAYLPEBLSALHSW
	1	1	FOTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
i		1	EGKGLSPIEPEEERLATLSEREIAMAVTAWEKGLESLPPLRPQQ
1	ŀ	i	NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1	j	ì	
1	1	[	RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQEICDKYHIIHA
	l	j	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
f	İ	1	TVEQLRCEHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI
	ļ.		NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEBWLGRTL
1			PGSDWTPNAQFITPFFGFREMPSKPRWQ*TRDLK\WGNPGTP*E
1	1		
	1	l .	GFRDK\VFYVWFDATIGYLSITANYTDQWBRWW\KNPBQVDLYQ
1	ł	·	FM\AKDNVPFHSLVFPSSALGARDNYTL\VSHLIATEYLNYEDG
1	1	1	k\fsksrgvgvfrdm\ahdtgippdisrfyl\lyirpegk\dsa
		Ì	FSWTDLLLKNNS\BLLNNLGNFINRA\GMPVSKPFGG\YVPEMV
i	<b>!</b>		LTPDDQRLLA\HVTLELQIIYIIQ\LLEKVRIRDALRSILTIS\RH
Ī			
1	İ	l	GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
1	I	l	QPYMPTVSATIQAQLQLPPPACSILLTMFLCTLPAGHQIGTVSP
1	1		LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1	1	1	IMDEVTKQGNIVRELKAQKADKNEVAASVAKLLDLKKQLAVAEG
1	1		KPPEAPKGKKKK
F682	2000		HPSLLGATPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
5896	2967	86	
	Į.		MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
]	İ	1	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWRQDDLTNQWLEW
	ŧ	]	BATELOPTLSAALYYL\VVQGKKG\EDVLGSVRTLTHIDHSLS
1	I	[	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
ł	Į.	Ì	FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
1	1	1	
}	ł	I	BGKGLSPIEPEEEELATLSEEBIAMAVTAWEKGLESLPPLRPQQ
1	I		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
1		1	RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA
1	I	l	DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1	I	1	TVEQLECENCARP\LADREVEGVCPFCGYEEARGDQCDKCGKLI
ł	1	I	
1	1	1	NAVELEKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLEEWLGRTL
1	<b>}</b>	I	PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\NGNPGTP*E
ł	1	ţ	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
1	I	ł	FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLNYEDG
1	I	l	
1	1	I	K\F\$K\$RGVGVFRDM\AHDTGIPPDI\$RFYL\LYIRPBGK\D\$A
1	ì	ł	FSWTDLLLKNNS\BLLNNLGNFINRA\GMFVSKFFGG\YVPENV
	1	<b>1</b>	LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
t	l	1	GNOYI \QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
ł	1	Į	OPYMPTVSATIQAQLQLPPPACSILLTMFLCTLPAGHQIGTVSP
1	I	ļ ·	
L	L	L	LFOKLENDQIESLRORFGGGQAKTSPKPAVVBTVTTAKPQQIQA

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, K=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
			L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
	į		KPPEAPKGKKKK
	5060		HPSLIGATPFYPPPSSPWPPPLYLPWNSHRKGRHFINQRGIHGE
5897	2967	86	
		ł	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
Ì		!	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
	i	l	EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
j		İ	RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPBELSALHSW
	i		
	1	ŀ	FOTLSTO\EPCOR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
	l	1	EGKGLSPIRPKEEELATLSEKEIAMAVTAWEKGLESLPPLRPQQ
	1		NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
	1	l	RLROWNTLYLCGTDEYGTATETKAL\EEGLTPQBICDKYHIIHA
		}	
į	l		DIY\RWFNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1	ĺ	[	TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
	l	1	NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
	1	l	PGSDWTPNAQFITPFFGFRENPSKPRWQ*TRDLK\WGNPGTP*R
l		Ī	GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
ļ		1	
I		l	FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
l	I	Ì	K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPBGK\DSA
ĺ			FSWTDLLLKNNS\BLLNNLGNFINRA\GMFVSKFFGG\YVPEMV
1	ļ	t	LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
İ	1		GNQYI\QVNBPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML
l	•	i	
l	,	!	QPYMPTVSATIQAQLQLPPPACSILLINFLCTLPAGHQIGTVSP
l	İ		LFQKLENDQIRSLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1	i	l .	LMD3VTKQGNIVRELKAQKADKNEVAAEVAKT.LDLKKQLAVAEG
l		ļ	КРРЕАРКСККК
	2025	86	HPSTLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
5898	2967	96	
i			
Į.	1	ţ	MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGFEDCVVFFLT RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
	·		RPKVPVLQLDS@NYLFSTSAICRYFF\LLSGNBQDDLTNQWLBW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFBELSALHSW
e ^r	·		RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNBQDDLTNQWLBW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
e ^c			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNBQDDLTNQWLBW EATELQFTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFBELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA BGKGLSPIEPBEBBLATLSBEKIAMAVTAWBKGLESLPPLRPQQ
at .			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS
÷			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNBQDDLTNQWLBW EATELQFTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFBELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA BGKGLSPIEPBEBBLATLSBEKIAMAVTAWBKGLESLPPLRPQQ
÷	•		RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVMNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQBICDKYHIIHA
÷			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNBQDDLTNQWLBW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFBELSALHSW FQTLSTO\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA RGKGLSPIEPBEBELATLSBEKHAMAVTAWBKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BSGLTPQBICDKYHIIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
e e			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNBQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFBELSALHSW FQTLSTO\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPREEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\REGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI
, e			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA DIY\RWPNISFDIPGETTTYQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEBWLGRTL
, e			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPREEELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLFKLBRRLBBWLGRTL PGSDWTFNAQFITFFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
÷			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQCKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA DIY\RWPNISFDIPGETTTYQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEBWLGRTL
e e			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPREEELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLFKLBRRLBBWLGRTL PGSDWTFNAQFITFFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
e e			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVMNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCCHCARF\LADRFVBGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFFLDLPKLBKRRLBEWLGRTL PGSDWTPNAQPITPFFGFREWPSRPRW^TRDLK\WGNPGTP*B GFEDK\VFYVNFDATIGYLSITANYTDOWERWN\KNFEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATKYLNYEDG
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEBLATLSEEKIAMAVTAWEKGLESLPPLRPQQ MPVLPVAGERNVLITSALPYVMNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVBGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFGFREWPSKPRWP*TRDLK\WGNPGTF*E GFEDK\VPYVNFDATIGYLSITANYTDOWERWN\KNPRQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISPDIFGRTTTPQQ\TKIT\QDIPQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLERRLEBWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTF*E GFEDK\VFYVNFDATIGYLSTTANYTDOWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTLVSHLLATKYLNYEDG K\FSKSCVGVPRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLKNNS\BILINNLGNFINRA\CMPVSKFFGG\YVPEMV
·			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPREEELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGLTPQBICDKYHIIHA DIY\RWFNISFDIFGFTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPFCYSEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLFKLBERLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYKDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYLLLYTEPGEK\DSA FSWTDLLKNNS\BILINNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGLTPQBICDKYHIIHA DIY\RWPNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBEWLGRTL EGSDWTPNAQFITPFFGFREWBSLPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCGVFRDM\AHDTGIPPDISRFYLLYLTPEGK\DSA PSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKFFGG\YVPEMV LXTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVUPPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGLTPQBICDKYHIIHA DIY\RWPNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBEWLGRTL EGSDWTPNAQFITPFFGFREWBSLPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCGVFRDM\AHDTGIPPDISRFYLLYLTPEGK\DSA PSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKFFGG\YVPEMV LXTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVUPPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML
·			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVMNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLERRLBEWLGRTL BGSDWTPNAQFITPFFGFREWBSKPRWG*TRDLK\WGNPGTT*E GFEDK\VPYVWFDATIGYLSITAMYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLLKNMS\BLLNNLGNF\NRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSRADRQRAFFVYGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEBBLATLSEEKIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVMNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\EBGLTPQBICDKYHIIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCCHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWO*TRDLK\WGNPGTP*E GFEDK\VFYVNFDATIGYLSITANYTDQWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLIATKYLNYEDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYTRPBGK\DSA FSWTDLLLKNNS\BILINLCNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVIRDALRSILTIS\RH CRQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLFAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYII\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTO\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQRICDKYHLIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPMO*TRDLK\WGNPGTT*E GFEDK\VFYVWFDATIGYLSITANYTDQMERWW\KNPEQVDLYQ K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLLKNNS\BILHNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KKJSBADARQRAGTVTGLAVNLAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNELCTLPRGEQIGTVSP LFQKLENDQIESLRQRFGGGGAKTSPKPAVVETVTTAKPQQIQA LMDBVTKQGNIVRBLKAQKADKNEVAABVAKLLDLKKQLAVABG
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIPQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBRWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTF*E GFEDK\VPYVNFDATIGYLSITANYTDQWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRGVGVPRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSYML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA K\PPEAPKGKKKK
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIPQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBRWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTF*E GFEDK\VPYVNFDATIGYLSITANYTDQWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRGVGVPRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSYML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA K\PPEAPKGKKKK
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBBWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITAMYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLMYEDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA PSWTDLLLKNMS\BLLNNLGWFINRA\CMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAOLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KNPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGGLTPQBICDKYHIIHA DIY\RWPNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVVLQD TVEQLRCGHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKRPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBEWLGRTL EGSDWTPNAQFITPFFGFREWBSLPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCGVFRDM\AHDTGIPPDISRFYLLYIPBGK\DSA PSWTDLLLKNNS\BILINNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA LMDBVTKQGNIVRBLKAQKADKNEVAABVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ EANEKAKBIDAKAEEFNIEKGRLVQTQRLKIMEYYEKKBKQIE
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYIL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWPNISFDIPGRTTTPQYTKIT\QDIFQQLLKRGFVLQD TYEQLRCCHCARF\LADRFVESOVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWO*TRDLK\WGNPGTT*E GFEDK\VFYVWFDATIGYLSTTANYTOQMERWW\KNFEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATKYLNYEDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLLKNNS\BILHNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALBSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAGTVTGLAVNLAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPRAGQIGTUSP LFQKLENDQIESLRQRFGGGGAKTSPKENAVETVTTAKPQQIQA KPPEAPKGKKKK NCPKSKEBFUGNAPSILFSPLRAAMALSDVDVKKQIKHMMAPIEQ GNKILMSTMRNQARLKVLRARNDLISDLLSEAKURLSRIVEDP
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYIL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPBELSALHSW FQTILSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHITHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TYEQLRCEHCARF\LADRFVESOVCPFCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWO*TRDLK\WGNPGTP*E GFEDK\VFYVNFDATIGYLSTTANYTDOWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCUGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKPFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNGYI\QVNEPW\KRIKGSERADRQRAFTVTGLAVNIAALLSVUL QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGIVSP LFQKLENDQIESLRQRFGGGGAKTSPKPAVVETVTTARPQQIQA KPPRAPKGKKKK CCPKSKEPMGVRAPSLFSPLRAMMALSDVDVKKQIKHMMAFIEQ QQKKILMSTMRNQARLKVLRARNDLISDILSEAKURLSRIVEDP EVYQGLDKLVLQGLURLBPVMIVRCRP\QDLLLVEARVCKAI
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYIL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWPNISFDIPGRTTTPQYTKIT\QDIFQQLLKRGFVLQD TYEQLRCCHCARF\LADRFVESOVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWO*TRDLK\WGNPGTT*E GFEDK\VFYVWFDATIGYLSTTANYTOQMERWW\KNFEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATKYLNYEDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA FSWTDLLLKNNS\BILHNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALBSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAGTVTGLAVNLAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPRAGQIGTUSP LFQKLENDQIESLRQRFGGGGAKTSPKENAVETVTTAKPQQIQA KPPEAPKGKKKK NCPKSKEBFUGNAPSILFSPLRAAMALSDVDVKKQIKHMMAPIEQ GNKILMSTMRNQARLKVLRARNDLISDLLSEAKURLSRIVEDP
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYIL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPBELSALHSW FQTILSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EKGLSPIEPBEBELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHITHA DIY\RWPNISPDIYSGTATETKAL\BEGLTPQBICDKYHITHA DIY\RWPNISPDIYSGTTTYQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLBEWLGRTL PGSDWTPNAQPITPFFGYREWPSRPRWQ*TRDLK\WGNPGTP*B GFEDK\VFYNFDATIGYLSTTANYTDQWERWW\KNPEQVDLYQ FM\AKDNYPHSLVPPSSALGAEDNYTL\VSHLLATBYLNYKDG K\FSKSRCYGVFRDM\AHDTGIPPDISRPYL\LYTRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKPFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIDALRSILTIS\RH GNQYI\QVMEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA KPPEAPKGKKKK NCPKSKBPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ QKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYGGLDKIVLQGLIRLIBEVMIVRCRP\QDLLLVEARVOKAI PEYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\ESGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTTPQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBRWLGRTL PGSDWTPNAQFITPPFGFREWPSKPRQ*TRDLK\WGNPGTF*E GFEDK\VPYVNFDATIGYLSITANYTDOWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRGVGVPRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMFVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPRGSILLTNFLCTLPAGEQIGTVSP LFDKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ QKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDD ENNEKABBIDAKAEREFNIBKGRLVQTQRLKIMEYYBKKBKQIR QKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDD EYYMTISOKHVEV\QIDKEA*LLAVECSWEVMEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI
5899	326	1078	RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPBEBELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCBHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBBWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ EM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA PSWTDLLLKNNS\BLLNNLGWFINRA\CMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSBADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAOLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KNPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ QKKILMSTMRNQARLKVLRRNDLISDLLSEAKURLSRIVEDP EANEKABBIDAKAEHBPNIEKGRLVQTQRLKIMEYYEKKEKQIR QQKKILMSTMRNQARLKVLRRNDLISDLLSEAKURLSRIVEDP PSYMTISQKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKWPEIRMALFGANTNRKFFI KAASRDSPCLEFCFLCGVSSHDLQHRWWYHRLSHLHSRLQDLLK
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSIPRWO*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\YSHLLATKYLNYEDG K\FSKSRCGVFRDM\AHDTGIPPDISRFYLLYIFPEGK\DSA PSWTDLLLKNNS\BILINNLGNFINRA\CMFVSKFFGG\YVPEMV LYPDDQRLLA\HVTLBLQHYRQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPRGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAABVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKURLSRIVEDP EVYQGLLDKINVLQGLIRLLBPUMIVRCRP\QDLLLVEAAVQKAI PEYMTISGKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEPCPLGGVSSIDLQHRMYYHRLSHLHSRLQDLLK CGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEELSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEBEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\EGGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVVLQD TVEQLRCEHCARF\LADRFVEGVCPFCGYEBARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBRRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSIPRWO*TRDLK\WGNPGTP*E GFEDK\VPYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\YSHLLATKYLNYEDG K\FSKSRCGVFRDM\AHDTGIPPDISRFYLLYIFPEGK\DSA PSWTDLLLKNNS\BILINNLGNFINRA\CMFVSKFFGG\YVPEMV LYPDDQRLLA\HVTLBLQHYRQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPRGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA LMDEVTKQGNIVRELKAQKADKNEVAABVAKLLDLKKQLAVAEG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKURLSRIVEDP EVYQGLLDKINVLQGLIRLLBPUMIVRCRP\QDLLLVEAAVQKAI PEYMTISGKHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEPCPLGGVSSIDLQHRMYYHRLSHLHSRLQDLLK CGVIYPALPQPNFKSLLPLAVHWHHTASKSLTCAWQQHEDHFEL
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYIL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPBELSALHSW FQTILSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEELATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWPNISFDIPGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD TYEQLRCCHCARF\LADRFVESOVCPFCGYBEARGDQCDKCGKLI NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBEWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWO*TRDLK\WGNPGTT*E GFEDK\VFYVWFDATIGYLSTTANYTDOWERWW\KNPEQVDLYQ FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATKYLNYEDG K\FSKSRCWGVFRDM\AHDTGIPPDISRFYL\LYTRPEGK\DSA ESWTDLLLKNNS\BILHNLGNFINRA\CMFVSKPFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALBSILTIS\RH GNQYI\QVNEPW\KRIKGSERADRQRAGTYTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTUSP LFQKLENDQIESLRQRFGGGGAKTSPKENVVETVTTAKPQQIQA KPPRAPKGKKKK NCPKSKEPBUGNAPSLEPSPLRAAMALSDVDVKKQIKHMMAFIEQ EVYGGLDKLVLQGLURLBPVMIVRCRP\QDLLLVEARVQKAI PEYMTISOKHVRV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEPCPLCGVSHDLQHRWWYHLSHLUSRLQDLLK CGVIYPALPQPNFKSLLPLAUHWHHTASKSLTCAWQQHEDHFEL KYANTVMRFDYVWULDHCRSASCYNSKTHQRSLDTASVDLCIKP
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTISAALYYL\VVQCKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVLWG\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWFNILGGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWFNILGGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWFNILGGTDEYGTATETKAL\BEGLTPQBICDKYHLIHA DIY\RWFNISPDIYGTTTYPQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLBKRLBRWLGRTL PGSDWTPNAQPITPFFGYREWPSRPRWQ*TRDLK\WGNPGTP*B GFEDK\VFYVNFDATIGYLSITANYTDOWERWN\NNFRQVDLYQ FM\AKDNVFHSLVPPSSALGAEDNYTL\VSHLLATBYLNYEDG K\FSKSRCYGVFRDM\AHDTGIPPDISRPYL\LYTRPBGK\DSA FSWTDLLLKNNS\BILINNLGNFINRA\CMFVSKPFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIDALRSILTIS\RH GNQYI\QVMEPW\RIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTARPQQIQA KPPEAPKGKKKK NCPKSKBPNGVRAPSLPSPLRAMALSDVDVKKQIKHMMAFIEQ QQKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYGGLLDKLVLQGLIRLLBPVMIVRCRP\QDLLLVEARVOKAI PEYMTISQRHVEV\QIDKEA*LAVECSWEVWEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCIEPCPLGVSSIDLQHRWWYHRLSHLHERLQDLLK KYANTVMRFDYVWLRDHCRSASCYNSKTHQRSLDTASVDLCIKP KTIRLDETTLFFTWPDGHVTKYDLNWLVKNSYBGQKQKVIQPRI
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLXLCGTDEYGTATETKAL\BEGLTPQBLCDKYHLIHA DIY\RWFINLSGTESYGTATETKAL\BEGLTPQBLCDKYHLIHA DIY\RWFINLSFDIFGRTTTTQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLERRLEBWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWQ*TRDLK\WGNPGTF*B GFEDK\VFYVNFDATIGYLSITANYTDOWERWN\NNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSCVGVPRDM\AHDTGIPPDISRPYL\LYTRPEGK\DSA ESWTDLLLKNNS\BLLNNLGNFINRA\CMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQPPPACSILLTNPLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KMPENTAGONIVRELKAQKADKNEVAABVAKLLDLKKQLAVABG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ ENNEKABBIDAKAEREFNIBRGRLVQTQRIKIMEYYBKKEKQIE PSYMTISQKHVRV\QIDKEA*LAVECSWEVWEYYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASROSPCLEPCPLCGVSSHDLQHRWWHRLSHLHSRLQDLLK KYIRLDETTLFTWPDGHVTKYDLINNLVKNSYBGGKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNPLLYGIAPVEN
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVIGSVRRTLTHIDHSIS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLFEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLYLCGTDEYGTATETKAL\BEGLTPQBICDKYHIIHA DIY\RWFNISFDIFGRTTTTPQ\TKIT\QDIFQQLLKRGFVLQD TVPQLRCBHCARF\LADRFVEGVCPFCGYBEARGDQCDKCGKLI NAVBLKKRQCKVCRSCPVVQSSQHLFLDLPKLBRRLBBWLGRTL PGSDWTPNAQFITPFFGFREWPSKPRQ*TRDLK\WGNPGTP*E GFEDK\VPYVNFDATIGYLSITANYTDQWERWN\KNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSRCVGVPRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA FSWTDLLLKNNS\BLLNNLGNFINRA\CMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSYML QPYMPTVSATIQAOLQLPPPACSILLTNFLCTLPAGEQIGTVSP LFQKLENDQIESLKQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQLKHMMAFIEQ QKKILMSTMRNQARLKVLRARNDLISDLLSEAKLRLSRIVEDP EVYGGLLDKLVLQGLLKLLRPVMIVRCRP\QDLLLVEAAVQKAI PSYMTISOKHVRV\QIDKEA*LAVECSWEVMEVYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASRDSPCLEFCPLCGVSSHDLQHRWWYHRLSHLHSRLQDLLK KYANTVMRFDYVWURDHCRSASCYNSKTHQRSLDTASVDLCIKP KYANTVMRFDYVWURDHCRSASCYNSKTHQRSLDTASVDLCIKP KYANTVMRFDYVWURDHCRSASCYNSKTHQRSLDTASVDLCIKP LINN&EIYQOQAVPSVDCQSFLETNEGLKKFLQNFLLYGIAFVEN VPPTQEHTEKLARRISLIRETIYGRMWYFTSDFSRGDTAYTKLA
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGNEQDDLTNQWLEW EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS RQ\NCPFLAGETESLADIVUWGALYPLLQDPAYLPEBLSALHSW FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA EGKGLSPIEPEEEBLATLSEERIAMAVTAWEKGLESLPPLRPQQ NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVPARYS RLRQWNTLXLCGTDEYGTATETKAL\BEGLTPQBLCDKYHLIHA DIY\RWFINLSGTESYGTATETKAL\BEGLTPQBLCDKYHLIHA DIY\RWFINLSFDIFGRTTTTQQ\TKIT\QDIFQQLLKRGFVLQD TVEQLRCEHCARF\LADRFVEGVCPPCGYBEARGDQCDKCGKLI NAVBLKKPQCKVCRSCPVVQSSQHLFLDLPKLERRLEBWLGRTL PGSDWTPNAQFITPFFGFREWPSRPRWQ*TRDLK\WGNPGTF*B GFEDK\VFYVNFDATIGYLSITANYTDOWERWN\NNPEQVDLYQ FM\AKDNVPFHSLVPPSSALGAEDNYTL\VSHLLATKYLNYEDG K\FSKSCVGVPRDM\AHDTGIPPDISRPYL\LYTRPEGK\DSA ESWTDLLLKNNS\BLLNNLGNFINRA\CMPVSKFFGG\YVPEMV LTPDDQRLLA\HVTLBLQHYHQ\LLEKVRIRDALRSILTIS\RH GNQYI\QVNEPW\KRIKGSRADRQRAFTVTGLAVNIAALLSVML QPYMPTVSATIQAQLQPPPACSILLTNPLCTLPAGEQIGTVSP LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA KMPENTAGONIVRELKAQKADKNEVAABVAKLLDLKKQLAVABG KPPEAPKGKKKK NCPKSKEPNGVRAPSLPSPLRAAMALSDVDVKKQIKHMMAFIEQ ENNEKABBIDAKAEREFNIBRGRLVQTQRIKIMEYYBKKEKQIE PSYMTISQKHVRV\QIDKEA*LAVECSWEVWEYYSGNQRIKVSN TLESRLDLSAKQKMPEIRMALFGANTNRKFFI KAASROSPCLEPCPLCGVSSHDLQHRWWHRLSHLHSRLQDLLK KYIRLDETTLFTWPDGHVTKYDLINNLVKNSYBGGKQKVIQPRI LWNAEIYQQAQVPSVDCQSFLETNEGLKKFLQNPLLYGIAPVEN

			No.
ID	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
! !	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
<b>l</b> 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
	sequence		QKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
1		ļ	
i i			/YKBLYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
!!			NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
1			NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
1 1		ĺ	KTHLDTVLPKLTCPQCNKBFPNQESLLKHVTIHFMITSTYYICE
			SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQKVFDSKVSIQLHL
1			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
			CIPCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
ľ			CIPCOBSPGIEVELQCISTINGSKINCKPCSKITATINGSKINCK
		1	REKHCVFETKTPNCGTNGASEQVQKEBVBLQTLLTNSQESHNSH
į <b>1</b>			DGSERDVDTSEPMYGCDICGAAYTM5TLLQN:HQLRDHNIRPGES
į I			AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
1			CPICGERPPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEBFL
, 1		İ	BHCQMHPDLRNSLTGFRCVVCMQTVTSTLBLKIHGTFHMQKTGN
; I			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
1			CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVCGL
į l			KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
] [		1	QVSPMPRISPSQSDEKKTYQCIKCQMVFYNENDIQVHVANHMID
1 1			EGLNHECKLCSQTFDSPAKLQCHLIEHSPEGMGGTFKCPVCFTV
1		1	PVOANKLOOHIPSAHGOEDKIYDCTQCPQKFFFQTBLQNHTMTQ
		ĺ	HSS
<u> </u>			LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*RBF
5902	712	209	
1 1			IPLKPRQ*BD*MFQSWLHAWGDTLBRAPEQCAMAMFGYMTDTGT
i I			VEPLQTVRVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
L	_ '.		BFSLSKHPQGTBVKAITYSAMQVYNBENPEVFVIIDI
5903	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
i i			PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
1 1			GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
[ ]			LPEAVLALYNSTRDRVAGESABPEPEPEADYYAKEVTRVLMVET
1		1	HNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
1 1			KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
i ·			ROWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
1 1			ATTHEMNRPPLILMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
i I			HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
1 1		1	GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
1 1			LPIVYY\VGRKPKVEQLSNMIVRSCKCS
<del>  </del>		1126	MMREIENAINTFKEEORLIYEELIKEEKTTNNELSAISRKIDIW
5904	3	1120	ALGNSETEKAFRAISSKYPYDKYTPSTLPEEVLDFEKFLQQTGG
		1	ROGAWDDYDHONFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
1		1	
1		1	HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
]			VLFHNKQEDNQKQKEEQRKKQKLAVEAWKKQKSIEMSMKCASQL
			KBEREKEKKHQKERQRQFKLKI_LLESYTQQKKEQEEFLRLEKEI
			KEEEBKEKKHOKEROROPKIKILLESYTOOKKEQEEFIRLEKEI REKAEKAEKRAADEISRFOERDLHKLELKILDROAKEDEKSO
			KEEEBKEKKHOKEROROPKIKILLESYTOOKKEQEEFIRLEKEI REKAEKAEKRAADEISRFOERDLHKLELKILDROAKEDEKSO
			KBEREKEKKHQKERQRQFKLKI_LLESYTQQKKEQEEFLRLEKEI
5905	287	2912	KBEEEKKKHQKERQRQFKLKI_LLESYTQQKKEQBEFLRLEKEI RBKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKBDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	KBEEEKEKKHQKERQRQFKLKI_LLESYTQQKKEQEEFLRLEKEI RBKAEKAEKRKNAADEISKFQERDLHKLELKILDRQAKBDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP
5905	287	2912	KBEBEKEKKHQKRRQRQPKLKI.LLESYTQQKKEQBEPLRLEKBI RBKAEKABKRKNAADBISHPOERDIHKLELKILDRQAKBDBKSQ KQRRLAKLKBKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNBKBIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
5905	287	2912	KBEBEKKKHQKRRQRQFKLKI.LLBSYTQQKKBQBEFLRLEKBI RBKABKABKRKNAADBISRFQERDLHKLBI.KILDRQAKBDBKSQ KQRRLAKI.KBKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTBKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFILHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH
5905	287	2912	KEEEKKKHQKRRQRQFKLKI.LLESYTQQKKEQEEFLRLEKEI RBKAEKABKRKNAADEISRFQERDLHKLELKILDRQAKBDEKSQ KQRRLAKI.KBKVENNVSRDPSRLY/NTHQRIGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNPLLHGTKNVTNSSSIRL>R QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLINLVDHTGVVRDL
5905	287	2912	KEEEKKKHQKRRQRQFKLKI.LLESYTQQKKEQEEFLRLEKEI RBKAEKAEKRNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKI.KEKVENNVSRDPSRLY/NTHQRIGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLЭR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPKKQSRCVNLEWH RFRFGGDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
5905	287	2912	KEEEKKKHQKRRQRQFKLKI.LLESYTQQKKEQEEFLRLEKEI RBKAEKAEKRNAADEISKFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHORIGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTYGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNPLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGINSGRIKIWDVYTGKILLMIVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS
5905	287	2912	KEEEKKKHQKRRQRQPKLKI.LLESYTQQKKEQEEPLRLEKEI RBKAEKAEKRKNAADEISHPOERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNLEWH RFFFGQDQLLLATGLNSGRIKIWDVTTGKLLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHRSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
5905	287	2912	KEEEKKKHQKRRQRQFKLKI_LLESYTQQKKEQEEFLRLEKEI RBKAEKABKRKNAADEISRFOERDIHKLEIJKILDRQAKEDEKSQ KQRRLAKIJKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH RPRFGQDQLILLATGINSGRIKIJWDYTTGKILLMIJVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN/MKVLRGHQNWVYL SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGIGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
5905	287	2912	KEEEKKKHQKRRQRQPKLKI.LLESYTQQKKEQEEPLRLEKEI RBKAEKAEKRKNAADEISHPOERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNLEWH RFFFGQDQLLLATGLNSGRIKIWDVTTGKLLINLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHRSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
5905	287	2912	KEEEKKKHQKRRQRQFKLKLILESYTQQKKEQEEFLRLEKEI RBKAEKABKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFILHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHONWYY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISFTVKYH*LLSKLIFOFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK
5905	287	2912	KBEEBKKKHQKRRQRQFKLKI.LLESYTQQKKEQBEFLRLEKBI RBKAEKABKRKNAADBISRFQERDLHKLELKILDRQAKBDBKSQ KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFILHGIKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RPRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHGNWYY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTJATNVLS WAERVASLATGLGATFTIG*SNLAFVLQSVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS*
5905	287	2912	KBEEBKKKHQKRRQRQFKLKLILESYTQQKKEQBEFIRLEKEI RBKAEKABKRKNAADBISRFQERDLHKLELKILDRQAKBDBKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNPLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNLEWH RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WABRVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSBTNLM*SI WLSNGFSVLFFGILSDSRDILRL*PNLKFVLIFF*K*CIUSVQK KKKPKRIALLQEBRLS*DKPPSSHLL*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYQMTYDRG*FGKNKMVKF*FIEM
5905	287	2912	KEEEKKKHQKRRQRQPKLKI_LLESYTQQKKEQEEPLRLEKEI RBKAEKAEKRKNAADEISHPOERDLHKLELKILDRQAKEDEKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKETVRLTTGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNLEWH RFFFGQDQLLLATGLNSGRIKIWDVTTGKLLLNLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKP*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
5905	287	2912	KBEBEKKKHQKRRQRQFKLKI.LLESYTQQKKEQBEFLRLEKBI RBKABKABKRKNAADBISHFOERDIHKIBIKILDRQAKBDBKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR  MASFPPRVNEKBIVGLTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGINSGRIKIWDVYTGKLLLMLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGIGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYLQMTYDRG*FGKNKMVKP*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSYYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
5905	287	2912	KBEEBKKKHQKRRQRQFKLKI.LLESYTQQKKEQBEFLRLEKEI RBKAEKABKRKNAADBISRFQERDIHKLELKILDRQAKBDBKSQ KQRRLAKLKBKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RPRFGQDQLLLATGLNSGRIKIWDVYTGKLLLMLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWV\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISFTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQBERLS*DKPPSSHLI*QTBVNIKILFRATLHS* LLIFRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM *LYYFHKIAFSPCNVV*HPCCLPKKPHLAVNILFACSICFSS*A QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK REGGL*YLTLFISVYFFS*LVFGINGFQYSFVVKLHCLYFMFRLI
5905	287	2912	KBEBEKKKHQKRRQRQFKLKI.LLESYTQQKKEQBEFLRLEKBI RBKABKABKRKNAADBISHFOERDIHKIBIKILDRQAKBDBKSQ KQRLAKLKEKVENNVSRDPSRLY/NTHORLGRTNQKDRTNRLM ATSTYPT*GYSNLETRNTEKSMR  MASFPPRVNEKBIVGLTIGELLAPAAPFDKKCGRENWTVAFAP DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPBKQSRCVNIEWH RFRFGQDQLLLATGINSGRIKIWDVYTGKLLLMLVDHTGVVRDL TFAPDGSLILVSASRDKTLRVWDLRDDGN\MKVLRGHQNWVY\ SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGIGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK KKKPKRIALLQEERLS*DKPPSSHLI*QTEVNIRILFRAILHS* LLIFRI*NCI*TYS*IIDPFYLQMTYDRG*FGKNKMVKP*FIEM *LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A QVGDPSLL*TSYYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK